THESIS

INVESTIGATING THE OSTEOGENIC POTENTIAL OF MULTIPOTENT MESENCHYMAL STROMAL CELLS THROUGH THE USE OF DNA MICROARRAY TECHNOLOGY AND BIOMATERIAL NANOTOPOGRAPHY

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ABSTRACT

INVESTIGATING THE OSTEOGENIC POTENTIAL OF MULTIPOTENT MESENCHYMAL STROMAL CELLS THROUGH THE USE OF DNA MICROARRAY TECHNOLOGY AND BIOMATERIAL NANOTOPOGRAPHY

Multipotent mesenchymal stromal cells (MSCs, also called mesenchymal stem cells), a heterogeneous population of adult progenitor cells commonly isolated from the bone marrow, are capable of differentiation into a wide variety of tissue types. The use of MSCs is gaining traction amongst researchers due to their ease of acquisition, ex vivo expandability, and encouraging potential for tissue regeneration. It is well established that MSCs can be induced to differentiate into osteoblasts when provided media supplemented with the synthetic glucocorticoid, dexamethasone, or growth factors, such as bone morphogenetic proteins (BMPs). However, recently osteogenesis has also been shown to be induced in MSCs cultured on substrates with modified surface nanotopographies. This work utilizes a combination of bioinformatics and biomaterial engineering to study MSC differentiation towards the osteogenic lineage as a result of two fundamentally different inductors; the osteogenic growth factor, BMP6, and substrate nanotopography.

BMP induced differentiation

BMPs are currently under intense investigation for therapeutic use as osteoinducers, and one of them, BMP2, is approved for use in spinal fusion. In collaboration with a bone biologist at UPenn, we performed extensive genomic analysis of differentiating human MSCs using Affymetrix microarrays. We discovered that suboptimal concentrations of BMP6 induced a short-term burst in gene activity of known negative regulators of the BMP pathway, and other negative regulators of cell differentiation, cell development and biosynthetic processes. On the other hand, osteogenic concentrations of BMP6 result in the long-term up-regulation of bone related transcription factors and bone marker transcripts. The data support a novel hypothesis that the up-regulation of BMP6 antagonists may be playing an important role in establishing a threshold for BMPs signaling, which must be surpassed to trigger differentiation.

Another set of studies explored the role of Osterix in BMP-mediated MSC differentiation. Osterix (OSX) is an osteogenic transcription factor vital to the process of bone formation. MSCs isolated from three human donors, were treated with siRNA to abrogate the transcription of OSX. Gene expression levels within normal and OSX knockout MSCs were compared in the presence and absence of BMP6 to identify potential genes under the transcriptional control of OSX. Our microarray data analysis suggests that OSX plays multiple functional roles, the most important of which includes the up-regulation of alkaline phosphatase, the up-regulation of genes encoding for proteoglycans involved in bone mineralization, the activation of osteoclastic activity through the suppression of osteoprotegerin (OPG), and the repression of several matrix

metalloproteinases (MMPs) responsible for the breakdown of extracellular collagen. Other downstream biological processes linked to osterix, as suggested by the microarray data, include the suppression of genes associated with cellular proliferation and vasculature development as well as the activation of genes associated with cell adhesion and cellular morphogenesis. While many of these proposed genetic relationships have yet to be confirmed by additional tests, our analysis of the DNA microarray data yields a number of novel testable hypotheses on the downstream functions of OSX.

MSC differentiation by nanotopography

MSCs can differentiate in response to a large number of cues, including, most intriguingly, the topography of the extracellular material around them. We performed experiments to investigate the effects of nanotopography on the long-term response of progenitor cells using polycaprolactone nanopillar and nanofiber surfaces seeded with rat MSCs. We found that after four weeks in normal growth media, MSCs cultured on nanofibers exhibit better adherence, increased proliferation, and maintain increasingly dense fibroblast-like morphologies. In contrast, MSCs seeded on nanopillar surfaces display lowered adherence, reduced proliferation, and adopt highly elongated cellular morphologies. Immunofluorescent staining of MSCs on PCL nanopillars reveals the presence of two bone marker proteins, osteopontin and osteocalcin, providing evidence for surface induced differentiation into osteoblast-like cells. Unlike the nanopillar topography, MSCs cultured on nanofiber and smooth PCL surfaces did not appear to undergo osteogenesis. Observed differences in cellular response to the PCL nanotopographies offer strategies to direct progenitor cell populations solely based upon submicron surface modifications. Our experiments suggest that PCL nanofiber

morphologies could assist in promotion of cell growth without recourse to growth factors, while nanopillar morphologies could be useful for promotion of osteogenesis without any chemical cues.

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Introduction

Multipotent Mesenchymal Stromal Cells

Multipotent mesenchymal stromal cells (MSCs) comprise a heterogeneous population of adult progenitor cells, which have the potential to differentiate into a variety of tissue types. Originally characterized over forty years ago as bone marrow-derived, plastic-adherent, colony forming fibroblasts, which retain the ability differentiate into bone tissue[1], MSCs have become a progressively more popular cell type for use in regenerative medicine. While bone marrow serves as the most common supply of MSCs, they can also be isolated from many other tissue sources, including: adipose[2], skeletal muscle[3], liver[4], synovial fluid[5], amniotic fluid[6], and brain[7]. In fact, evidence is pointing to the notion that MSCs reside in almost all tissue types and organs[8]. Once isolated, placed in the proper environment and treated with appropriate cellular cues, MSCs have been induced to differentiate into cells of both mesenchymal lineages; bone[9], cartilage[10], fat[11], muscle[12], tendon[13], and non-mesenchymal lineages; including endothelial[14], neuronal[15], and hepatic[16] tissues.

While MSCs are praised for their ease of acquisition, ex vivo expandability, and potential to revolutionize modern medicine, they can only undergo a finite number of cell divisions ex vivo, approximately forty doublings, before they show signs of senescence and apoptosis[17]. Therefore, the classification of MSCs as a true stem cell population has been brought into question. To address this concern, it has recently been suggested that a

key difference between the in vitro cell culture environment and an in vivo setting is the amount of oxygen available for cell consumption. MSCs show enhanced expansion and proliferation in hypoxic tissue environments[18], such as the bone-marrow, leading to the perception that MSCs utilize low oxygen environments to proliferate and differentiate when exposed to higher oxygen levels.

One issue currently impeding MSC research is the lack of globally accepted methods of extraction, isolation, and cellular expansion, rendering direct comparisons of results across separate studies nearly impossible. In an attempt to unify the scientific community, the International Society for Cellular Therapy (ISCT) released a position statement in 2006 establishing a minimal set of three criteria which define MSCs[19]. The ISCT proposed that a multipotent mesenchymal stromal cell must be plastic adherent, maintain specific surface antigen expression, and have multipotent differentiation potential. More specifically, MSCs must be positive for a select set of surface markers (CD73, CD90, CD105), negative for contaminating hematopoietic surface markers (including CD34, CD45, CD14, CD19), and they must be able to differentiate into osteoblasts, chondroblasts and adipocytes in vitro. It is important to understand that MSCs are a plastic adherent, heterogeneous population of cells; surface markers capable of specifically identifying MSCs from other cell types have yet to be identified, complicating their classification.

MSCs have been utilized in a wide range of in vivo animal disease models to study their therapeutic effectiveness with encouraging results. MSCs aid in the prevention of graft-versus-host disease[20], improve survival following endotoxin induced acute lung injury[21], and improve arthritic symptoms of collagen induced arthritis[22] in mouse models.

A skin graft transplantation study conducted using baboons revealed MSCs to prolong transplant survival by decreasing the immune response, more specifically by reducing the proliferation of lymphocytes. In rats, MSCs have been observed to improve the healing of critical sized bone defects[23] and improve glomerular healing following experimentally induced glomerulonephritis[24].

In addition to encouraging results in animal models, MSCs have also been successfully used to treat human maladies in the clinical setting. Direct transplantation of autologous bone marrow derived MSCs improve the healing and function of critical-sized bone defects[25] and aids in the repair of articular cartilage[26], while intracoronary administration of these cells results in improved left ventricular function in patients prone to myocardial infarctions[27]. Allogenic marrow derived MSCs, injected intravenously, have resulted in improved bone growth in children with osteogenesis imperfecta[28] and increased nerve conduction velocities in patients with metachromatic leukodystrophy[29]. Patients suffering from multiple sclerosis may be seeing a new MSC treatment option in the future. Phase 1 clinical trials, planning to utilize the immunosuppressive nature of marrow derived MSCs in an attempt to lessen the ongoing damage attributed to multiple sclerosis, are set to get underway. The use of MSCs in a clinical setting is not strictly limited to bone marrow derived cells, as the recent use of adipose derived MSCs was shown effective in the treatment of fistulas associated with Crohn's disease[30].

One desirable aspect of MSC therapy is the ability for these cells to home in on, or migrate towards, sites of injury. It is currently thought that inflammation itself acts as a major cue for directing the migration of transplanted MSCs. A rat myocardial infarction model shows that injected MSCs migrate well in non-infarcted hearts; however, MSCs

remain in the border zone of infarcted hearts and begin to express myocytic markers[31]. Intra-arterial infusion of MSCs was also shown to migrate to the kidneys of rats with ischemia-induced acute renal failure and improve renal function, increase cellular proliferation and reduce apoptosis[32]. Several cases of MSC homing in human patients have been reported, including the migration to the bone marrow following intravenous injection of MSCs to treat osteogenesis imperfecta[28].

MSC Differentiation

Prior research with MSC populations have shown that they can be induced to differentiate into many cell types in response to a wide variety of stimuli, including soluble cues[33], surface chemistry[34], matrix elasticity[35], seeding density[36], and cell geometry[37]. Establishing the groundwork for MSC differentiation, Pittenger and colleagues successfully maintained and expanded populations of undifferentiated MSCs in vitro and were capable of inducing differentiation into the adipocytic, chondrocytic, and osteoblastic cell lineages depending on the chemical contents added to the cell culture media[33]. Isolated and expanded MSCs from 50 human donors were investigated, with all MSCs responding positively to the three differentiation assays. Two populations of human fibroblasts, terminally differentiated cells similar in morphology to MSCs, failed to differentiate into any of the three lineages. To rule out the possibility of MSCs being comprised of a population of committed progenitor cells, with each cell destined for only one fate, Pittenger showed that MSCs from colonies derived from a single cell were also capable of differentiation into all three cell lineages[33].

It is becoming increasingly evident that the differentiation of MSCs is not only sensitive to soluble media components, but to many different aspects of the cellular

microenvironment. A study utilizing functionalized self-assembled monolayers containing a wide range of surface chemistries shows that positively charged monolayers supports both adipocytic and osteoblastic differentiation, while neutral hydrophilic monolayers selectively permit osteoblastic differentiation, inhibiting adipogenesis[34]. In other work, collagen coated, polyacrylamide gels of varying degrees of elasticity were found to have a drastic effect on the fate MSCs. MSCs on stiff gels underwent osteogenesis, while those seeded on gels with lower elastic moduli were found to differentiate into myocytic and neuronal lineages[35].

Cell density is also thought to be important in MSC fate determination. Using mixed media comprised of adipogenic and osteogenic cues, McBeath and colleagues showed that higher MSC densities promoted differentiation into adipocytes and lower densities permitted osteogenesis[36]. In order to further investigate this phenomenon, fibronectin islands of different areas were used in single cell experiments. Large islands, which allow for cellular spreading, favored osteogenesis, while small islands, which maintain a rounded cell morphology, favored adipogenesis[36]. These two concepts are inherently related; cells seeded at low densities have room to spread, while those at higher densities are forced to remain rounded due to the steric interactions of surrounding cells. Even more recently, cellular geometry has been shown to direct MSCs down specific lineages. A microcontact printing technique, allowing for the patterning of individual cellular shapes on a substrate, was used to show that MSCs with increased contractility led to preferential osteogenesis, while those with low contractility preferred adipogenesis[37]. Clearly, MSC differentiation is a process greatly affected by the surrounding cellular environment in which the cell resides. A detailed picture of the

multiple signaling pathways responsible for eliciting MSC differentiation is beginning to emerge as a result of the concerted efforts of researchers worldwide.

Bone Morphogenetic Protein Induced Osteogenesis

While synthetic chemicals are routinely used in the lab to induce MSC differentiation in vitro, MSC differentiation in vivo relies on the chemical and physical properties of the surrounding natural environment. Paracrine and autocrine signaling by growth factors is known to play a large role in determining the end fate of stem cells. Osteogenesis, or more simply, the formation of bone, occurs when MSCs are presented with specific growth factors, termed bone morphogenetic proteins (BMPs). Knowledge of the osteoinductive potential of BMPs has increased considerably ever since Urist's 1965 discovery of reproducible ectopic bone formation induced by allogenic implantation of de-mineralized bone matrix[38]. The term 'bone morphogenetic protein' was introduced in 1971 after enzymatic digestion of de-mineralized bone matrix abrogated its ability to induce bone formation[39]. Over the years, work to isolate and characterize BMPs[40,41] eventually led to their molecular cloning[42,43], allowing for the wide spread study of the osteogenic growth factors. There are currently nineteen BMPs which have been identified and given main physiological roles, five of which are capable of inducing complete bone morphogenesis[44].

BMPs belong to the Transforming Growth Factor β (TGFβ) superfamily of signaling molecules and are capable of binding to the extracellular matrix (ECM), soluble antagonists, co-receptors and transmembrane receptors[45]. BMPs present themselves as dimers, held together by disulfide bonds, and are known to exist in homodimeric and heterodimeric form both in vitro and in vivo[46]. BMP heterodimers are thought to have

increased signaling capabilities compared to homodimers. For example, BMP2/7 is more effective at inducing osteogenesis than either the BMP2 or BMP7 homodimers because it is not as effectively antagonized by the presence of the BMP antagonist, noggin[47]. In addition to playing an important role in the differentiation of MSCs into osteoblasts, BMPs appear to be essential for the proper development of the majority of organs in vertebrates[45].

Osteogenesis is initiated through the binding of BMP ligands to heterodimeric receptor complexes, formed from type I and type II transmembrane BMP receptors. There are currently six BMP receptors which have been identified, three type I (ActR1a, BR1a , and BR1b) and three type II (ActRIIa, ActRIIb, BRIIa)[48]. Each receptor contains an extracellular binding domain and an intracellular serine/threonine kinase domain. The BMP signaling pathway is initiated when a BMP ligand binds to a preformed receptor complex, allowing the type II receptor tail domain, a constitutively activate kinase, to phosphorylate and activate the type I receptor tail domain. Once activated, the type I receptor transmits the BMP signal through the phosphorylation of a group of cytoplasmic proteins known as receptor smads or R-Smads (Smad1, Smad5, Smad8). Upon phosphorylation, R-smads multimerize with other cytoplasmic smad molecules known as Co-Smads (Smad4) and translocate into the nucleus, where they function as transcription factors, activating genes vital to the process of osteogenic differentiation[49].

BMP signaling is a highly regulated process, during which many proteins play roles in enhancing and attenuating the signaling event. Some membrane bound co-receptor molecules are known to potentiate BMP signaling, including Betaglycan[50,49] and the repulsive guidance molecules (RGMs)[51], while others are known to function as decoy

receptors for BMP ligands, inhibiting the signaling response. Secreted inhibitory molecules, known as BMP antagonists, assist in dampening osteogenic signals by binding to BMP ligands in the extracellular environment, thus preventing their association with receptor molecules[52]. Attenuation of BMP signaling is also performed in the intracellular environment. A type of inhibitory smad protein, known as I-Smads (Smad6 and Smad7), functions to silence BMP signaling in multiple ways including, preventing R-Smad phosphorylation and acting as a transcriptional repressor[49].

The Food and Drug Administration (FDA) has authorized the approved use of tissue engineering constructs which employ the use of recombinant human BMP2 (rhBMP2). Infuse® by Medtronic has been FDA approved since 2002 for the treatment of degenerative disc disease in the lower back by facilitating spinal fusions. The technology utilizes rhBMP2 seeded within an absorbable collagen sponge at a concentration of 1.5mg/cc, which is used to support bone growth when implanted in the body. Over past several years, the FDA has approved additional clinical uses for the Infuse® bone graft, including the repair of compounded lower leg fractures in 2004 and its use in reconstructive surgery throughout maxillofacial regions in 2007[53]. Another BMP containing product hasn't been as successful. OP-1 Putty® by Stryker is generated using powdered rhBMP7, also known as osteogenic protein-1, combined with bovine collagen, and mixed in a saline solution to form a putty-like material. The material was approved for use under the Humanitarian Device Exception program for bone regeneration in spinal fusions in 2001. However, subsequent research revealed that while OP-1 Putty® didn't cause adverse harm, it did not heal spinal fusions any better than standard autogenic bone grafts[54], prompting the FDA to reject its application for pre

market approval in 2009. The success and failure of OP-1 Putty® has illustrated that while bone morphogenetic proteins show great potential in regenerating bone tissue, there is still more to be learned to maximize their potential.

Nanotopography Induced Osteogenesis

Over the past decade, the use of nanotopography driven cellular response has been an exciting topic for biomaterial and tissue engineers looking to modulate the fate of stem cells through material surface properties. Research conducted by members of the Biomaterials and Surfaces Micro-Nano Engineering Laboratory (BSμnEL) at Colorado State University has extensively investigated the response of rat MSCs to two different polymer nanotopographies, nanopillars and nanofibers. Fabricated out of an FDA approved, biodegradable and bioresorbable, polymer called polycaprolactone (PCL), the two surface topographies were both shown to support MSC adhesion, viability and aggregation[55,56]. When cultured in the presence of soluble osteogenic cues, MSCs on PCL nanopillars and nanofibers exhibited increased bone protein production and mineralization compared to planar controls. The enhanced osteogenic response of MSCs to PCL nanotopographies provides a solid foundation for the development of polymeric three-dimensional scaffolds for bone tissue engineering.

One of the leading causes of orthopedic implant failure is soft tissue encapsulation, a condition characterized by the formation of fibrous tissue surrounding the implant instead of the desired bone tissue[57]. The resultant wear and abrasion at the biomaterial-tissue interface reduces the average lifespan of titanium implants to 10-15 years, after which they must be replaced. This has lead to increased interest in material topographies capable of directing osteogenesis and supporting osteointegration. A

multitude of techniques have been proposed and tested to alter the surface nanotopography of titanium, including polishing, etching, blasting and oxidization[58]. The increase in surface roughness imparted by the addition of nanostructures has been shown to increase the strength of bone bonding, leading to the development of implants with increased osteointegration capabilities. For example, an in vivo study comparing titanium dioxide nanotube implants with gritblasted titanium dioxide implants in rabbits found a significant increase, over 9-fold, in the bone bonding tensile strength of the nanotube surfaces[59]. Thus, the use of nanotopography will undoubtedly play a major role in the future of bone implant design and fabrication.

One drawback of the numerous in vitro studies comparing surface nanotopographies for MSC differentiation and integration involves the use of cell culture media containing osteogenic supplements. While the results suggest that select nanotopographies increase osteoblast differentiation, the use of the glucocortical steroid, dexamethasone, complicates matters. Due to the uncharacterized effects of the addition of dexamethasone to the human body, some researchers have focused their attention on biomaterial surfaces which are capable of inducing osteogenic differentiation in the absence of any soluble cues. For example, one study found that the addition of disordered nanopits, approximately 120nm in diameter and 100nm deep, to a polymethyl-methacrylate (PMMA) surface resulted in the differentiation of human MSCs into osteoblast-like cells without the addition of osteogenic media[60]. Further, microarray analysis revealed that additional pathways, seemingly unrelated to bone, were activated in the presence of dexamethasone which were not activated by the nanopit topography, including genes related to the digestive system and hair, skin, and respiratory

development[60]. The activation of genes unrelated to bone production is a cause for concern, as there may be unintended cellular consequences to the use of dexamethasone, strengthening the push to establish surface driven control over differentiation.

In addition to altered polymer surfaces, MSCs have been shown to undergo nanotopography induced osteogenesis on titanium dioxide nanotube surfaces with well-defined dimensions. A study comparing different nonordered nanotube sizes revealed that MSCs seeded on nanotubes with a diameter of 70-100nm underwent differentiation into osteoblast-like cells in the absence of osteogenic media. While cell adhesion was reduced, MSCs adopted very elongated morphologies, suggesting that increased intracellular tension and limited attachment points results in the driving force for osteoblastogenesis[61]. In contrast, MSCs seeded on 30nm nanotubes and smooth titanium dioxide surfaces had better adherence and spread more uniformly, but they did not show any up-regulation of osteoblast bone markers. The authors proposed that protein adsorption plays a major role in the observed response, as significantly more protein was present on the smooth titanium samples and those with smaller nanotube diameters than on the 100nm nanotubes[61]. The reduced number of bound proteins could potentially explain the reduction in adherence and the increased elongation observed on nanotubes, as MSCs would likely have fewer points for cell attachment, spreading over longer distances to effectively adhere.

The use of nanotopography to alter the fate of stem cells is an emerging and very exciting field. Nanotopographical control over osteoblastogenesis appeals to investigators who wish to eliminate the need for soluble cues and their unintended side effects. While researchers have shown that certain surfaces are capable of inducing MSC osteogenesis, a

significant amount of work needs to be done in order to obtain an understanding of the mechanisms driving such behavior.

DNA Microarray Technology

DNA microarrays encompass a high-throughput technology which allows for the simultaneous measurement of all the gene expression, including tens of thousands of transcripts, within a particular organism or population of cells at a given moment in time. Microarrays utilize the messenger RNA (mRNA) produced by cells as a measure of gene expression, with the central assumption that the amount of a particular mRNA within a cell population is proportional to the activity of its associated gene. With the inception of DNA microarrays in the early 90's, there has been a substantial increase in the number and types of arrays produced. Investigators have several choices in microarray technology resulting from the development of biology-specific chip types, including gene expression arrays[62] and single nucleotide polymorphism (SNP) arrays[63]. Microarrays can be advantageous over other technologies, such as quantitative real-time polymerase chain reaction (RT-PCR), in that they allow for the simultaneous comparison of gene expression from a very large number of genes and can be used to indentify groups, or clusters of differentially expressed genes with similar biological functions.

In general, microarray technology can be split into two main groups, cDNA and oligonucleotide arrays, depending on the probe type. Microarray probes comprise a portion of single-stranded DNA which is complimentary to a transcript of interest and permanently affixed to a solid support, called the chip. In cDNA microarrays, the probes consist of PCR products obtained from cDNA libraries using gene specific primers, and they are printed onto a glass slide. Whereas oligonucleotide arrays, developed by

Affymetrix, utilize short, 25-mer, oligonucleotide strands which are printed onto silicon wafers using photolithography for their probes. Each array type has its own advantages and disadvantages[64]. For example Affymetrix oligonucleotide arrays can be designed in such a way that their probes represent the most unique portion of a gene, allowing for the detection of mRNA levels from very similar transcripts and splice variants. However, Affymetrix arrays are especially costly, hampering their use in the academic setting. In contrast, spotted cDNA microarrays allow for greater flexibility and customization for smaller scale experiments, however, it is common to observe cross hybridization preventing the detection of closely related transcripts.

Another key difference between Affymetrix oligonucleotide arrays and spotted cDNA arrays is the manner in which two samples are compared. A comparison of differentially expressed genes occurs on a single chip in cDNA arrays and it occurs between two or more chips when oligonucleotide array technology is used. Suppose one wants to compare gene expression in a population of tumor cells and normal cells. When using a cDNA array, the mRNA is extracted from both cell populations and converted into fluorescently labeled cDNA; the tumor cells are typically labeled red (Cy5) and the control cells labeled green (Cy5). Following labeling, cDNA from both cell populations is allowed to hybridize to a single array, forcing a competition between the two samples for probe hybridization. Any transcript which is up-regulated in the cancer cells will result in a greater amount of red labeled cDNA, and the corresponding spot will appear red on the microarray. If a transcript is down-regulated in the cancer cells, the spot will appear green. When equal amounts of the transcript appear in both populations, as in a non-differentially expressed gene, the two colors will essentially cancel out, resulting in a

yellow spot. On the contrary, when using Affymetrix oligonucleotide arrays, the mRNA from each cell population is converted to biotin-labeled cRNA or cDNA, depending on the chip type. The label transcripts are subsequently fragmented and allowed to hybridize to individual chips. Comparisons of gene expression values are performed by comparing probe intensities across chips. Therefore, an up-regulated gene in a cancer cell population will have greater probe intensities, when compared with the same gene from the control cell population. Notice that the term probe “intensities” is plural, as a result of Affymetrix arrays having multiple 25-mer probes for each transcript of interest.

The subsequent research in this thesis utilizes Affymetrix arrays; therefore, some background information on the processing of oligonucleotide arrays is essential. After mRNA extraction, labeling, chip hybridization and scanning, additional steps, including normalization, background subtraction and expression value summarization must be performed before gene expression levels can be compared. Background subtraction corrects for non-specific binding and optical noise. It can be thought of as adjusting the data for the ambient intensity. Depending on the chip type, different forms of background correction are performed. Affymetrix chips commonly have probes with slightly incorrect sequence alterations, termed mismatch probes, to detect for nonspecific binding. The intensities of mismatch probes can be subtracted from the perfect match probes to correct for background noise. Another form of background subtraction involves calculation of local background noise by taking the 5^{th} percentile of intensities within a defined region of the chip and subtracting it from all intensity values within the region.

Normalization attempts to correct for systematic variation that commonly occurs within microarray studies for the purpose of comparing multiple arrays. Assuming equal

starting amounts of mRNA from each sample to be compared, sources of variation, including labeling efficiency, hybridization times, and scanning, can result in chips from the same study having very different overall intensities. The purpose of normalization is to bring the relative intensities of each chip to approximately equal levels so that they may be compared. There are multiple methods to normalize DNA microarrays. Simple scaling involves re-scaling all the chips within an experiment to equalize the average intensity across all chips. Microarrays can also be normalized based on a group of housekeeping genes, those whose expression value is expected to remain constant across all samples. Quantile normalization is performed by forcing the distribution of probe intensities to be equal in all samples. Other forms of normalization involve the impromptu detection of genes with very little change in expression across samples, and using them as housekeeping genes for normalization.

After background correction and normalization, expression value summarization is performed. The purpose of this last step is to advance from the multiple intensity values of the probes within a particular gene's probe set to one value which is representative of the gene's overall expression level. Many different models have been developed and used for expression value summarization. Affymetrix's Microarray Suite model, MAS5[65], DNA-Chip Analyzer's (dChip) PM-MM and PM-only multiplicative model based expression index (MBEI) models[66,67], and the Robust Multi-array Average (RMA) model[68] are all commonly used to obtain expression values. Currently no one model is satisfactory for all purposes and depending on who is asked the question the response will differ. DNA microarrays in this work were analyzed using dChip's MBEI models.

Chapter 1: MSC Response to Suboptimal and Osteogenic Concentrations of BMP6

Motivation

Previous work conducted by our experimental collaborators reveal BMP6 to be the most potent in vitro inducer of MSC osteoblast differentiation out of all the osteogenic BMPs[69]. The addition of BMP6 to human MSCs results in the up-regulation of genes consistent with osteoblast differentiation, including major bone associated transcription factors and marker proteins. Further, BMP6 was the only BMP to be significantly expressed shortly following treatment with bone differentiation media containing the osteogenic inducer, dexamethasone[69]. BMP6 is also secreted by osteoclasts, providing a mechanism by which the bone resorbing cells are able to recruit osteoprogenitors to the site of remodeling and induce bone formation via BMP pathway activation[70,]. The ability of BMP6 to induce the osteogenic differentiation of adult stem cells makes it a desirable candidate for further research in the field of bone tissue regeneration.

Increased understanding of the genetic changes which occur following treatment of hMSCs with BMP6, provided by DNA microarray technology, may help determine future avenues for treatment of a wide variety of bone disorders and injuries. In this work, human marrow derived MSCs obtained from a single individual were cultured in serum-free media containing two different amounts of BMP6, a suboptimal dose of 2nM and an effective dose of 20nM. Cells from each treatment condition were harvested at

two separate time points following BMP6 delivery, and the mRNA was extracted for detection on Affymetrix oligonucleotide gene arrays. The subsequent analysis of this microarray data provides unique insight into BMP6 signaling and its regulation.

DNA Microarray Analysis

Adult MSCs, cultured under serum-free conditions, were harvested 4 and 10 days post BMP6 treatment, and the mRNA was extracted for microarray profiling using the Affymetrix HG-U133 Plus 2.0 Genechip® platform, a comprehensive 3' in vitro transcription (IVT) array capable of detecting the expression of over 47,000 transcripts. A total of six microarrays were incorporated into the analysis, one for the baseline control condition and two for the experimental samples provided with BMP6 (2nM and 20nM) at each of the two time points. It must be noted that the arrays utilized for this experiment were a subset of a larger study on the over-expression of a bone transcription factor, osterix, and its response to BMP signaling. Therefore, both the baseline and experimental MSCs were manipulated to over-express GFP prior to BMP6 treatment and microarray profiling.

Initially, the microarrays are visually inspected to rule out any surface scratches, abnormally bright or dark spots, or any other irregularities that may indicate a faulty chip. The array summary provided by the DNA-Chip Analyzer (dChip) software package did not flag any chips with a warning, indicating that all the chips met acceptable criteria for further analysis[67] **(Table 1.1)**. The percentage of genes called present was well over 50% on each chip. Affymetrix considers the total amount of genes marked as present as a quality control assessment for the in vitro transcription procedure, and values for the percentage of genes called present typically range between 30-50%. In addition the

percentage of probe sets classified as array outliers and individual probes classified as single outliers by were well below 5%, a score indicative of a problematic chip. The median intensity values reveal that the 4 Day 2nM BMP6 array has a much lower median intensity value compared to the other five chips, stressing the need for normalization.

Table 1.1 - dChip BMP6 Array Summary

Number	Array	Median Intensity (unnormalized)	P call %	% Array outlier	% Single outlier
1	4 Day GFP	331	59.4	0.34	0.094
2	4 Day GFP 2nM BMP6	152	58	0.71	0.161
3	4 Day GFP 20nM BMP6	259	58	0.507	0.122
4	10 Day GFP	349	54.5	0.26	0.08
5	10 Day GFP 2nM BMP6	348	54.4	0.417	0.124
6	10 Day GFP 20nM BMP6	305	56.6	0.631	0.101

dChip's invariant set normalization method was employed to bring the median intensity value for each chip to a comparable level. Raw data from each chip was normalized to the baseline array with median brightness level provided by the intensity values[66]. In this case, the baseline array was selected to be the day 4 control array. In general, the microarray normalization should be based on a set of non-differentially expressed control or housekeeping genes. Instead of using predetermined housekeeping genes, dChip selects for a list of controls ad-hoc using an iterative procedure. Briefly, the invariant set normalization performed by dChip selects for a list of non-differentially expressed genes by establishing thresholds for a probe's proportion rank difference (PRD). The PRD is calculated by taking the difference in ranks of a particular probe between the array to be normalized and the baseline array, and dividing it by the total number of probes contained within the chip. If a probe clears the established threshold, typically around 0.003 – 0.007, it is saved for the next round of iteration. The procedure is again repeated, but with a decreased number of probes. After several rounds, the

number of selected probes will no longer decrease in size and the resultant list of genes form the "invariant set". The process of normalization is finalized when the array to be normalized is plotted against the baseline array and the points are shifted such that the identity line runs though the points comprising the invariant set. Following normalization, the microarrays have very similar overall brightness levels, allowing for chip-to-chip comparisons.

Once chips are normalized, the microarrays need to be modeled to establish expression levels for a particular gene. Each gene's individual expression level results from the information contained within its probe set. For the HG-U133 Plus 2.0 array, there are twenty probes within a probe set, ten perfect match (PM) and ten mismatch (MM) probes. A PM probe consists of millions of copies of a single 25 base pair long strand of DNA complementary to a transcript of interest, while the corresponding MM probe is identical with the exception of a different nucleotide at the 13^{th} position. The mismatch probes allows for background correction, as it is assumed that any labeled transcript binding to a MM probe is also capable of binding to its PM equivalent. To account for the probe variability in computing expression values, dChip utilizes a statistical model which provides a weighted average of perfect match and mismatch differences (PM–MM) for the estimated expression index[67]. In brief, each probe is provided with a sensitivity index, which is a value describing the affinity of a probe for its particular target. One could imagine that a probe with higher CG content should have a higher probe sensitivity index, due to the fact that three intramolecular hydrogen bonds form between the base pairs Cytosine and Guanine, as opposed to two hydrogen bonds forming between Adenine and Thymine. The model operates by iteratively fitting values

for probe sensitivity index estimates and expression indices, using least squares estimation, ultimately converging on one common expression index for all probes within a particular probe set. The PM-MM dChip model is shown below[67].

$$Y_{ij} = PM_{ij} - MM_{ij} = \theta_i \varphi_j + \varepsilon_{ij} \quad \sum_j \varphi_j^2 = J,\ \varepsilon_{ij} \sim N(0, \sigma^2)$$

PM_{ij} is the perfect match intensity for the j^{th} probe pair within the i^{th} array, while MM_{ij} is the mismatch intensity. The rate at which the j^{th} probe pair increases in intensity after hybridization, φ_j, is also known as the probe sensitivity index, and the resultant expression index for the i^{th} array is θ_i. εij is the random error associated with the model. In order to estimate values for a gene's expression value, the model must be constrained in some way. The designers chose to constrain the model by making the sum of squares of the probe sensitivity indices equal to the total number of probes, J. Assuming the φ's are known within a probe set, the least squares estimate for θ is[67]:

$$\theta = \frac{\sum Y_j \varphi_j}{\sum \varphi_j^2} = \frac{\sum Y_j \varphi_j}{J}$$

Once expression values for all genes are obtained, probe sets of interest were filtered from the data for further analysis. In order for a gene to be filtered, it must satisfy three criteria; it must possess sufficient variation across chips, it must be present across chips, and it must surpass minimal expression limits. More specifically, a filtered gene must have a coefficient of variation greater than or equal to 0.33, it must be called present in at least 20% of the chips used, and it must have an expression value greater than 20 in at least 50% of the chips examined. Following the establishment of a list of filtered genes, the expression levels in the experimental samples were compared amongst control samples to determine which genes are differentially expressed in response to suboptimal

and osteogenic quantities of BMP6. Gene expression levels were compared pair-wise, with the criteria utilized by dChip identifying differentially expressed genes set to be |lower 90% C.I. of fold change| ≥ 1.5 and |difference in expression values| ≥ 100.

Gene lists specific to the biological processes of BMP signaling, bone mineralization, bone remodeling, ossification, osteoblast differentiation and Wnt signaling were generated by the dChip software package in conjunction with the Gene Ontology (GO) database and were subsequently combined into one bone-related master gene list. This master list was compared against the lists of differentially expressed genes (DEGs) in response to 2 or 20nM BMP6 to determine the effects BMP6 has on the expression of genes important to bone formation.

To determine if other biological processes are significantly affected by the presence of BMP6 signaling, DEG lists were submitted to the Database for Annotation, Visualization and Integrated Discovery (DAVID)[71,72]. DAVID, an online database created by the National Institute of Allergy and Infectious Disease (NIAID) and the National Institute of Health (NIH), allows for one to determine if certain biological themes, particularly GO terms, are enriched or overrepresented within a DEG list. Using DAVID's EASE score, a conservative version of Fisher's Exact P-value, one can determine if a particular biological process in more represented within an experimentally derived DEG list than it would be if a gene list of the same size was randomly selected from the gene pool. Because many of the annotation terms can be similar in nature, the creators of DAVID have implemented a functional annotation clustering tool, which groups and displays functionally related terms together allowing for clearer interpretation of the biological changes associated with an experiment.

Results

Differential Expression Genome Wide

The total numbers of differentially expressed probe sets in response to the two quantities of BMP6 reveal considerably different cellular responses. DNA microarray data from MSCs treated with a 2nM BMP6 showed far fewer genes to be significantly expressed over both time points compared with MSCs treated with a tenfold increase in concentration, 747 vs. 2,427 probe sets **(Figure 1.1)**.

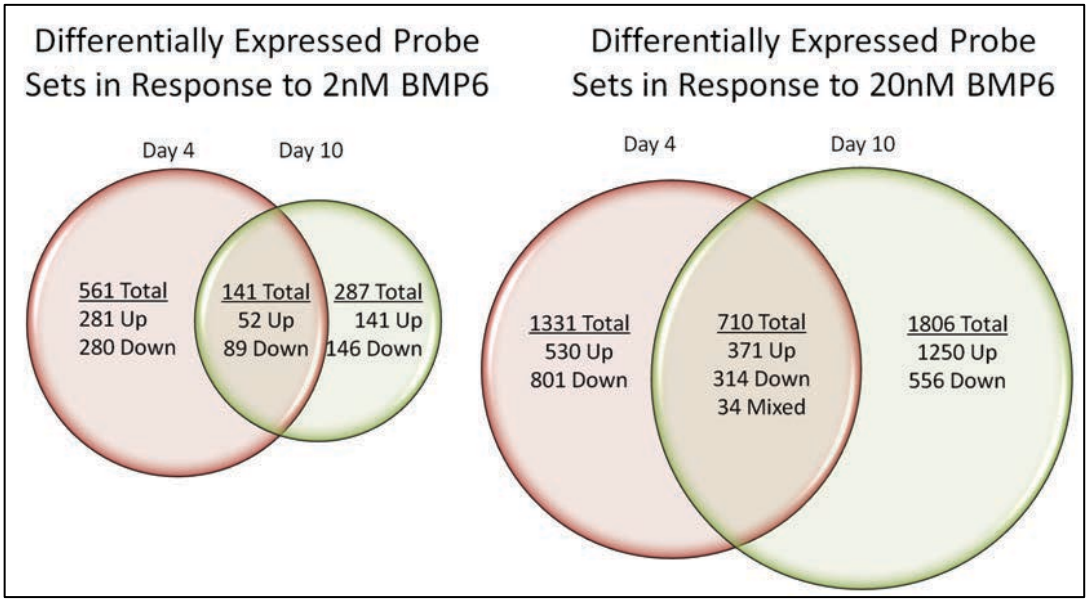

Figure 1.1 - Genome Wide Trends in Expression Following Treatment with 2nM and 20nM BMP6

Four days after administering 2nM BMP6, a total of 561 probe sets were significantly expressed, with the number of up-regulated and down-regulated transcripts roughly equal. After ten days, the number of differentially expressed probe sets almost halved, to 287, indicating that a 2nM dose of BMP6 results in more gene activity occurring earlier rather than later. Additionally, of the 141 probe sets identified as differentially expressed at both days, 112 of them had reduced fold changes at day 10 compared with day 4, relative to the control arrays.

On the contrary, MSCs treated with 20nM BMP6 had in increased differential expression genome wide. After four days of exposure, a total of 1,331 probe sets were significantly expressed with the majority, ~60%, of transcripts down-regulated. By the tenth day in culture, the number of differentially expressed probe sets increased to 1,806, with the majority, ~70%, up-regulated, indicating a shift from overall repression to activation. Of the 710 probe sets differentially expressed at both time points, 497 had increased fold changes at day 10 compared to day 4, relative to the controls. Unlike the 2nM data, genes appeared to be even more affected by the larger BMP6 dose by day 10. Interestingly, 34 probe sets fall into the mixed category, implying that they were up-regulated at day 4 and down-regulated at day 10 or vice versa.

Overall, the genome wide trends suggest that suboptimal doses of BMP6 cause an initial burst in gene transcription which peaks in activity and then begins to return to normal levels. The response to 20nM BMP6 is different. Considerably more genes are affected and they become increasingly activated or repressed over the course of time. To understand this observation, genes related to the regulation of BMP signaling and bone formation were thoroughly investigated.

Suboptimal Amounts of BMP6 (2nM) Fail to Drive MSC Osteogenesis and Elicit Considerable Short-Term Changes in the Expression of Negative Regulators of BMP Signaling

Further analysis into the unsuccessful differentiation of MSCs in response to suboptimal BMP6 levels revealed interesting results among transcripts contained within the bone-related gene list. As expected, some transcripts satisfied the dChip comparison criteria for a differentially expressed gene at both day 4 and day 10, while others satisfied the criteria for only one of the two time points. The majority of the significantly

expressed transcripts could be placed within one of three categories; negative regulators of BMP signaling, positive markers and potentiators BMP signaling and osteogenesis, and modulators of the Wnt receptor signaling pathway. A legend to interpret the following tables can be found below **(Figure 1.2)**.

Increase in Expression at Day 4	Decrease in Expression at Day 4	Did not Satisfy Model Criteria at Day 4
Increase in Fold Change at Day 10 from Day 4	Decrease in Fold Change at Day 10 from Day 4	**Did Not Satisfy Model Criteria at Day 10

Figure 1.2 - Legend for Interpretation of Microarray Results

Similar to the trends seen genome wide, differentially expressed bone-related transcripts, had larger |fold changes| relative to the control chip at the first time point, indicative of temporary change **(Table 1.2)**. Included within the list of differentially expressed genes at both days were two negative regulators of BMP signaling, the BMP specific inhibitory smad (SMAD6) and gremlin 2 (GREM2). The increased expression of SMAD6 likely serves to hinder BMP6 signaling through its inhibitory roles in binding to the BMP type I receptor, effectively blocking the phosphorylation of R-smads[49]. Moreover, SMAD6 is thought to disrupt the formation of smad complexes by competing for co-smad binding[73], and it has been shown to act as a transcriptional co repressor for osteogenic transcripts[74]. Thus, SMAD6 can function in multiple ways to thwart BMP6 signaling. Further, GREM2, a BMP antagonist[52], functions to inhibit BMP signaling through the sequestration of BMP molecules in the extracellular environment.

Other negative regulators of the BMP signaling pathways were up-regulated at the 4 day time point only. Activated genes of interest include the other inhibitory smad, (SMAD7), histone deacetylase 7 (HDAC7), and another BMP antagonist, noggin (NOG). SMAD7, like SMAD6, encodes for an inhibitory smad which prevents receptor smad phosphorylation, thus blocking ligand induced signaling. While SMAD6 preferentially

Table 1.2 - Differential Expression of Bone Related Genes in Response to a Suboptimal (2nM) BMP6 Concentration

Probe Set	Gene	Accension	4 Day Control	4 Day 2nM BMP6	4 Day Fold Change	10 Day Control	10 Day 2nM BMP6	10 Day Fold Change
Negative Regulators of BMP Signaling and Osteogenesis								
240509_s_at	**GREM2**	BF064262	15.32	118.49	**7.73**	46.36	192.53	**4.15**
231798_at	**NOG**	AL575177	46.78	290.9	**6.22**	32.47	34.09	**1.05****
207069_s_at	**SMAD6**	NM_005585	298.92	920.71	**3.08**	355.81	809.88	**2.28**
217937_s_at	**HDAC7**	NM_016596	364.31	632.17	**1.74**	304.03	305.54	**1****
204790_at	**SMAD7**	NM_005904	2713.04	4678.29	**1.72**	2241.18	2850.26	**1.27****
Positive Markers and Potentiators of BMP Signaling and Osteogenesis								
208937_s_at	**ID1**	D13889	121.29	4504.84	**37.14**	267.43	3273.8	**12.24**
210881_s_at	**IGF2**	M17863	93.74	590.55	**6.3**	132.89	537.53	**4.04**
227719_at	**SMAD9**	AA934610	328.57	1463.21	**4.45**	404.8	963.66	**2.38**
217511_at	**KAZALD1**	W28828	112.71	276.23	**2.45**	201.2	426.79	**2.12**
213707_s_at	**DLX5**	NM_005221	311.68	708.81	**2.27**	357.93	803.63	**2.25**
203426_s_at	**IGFBP5**	M65062	98.26	218.16	**2.22**	355.83	457.79	**1.29****
241986_at	**BMPER**	AI423201	480.37	318.93	**-1.51**	1205.86	756.75	**-1.59**
209541_at	**IGF1**	AI972496	248.8	77.88	**-3.19**	1233.07	790.05	**-1.56****
236028_at	**IBSP**	BE466675	3607.92	627.32	**-5.75**	1681.29	918.81	**-1.83**
211518_s_at	**BMP4**	D30751	1146.8	131.27	**-8.74**	2341.4	440.52	**-5.32**
Modulators of Wnt Signaling								
214520_at	**FOXC2**	NM_005251	239.12	537.2	**2.25**	163.36	149.94	**-1.09****
204452_s_at	**FZD1**	AF072872	178.79	400.49	**2.24**	274.99	398.49	**1.45****
203222_s_at	**TLE1**	NM_005077	129.74	120.03	**-1.08**	141.87	257.23	**1.81**
218665_at	**FZD4**	NM_012193	341.85	530.4	**1.55**	361.07	632.46	**1.75**
221029_s_at	**WNT5B**	NM_030775	2437.24	1410.02	**-1.73**	2587.77	1717.37	**-1.51****

inhibits BMP signaling, SMAD7 acts more as a general inhibitor of TGFβ superfamily signaling[75]. HDAC7, while not a direct modulator of BMP signaling, has been shown to repress a key osteogenic transcription factor, RUNX2[76]. NOG, like GREM2, functions by binding to BMPs in the extracellular environment and preventing their signaling activities through the intended BMP receptors. When over-expressed, BMP antagonists, noggin and gremlin, result in the inhibition of osteoblastic differentiation as well as decreased osteoblast function. On the other hand, both noggin and gremlin are vital for cell viability and they are both found to increase in expression in response to BMPs[52]. The initial up-

regulation of GREM2, SMAD 6 and SMAD7, NOG and HDAC7 likely serves in the burst of negative regulatory activity aiding in the prevention of osteoblastogenesis.

While several genes inhibitory to BMP signaling were up-regulated, other genes responsible for potentiating BMP signaling events were down-regulated, including BMP4, BMPER, and IGF1. Down-regulated at both time points, BMP4 encodes for a member of the bone morphogenetic protein family, and similar in function to BMP6, it is capable of inducing osteoblast differentiation[77]. The one bone-related transcript down-regulated at day 10 only encodes for BMP endothelial regulator (BMPER), an extracellular matrix protein which is required for BMP4 to exert its activating role on receptor Smad1 and Smad5[78]. The down-regulation of BMPER may be coupled with the down-regulation of BMP4 or vice-versa. Another signaling molecule, insulin-like growth factor 1 (IGF1) is also thought to aid in bone development. The addition of IGF1 increases markers of early osteogenic differentiation in MSCs[79].

The addition of 2nM BMP6 induces the largest fold changes in expression amongst a group of genes having inhibitory roles in BMP signaling and therefore does not appear to be an effective concentration for osteoblast differentiation. However, several of the up-regulated transcripts do actually potentiate osteogenic BMP signals and would be expected to have increased expression levels during successful osteogenesis including the receptor smad (SMAD9), a BMP responsive gene known as the inhibitor of DNA binding-1 (ID1), and the osteogenic transcription factor distal-less homeobox 5 (DLX5). The up-regulation of SMAD9, also known as Smad8, one of three receptor smads responsible for transmitting signals from the different BMPs, likely serves to maintain or even to increase the BMP signaling response. ID1, a transcription factor

known to be activated by smad1-smad4 nuclear complexes, is thought to function as a molecular switch, inhibiting developmental pathways such as myogenesis or neurogenesis[80]. The up-regulation of ID1 may act to promote the initiation of osteogenesis by inhibiting other hMSC differentiation pathways. However, it was discovered that an additional role for SMAD6 is to repress BMP-induced ID1 transcription by recruiting a transcriptional co-repressor, CtBP[81]. The decreased values of ID1 expression at day 10 compared with day 4, could be attributed to the presence of the inhibitory smad. In addition to ID1, DLX5 is an important transcription factor for osteogenic differentiation. DLX5 drives runt-related transcription factor 2 (RUNX2) activation and has been shown to be activated via the BMP signaling pathway[82]. Further, DLX5 null mice had reduced expression levels of vital transcription factors, RUNX2 and osterix (OSX), as well as reduced levels of bone markers, osteocalcin (OCN), and bone sialoprotein (IBSP)[83].

Given the significant up-regulation of DLX5, one would expect to see activation of downstream transcription factors RUNX2 and OSX. However, there was no detection of significant increases in expression of either of the master bone regulators, implying failed differentiation. Another key indicator for the lack of successful osteogenic differentiation, in addition to the initial activation of BMP signaling inhibitors and the absence of RUNX2/OSX, is the down-regulation of IBSP at both time points. Bone sialoprotein is a major structural protein within the bone matrix[84], and elevated mRNA levels of IBSP, quantified using real-time RT-PCR, can be used as a marker to monitor the extent of MSC osteogenic differentiation in vitro[85]. In addition to the negative regulatory functions of the BMP antagonists and the inhibitory smad molecules, HDAC7,

which is significantly up-regulated at day 4 only, has been reported to function as a repressor for RUNX2[76], and may partially explain the lack of RUNX2 activation.

Human multipotent stromal cells did not differentiate into osteoblasts when given a suboptimal (2nM) dose of BMP6. The lack of differentiation is evident given the absence of RUNX2 and OSX activation, as well as the lack of expressed osteogenic markers such as osteopontin, osteocalcin, and bone sialoprotein. In fact, bone sialoprotein was actually down-regulated in response to suboptimal amounts of the growth factor. Additionally, many of the bone related genes differentially expressed in response to 2nM BMP6 play a role in dampening the cell's reaction to osteogenic signals. The initial large fold change increases in BMP antagonists such as gremlin, noggin, histone deacetylase and the inhibitory smads, along with the down-regulation of BMP4 and IGF1, support the notion that small amounts of BMP6 are not osteoinductive, but instead activate or de-activate genes in an attempt to shut down osteogenic signaling. While a concentration of 2nM BMP6, which equates to 1.2 molecules per cubic microliter, does in fact up-regulate a few transcripts associated with osteogenesis, negative regulators of BMP signaling, which function to suppress differentiation, are up-regulated to a much greater extent. Thus by day 10, the effects of BMP signaling appear to have faded. These results were validated through experimental observations, which conclude that differentiation was unsuccessful for hMSCs provided with 2nM BMP6.

Osteogenic Amounts of BMP6 (20nM) Induce Bone Differentiation of MSCs through the Activation of Major Osteogenic Transcription Factors

Similar to the trends seen genome wide, the expression levels of bone-related transcripts in response to 20nM BMP6 show that a majority of differentially expressed genes are initially up-regulated or down-regulated at day 4 and further up-regulated or

down-regulated by day 10. Again, this behavior is opposite to the suboptimal BMP6 data, in which significant gene expression appears to peak and then begins to return to baseline levels. In addition to significant expression changes in many of the same genes inhibitory to osteogenesis, 20nM BMP6 also resulted in significant activation of genes which are required for successful osteogenic differentiation. Considerably more bone-related genes, including bone markers and osteogenic transcription factors, were significantly expressed in response to 20nM BMP6 at both time points **(Table 1.3)**.

Negative regulators of BMP signaling, SMAD6, SMAD7, GREM2, and NOG, while still up-regulated at both time points, were not expressed at high enough levels to have fold change increases proportional to the increase in BMP6 concentration. For example, while the BMP6 concentration increased ten-fold between the two experiments, the 4 day fold changes in mRNA expression values of negative BMP regulators did not. SMAD6 increased by a factor of ~2.95, SMAD 7 increased by a factor of ~1.23, GREM2 increased by a factor of ~5.22, and NOG increased by a factor of ~5.77. Unlike the majority of the differentially expressed genes in response to 20nM BMP6, SMAD6, GREM2, and NOG also experienced a decrease in expression levels by day 10 relative to the expression levels at day 4. Taken together, these observations suggest that 20nM BMP6 may serve as an effective amount for osteogenesis by saturating the proteins responsible for the negative feedback loops associated with BMP signaling. Thus, greater amounts of BMP6 may overwhelm the threshold established by negative regulators, allowing for differentiation to occur.

A major indicator for the successful differentiation of hMSCs provided with 20nM BMP6 is the increased expression of several key transcription factors. The up-

Table 1.3 - Differential Expression of Bone Related Genes in Response to an Osteogenic (20nM) BMP6 Concentration

Probe Set	Gene	Accension	4 Day Control	4 Day 2nM BMP6	4 Day Fold Change	10 Day Control	10 Day 2nM BMP6	10 Day Fold Change
Negative Regulators of BMP Signaling and Osteogenesis								
240509_s_at	GREM2	BF064262	15.32	619.28	40.41	46.36	1689.73	36.45
231798_at	NOG	AL575177	46.78	1679.82	35.91	32.47	614.56	18.93
207069_s_at	SMAD6	NM_005585	298.92	2713.87	9.08	355.81	2824.4	7.94
204790_at	SMAD7	NM_005904	2713.04	5786.07	2.13	2241.18	5015.83	2.24
Positive Markers and Potentiators of BMP Signaling and Osteogenesis								
1552340_at	OSX	NM_152860	35.92	945.41	26.32	13.26	4440.75	334.92
208937_s_at	ID1	D13889	121.29	9312.14	76.78	267.43	10372.9	38.79
210881_s_at	IGF2	M17863	93.74	1172.7	12.51	132.89	1340.38	10.09
213707_s_at	DLX5	NM_005221	311.68	2245.67	7.2	357.93	3037.97	8.49
227719_at	SMAD9	AA934610	328.57	4566.77	13.9	404.8	3379.26	8.35
217511_at	KAZALD1	W28828	112.71	569.44	5.05	201.2	1129.33	5.61
205289_at	BMP2	AA583044	47.66	195.41	4.1	159.95	778.19	4.87
209541_at	IGF1	AI972496	248.8	888.42	3.57	1233.07	5419.01	4.39
209875_s_at	SPP1	M83248	2125.2	4112.18	1.93	3218.01	13672.51	4.25
232231_at	RUNX2	AL353944	1849.14	3243.42	1.75	1483.24	3620.05	2.44
236028_at	IBSP	BE466675	3607.92	2626.29	-1.37	1681.29	6262.53	3.72
203426_s_at	IGFBP5	M65062	98.26	89.8	-1.09	355.83	1019.13	2.86
206788_s_at	CBFB	AF294326	763.97	1109.42	1.45	736.36	1888.72	2.56
204595_s_at	STC1	AI300520	265.7	412.32	1.55	83.44	509.14	6.1
241986_at	BMPER	AI423201	480.37	361.27	-1.33	1205.86	268.75	-4.49
211518_s_at	BMP4	D30751	1146.8	111.41	-10.29	2341.4	51.78	-45.22
Modulators of Wnt Signaling								
203698_s_at	FRZB	NM_001463	9.62	132.41	13.76	61	710.02	11.64
221558_s_at	LEF1	AF288571	439.35	1122.16	2.55	344.96	2083.59	6.04
221245_s_at	FZD5	NM_030804	137.86	428.33	3.11	218.4	1278.27	5.85
224325_at	FZD8	AB043703	293.21	1102.27	3.76	471.55	2524.25	5.35
227250_at	KREMEN1	BF221745	270.79	402.09	1.48	379.04	1936.32	5.11
228284_at	TLE1	BE302305	203.49	451.54	2.22	218.93	779.03	3.56
204602_at	DKK1	NM_012242	2543.3	5093.18	2	1878.85	6050.36	3.22
223679_at	CTNNB1	AF130085	520.34	640.33	1.23	206.89	666.27	3.22
202036_s_at	SFRP1	AF017987	67.06	59.49	-1.13	88.43	254.37	2.88
204451_at	FZD1	NM_003505	2119.15	6444.86	3.04	2765.58	7348.44	2.66
218665_at	FZD4	NM_012193	341.85	1314.51	3.85	361.07	795.52	2.2
219683_at	FZD3	NM_017412	131.59	94.93	-1.39	84.9	194.02	2.29
213260_at	FOXC1	AU145890	2165.17	3445.01	1.59	1276.97	1833.6	1.44**
214520_at	FOXC2	NM_005251	239.12	465.47	1.95	163.36	225.95	1.38**
224199_at	DKK2	AB033941	389.53	656.01	1.68	340	216.96	-1.57
221029_s_at	WNT5B	NM_030775	2437.24	843.07	-2.89	2587.77	496.62	-5.21
204051_s_at	SFRP4	AW089415	2098.72	1345.91	-1.56	2559.33	389.63	-6.57

regulation of OSX, RUNX2, and DLX5, all of which are vital to the process of osteogenesis, is seen at day 4 and further up-regulation is seen at day 10. With the largest fold change of any gene contained within the bone-related gene list, OSX increased ~335 fold relative to the control cells by day 10. Osterix has been shown to be required for osteoblast differentiation. Knockout mice are incapable of bone formation, and while their MSCs were shown to invade the endochondral cartilage matrix, they failed to differentiate into osteoblasts and deposit bone matrix[86]. The expression of RUNX2 was still elevated in the OSX knockout MSCs, indicating that osterix acts downstream of RUNX2[86]. RUNX2, is also up-regulated at both time points, but nowhere near the extent of OSX up-regulation. Similar to the murine OSX knockouts, RUNX2-null mice die at birth and lack both mature osteoblasts and skeletal ossification[87]. Not only is Runx2 important for initiating osteogenesis, but it is also expressed throughout the life of osteoblasts, as the expression of RUNX2 in terminally differentiated osteoblasts is thought to regulate the expression of bone matrix proteins[88]. DLX5 is a member of the distal-less homeobox protein family and functions as a transcription factor responsible for the activation of RUNX2 in response to BMP signaling[82]. The increase in expression of DLX5, RUNX2, and OSX suggests that 20nM BMP6 is an adequate amount to induce osteogenesis.

Genes which act as positive reinforcement for osteogenesis were also significantly affected in response to 20nM BMP6 at both time points. The up-regulation of SMAD9, IGF1, IGF2, and BMP2 may serve to enhance the osteogenic response of hMSCs to the increased BMP6 concentration through increased action of BMP signaling

pathways[89,90,91]. Positive markers for osteoblast differentiation were also found to increase in expression at both day 4 and day 10. The up-regulation of osteopontin (SPP1) provides indication of successful osteogenesis; SPP1 is often used as a marker to monitor the extent of hMSC osteogenic differentiation[85]. The Kazal-type serine peptidase inhibitor domain 1 (KAZALD1), also known as Bono1, has been shown to be expressed in functional osteoblasts and is associated with regions of matrix mineralization[92], thus its up-regulation further supports hMSC differentiation.

While SPP1 and KAZALD1 had increased expression levels at both time points, several other markers for osteoblast differentiation were only up-regulated at the 10 day mark, including core binding factor beta (CBFB), and IBSP. CBFB is the non-DNA binding partner of RUNX2, and it is thought to allosterically increase the binding affinity of RUNX2 for its promoter regions. Furthermore, CBFB can increase the lifetime of RUNX2 by suppressing its degradation[93]. Opposite in trend from its 2nM BMP6 induced repression, IBSP is up-regulated upon the addition of 20nM BMP6. IBSP has the ability to nucleate hydroxyapatite crystal formation, indicating an initial role in bone mineralization, and it allows for cellular attachment to the extracellular matrix through RGD amino acid sequences[84]. The increase in bone sialoprotein expression at day 10 is another sign that 20nM BMP6 is sufficient to cause hMSC differentiation into functional osteoblasts. Moreover, the up-regulation of STC1, or stanniocalcin 1, may aid the osteogenic process by playing a role in preventing hMSC apoptosis[94].

A handful of genes were repressed over the course of the experiment, including osteoprotegerin (TNFRSF11B), and BMP4. Also known as OPG, TNFRSF11B, acts to bind the receptor activator of nuclear factor kappa-β ligand (RANKL) and protects the

skeleton from excessive bone resorption by preventing RANKL from binding to the osteoclast bound receptor, RANK[95]. The decreased expression levels of osteoprotegerin indicate that osteoclasts may be required for complete osteoblast maturation. Interestingly, BMP4 is down-regulated in response to both suboptimal and osteogenic doses of BMP6, while BMP2 is up-regulated only after hMSCs are provided with the higher BMP6 dose. Both BMP2 and BMP4 preferentially signal through identical receptor complexes[96], and they both are capable of inducing complete osteogenesis. Thus, it is puzzling that upon addition of BMP6, one is activated while the other is repressed. Maybe BMP2 and BMP4 are not as similar in function as previously thought?

A large number of genes up-regulated by 20nM BMP6 play a role in the Wnt receptor signaling pathway, confirming the existence of crosstalk between BMP signaling and other osteogenic signaling pathways. Components of the Wnt signaling cascade up-regulated at both time points include multiple members of the Wnt receptor family of frizzled proteins, (FZD1, FZD4, FZD5, and FZD8), Wnt signaling inhibitors; frizzled-related protein (FRZB), and dickkopf-related protein 1 (DKK1), and downstream effector molecules; forkhead box protein 2 (FOXC2), lymphoid enhancer-binding factor 1 (LEF1) and transducin-like enhancer protein 1 (TLE1). The microarray data also reveals other Wnt signaling molecules which were up-regulated on day 10 only, including β-catenin (CTNNB1), secreted frizzled-related protein 1 (SFRP1), the Wnt frizzled receptor (FZD3) and Wnt signaling ligand (WNT5B). One function of the frizzled receptors is to bind secreted Wnt signaling molecule on the cell surface, leading to the stabilization of β-catenin[50]. This allows for the association between β-catenin and transcription factors LEF1/TCF to modulate osteogenic transcription factor expression[97]. The activation of

FOXC2 has been shown to stimulate osteoblast differentiation. FOXC2 over-expression leads to increased protein levels of β-catenin and increased transcriptional activity of Wnt-related transcription factors[98]. In contrast, the up-regulation of Wnt signaling antagonists FRZB[99], DKK1[100], SFRP1[101], and the transcriptional co repressor TLE1[102], may provide negative feedback, dampening Wnt signaling in response to the increase in expression of multiple frizzled family members, the up-regulation of transcription factor LEF1, and the increased levels of LEF1's co-activator β-catenin.

The largest portion of genes associated with Wnt signaling was up-regulated; however, some Wnt-related genes were down-regulated, including the down-regulation of the Wnt signaling ligand, WNT5B, at both time points and secreted frizzled-related protein 4 (SFRP4) at day 10 only**.** WNT5B and SFRP4 are both Wnt signaling antagonists responsible for inhibiting canonical Wnt signaling; WNT5B is thought to be a strong enhancer of adipogenesis[103], while SFRP4 is thought a potent inhibitor of angiogenesis[104] and increases in expression levels during adipogenesis of adipose-derived mesenchymal stem cells[105]. The down-regulation of these two genes likely supports the osteogenic process by preventing adipogenic differentiation and aiding in the coupling of angiogenesis with bone formation.

Human multipotent stromal cells provided with 20nM BMP6 successfully differentiated along the osteoblast cell lineage. This was evident in the DNA microarray analysis of bone-related transcripts and further validated by experimental observations. A substantially larger number of genes were affected by the addition of 20nM BMP6 in comparison with 2nM, and the trend in expression was noticeably disparate (see **Appendices 1.1-1.4** for full list of bone-related differentially expressed genes). The

majority of initially activated or repressed transcripts further maintained their activation or repression at day 10, whereas the genes affected by 2nM BMP6 appear to initially turn on or off and begin returning to baseline levels by day 10**.** While most of the same negative regulators of BMP signaling were up-regulated in response to both concentrations of BMP6, the increase in expression fold-changes of gremlin, noggin, and Smad6/7 was not proportional to the ten-fold increase in BMP6 concentration. It is therefore suggested that the 20nM BMP6 concentration is able to saturate the threshold established by the negative regulators of BMP signaling. The sustained up-regulation of master bone regulators DLX5, RUNX2, and OSX, and the eventual up-regulation of bone specific markers OPN and IBSP are key indicators of osteogenesis, and mark a drastic difference in overall gene expression between the two different BMP6 concentrations. The additional activity from Wnt-related genes likely plays a role in enhancing BMP6 induced osteogenesis, and the data suggests that BMP-Wnt crosstalk may be necessary for differentiation to occur.

Activation and Repression of Additional Biological Processes in Response to BMP6

In addition to solely focusing on transcripts related to osteoblast differentiation and bone formation, the genome wide DEG lists, in response to both BMP6 concentrations, were provided to DAVID in order to determine if additional biological processes were significantly overrepresented. While the HG U133 Plus 2.0 microarray has probes for over 47,000 different transcripts, only 13,528 of them are recognized by DAVID as associated with a particular Gene Ontology biological process term. The goal of the DAVID analysis is to determine if an experimentally derived DEG list contains subgroups of genes related to a specific biological process in greater proportions than if

an identically sized DEG list were to be selected at random. DAVID accomplishes this by using a modified version of Fisher's Exact Test.

The following passage provides some brief information, by means of example, to interpret the subsequent figures. A total of 370 probe sets were significantly up-regulated in response to 2nM BMP6 over both time points, as determined by dChip. Of those 370 probe sets, DAVID eliminated gene redundancies and non associated terms to identify 227 individual genes linked to a particular biological process term, as determined by the Gene Ontology database. Now out of these 227 differentially expressed genes, 25 are associated with skeletal system development, and out of the total number of genes linked to a biological process term, 319 are associated with skeletal system development. Fisher's Exact Test determines if obtaining 25/227 is more random than chance when compared to the human background of 319/13,528.

The EASE score is a conservative version of Fisher's Exact Test, whereby the number of enriched genes related to a specific biological process term is reduced by one. In the case of skeletal system development in response to 2nM BMP6, 24 instead of 25 genes would be used to calculate the EASE Score. A two-by-two contingency table (blue) is constructed out of the DAVID results (bold) and the EASE score is the calculated p-value from a one tail Fischer's Exact Test **(Figure 1.3)**. In this case the probability of randomly selecting 227 genes out of the genome and having 24 of them be associated with skeletal system development is very low, p = 7E-10, thus it is significantly enriched.

	In DEG List	Not in DEG List	**Total**
Involved in Skeletal System Development	24 (**25**-1)	295	**319**
Not Involved in Skeletal System Development	203	13,006	13,209
Total	**227**	13,301	**13,528**

a	**b**	**a+b**
c	**d**	**c+d**
a+c	**b+d**	**n**

$$p = \frac{(a+b)!(c+d)!(a+c)!(b+d)!}{a!b!c!d!n!}$$

Figure 1.3 -- Example of a Two-by-Two Contingency Table and EASE Score Calculation Used by DAVID

The most overrepresented biological process within the genes up-regulated by 2nM BMP6 was skeletal system development, confirming that the bone related transcripts were a good choice for examination in the initial microarray analysis **(Figure 1.4)**.

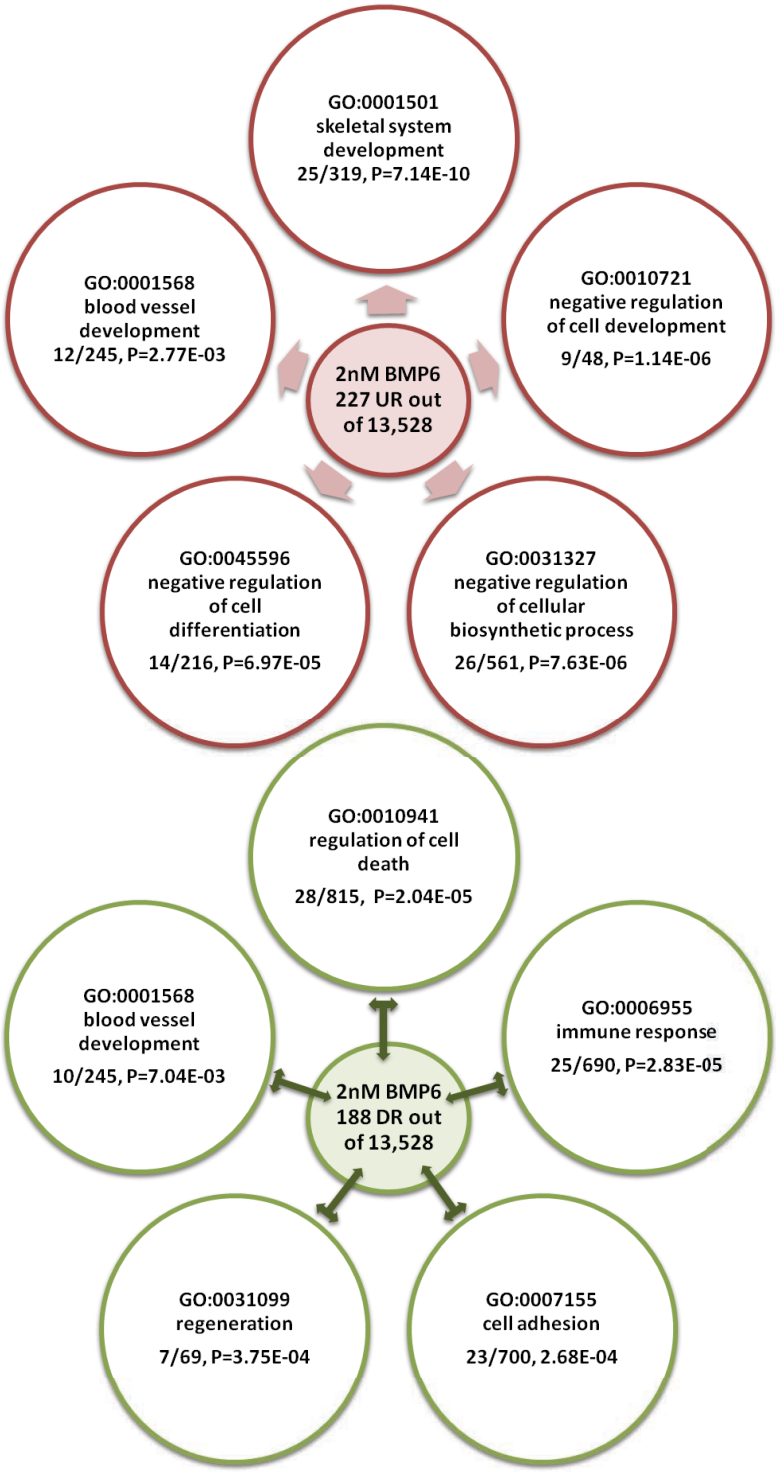

Figure 1.4 - Overrepresented Biological Processes within Significantly Up-Regulated and Down-Regulated Genes (2nM BMP6)

Additional enriched biological processes in response to 2nM BMP6 were inhibitory in nature, including the negative regulation of cell development, differentiation, and biosynthetic processes. Significantly overrepresented biological processes within the down-regulated genes include regulation of cell death, the immune response, regeneration, and cellular adhesion. The biological process of blood vessel development was also enriched for, indicating that even small amounts of BMP6 modulate the process of angiogenesis. The results from the DAVID analysis confirm the general trends seen in the expression of bone-related transcripts and transcripts genome wide; 2nM BMP6 appears to primarily affect genes and biological processes which prevent cellular change from occurring. Complete lists of differentially expressed genes within each overrepresented biological process in response to 2nM BMP6 can be found in **Appendices 1.5-1.6**.

On the other hand, the overrepresented biological processes in response to 20nM BMP6 are indicative of broad cellular change **(Figure 1.5)**. Similar to the 2nM case, the most overrepresented biological process within the up-regulated transcripts is skeletal system development. Notice however, the significant increase in the strength of the EASE Score to a p-value of 1.66E-16! Unlike the 2nM data, the biological processes of extracellular structure organization, the Wnt receptor signaling pathway, and osteoblast differentiation were also significantly enriched. Notice here that the enriched biological processes are related to cellular change as opposed to the negative regulation of cellular change. It is also important to note that the statistical significance of biological process enrichment in response to 20nM BMP6 is orders of magnitude greater than those enriched at a suboptimal dose. Overrepresented biological processes within the down-

regulated transcripts are somewhat similar to those enriched for at the lower BMP6 dose. Genes related to the regulation of cell death, blood vessel development, and cell adhesion appear to be down-regulated following BMP6 signaling, with greater gene enrichment at

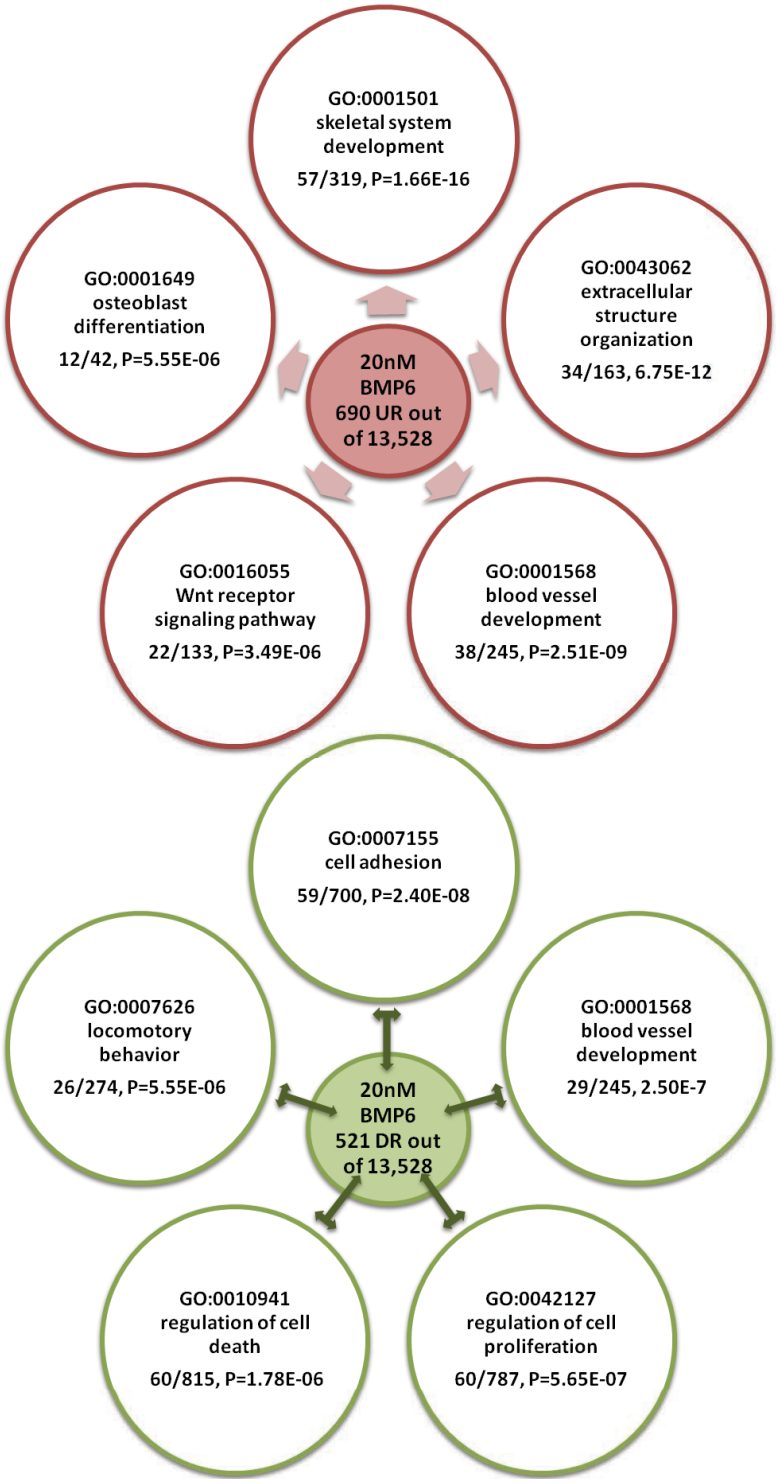

Figure 1.5 - Overrepresented Biological Processes within Significantly Up-Regulated and Down-Regulated Genes (20nM BMP6)

larger BMP6 doses. However, no longer are the processes of regeneration and the immune response significantly enriched, instead we see enrichment in genes related to cell proliferation and locomotory behavior. This makes sense as MSCs typically halt proliferation and migration during the process of differentiation. Complete lists of differentially expressed genes within each overrepresented biological process in response to 20nM BMP6 can be found in **Appendices 1.7-1.8**.

The DAVID results reaffirm the previous analysis conducted on the bone-related genes, as transcripts relating to both osteoblast differentiation and Wnt receptor signaling were found to be significantly overrepresented in response to an osteogenic concentration and not a suboptimal concentration of BMP6. Additionally, the overrepresented biological processes in response to a 2nM BMP6 were largely inhibitory in nature.

Discussion

DNA microarray results obtained from hMSCs treated with two different amounts of BMP6 confirmed experimental observations of a BMP6 dose dependence for successful osteogenesis. A 2nM quantity of BMP6 was suboptimal for osteoblast differentiation as indicated by the absence of expression of regulatory transcription factors (DLX5, RUNX2, OSX) and bone marker proteins (OPN, ISBP). Suboptimal BMP6 treatment induced a burst of gene activity at day 4, with expression levels much less pronounced at day 10, indicative of a temporary genetic response. Additionally, a large number of the differentially expressed genes in response to 2nM BMP6 play inhibitory roles in BMP and Wnt signaling pathways. The initial up-regulation of BMP antagonists (SMAD6/7, GREM2, and NOG) likely serves to dampen the osteogenic

effects of BMP6 when provided at such low quantities, and the repression of genes which can positively influence BMP signaling and/or osteogenesis (BMP4, USP9X, and IGF1) provides further evidence of the cell's attempt to halt the differentiation process. Further, significantly enriched biological processes included negative regulators of cellular development and differentiation. The hypothesis generated from the micro array results suggest that upon addition of a suboptimal amount of BMP6, hMSCs up-regulate BMP/Wnt inhibitors and antagonists in an attempt to prevent cellular change from occurring. The expression levels of these negative regulators likely establish a threshold which BMP6 must surpass in order to become osteoinductive. hMSCs may employ this strategy in order to prevent spurious differentiation upon encountering very low concentrations of BMP6 or to act as a buffer against minor changes in extracellular growth factor concentration. It must be stated that the 2nM concentration of BMP6 doesn't purely up-regulate negative feedback loops, as positive regulators of BMP signaling were also up-regulated. The ultimate fate of the cell depends upon the relative strength of these two kinds of regulators. This study suggests that feedback regulation of BMP signaling is extremely significant for the cell differentiation decision process.

The 20nM quantity of BMP6 was an adequate amount to induce osteoblast differentiation. Increased expression levels of osteogenic transcription factors (DLX5, RUNX2, and OSX) and bone marker transcripts (IBSP, OPN, and KAZALD1) confirmed experimental observations of successful differentiation of hMSCs into osteoblasts when treated with 20nM BMP6. The general trend of gene expression signifies long term genetic change, as the majority of genes expressed or repressed at day 4 were further expressed or repressed at day 10. This trend is not limited to the bone-associated gene list

and is seen in other functionally related genes, confirming long term cellular change. While the activation of many of the same negative BMP and Wnt signaling regulators (SMAD6/7, GREM2, NOG, KREMEN1) still occurred when hMSCs were provided with 20nM BMP6, the increase in fold changes was not proportional to the ten-fold increase in BMP6 concentration, and unlike the majority of DEGs, they decreased in fold change by day 10 relative to the control arrays. Thus, it appears that a sufficient BMP6 quantity induces osteogenic differentiation of hMSCs by saturating the negative feedback loops associated with BMP/Wnt signaling. In addition to the increased expression of vital transcription factors and bone markers, many members of the Wnt signaling cascade were also up-regulated. Wnt receptors (FZD1, FZD3, FZD4, FZD5, and FZD8), antagonists (FRZB, DKK1, and SFRP1), and transcription factors (CTNNB1 and LEF1) increased in expression throughout the time course. Therefore, activation of Wnt signaling genes appears necessary for BMP6 to induce osteogenic differentiation.

The fact that such a large number of Wnt related genes were differentially expressed in response to a sufficient BMP6 signal is not surprising, as recent evidence suggests that both pathways are necessary for DLX5, and RUNX2 expression. Conserved consensus sequences for the binding of LEF1 and the smad transcription factors are contained within the proximal promoter region of DLX5 and in the upstream promoter elements of RUNX2[97]. In addition, β-catenin and smads associate into functional complexes which are then recruited to the above promoters, and the combination of BMP and Wnt signaling molecules leads to cooperative induction of the osteogenic genes[97]. By providing hMSCs with 20nM BMP6, the microarray data and subsequent DAVID analysis suggests that a large number of Wnt related genes are significantly affected. The

activation or repression of these genes likely serves to cooperatively enhance the osteogenic response, and may even be required for complete osteoblastogenesis.

Due to data limitations, there exists a lack of statistical support for our conclusions, as only one DNA microarray was conducted per experimental condition resulting in the smallest sample size possible. This is not uncommon for microarray studies, as the cost of the arrays alone imparts a substantial financial toll. Follow up work will need to be conducted on hMSCs from multiple donors using a more cost effective technique, such as RT-PCR, to confirm the effects of suboptimal and osteogenic concentrations of BMP6 with statistical significance. Regardless, the current analysis provides abundant information on the state of gene expression during BMP6 induced osteogenesis, and offers new insight into the dose dependent BMP6 response that is observed experimentally.

Chapter 2: The Functional Roles of Osterix

Motivation

Osterix (OSX), also known as SP7, is considered to be a master regulator for the differentiation of human MSCs cells along the bone producing osteoblastic cell lineage. OSX null mice fail to form endochondral and intramembranous bone, even though blood vessels, osteoclasts, and MSCs are observed to invade the collagen matrix. The lack of ossification throughout the murine bones resulted in aberrant skeletal formation consisting solely of cartilaginous structures[86]. As mentioned beforehand, OSX is thought to be expressed downstream of RUNX2, another master transcription factor important to both osteogenesis and chondrogenesis; Osteoblasts of OSX null mice express RUNX2 at levels comparable to wildtype osteoblasts, while OSX is not expressed in RUNX2 null mice[86]. Recent investigation into growth factor signaling via the bone morphogenetic protein pathway has shown BMP2 and BMP6 dependent activation of OSX[106,69]. Further, our previous microarray analysis reveals over a 300 fold change increase in osterix mRNA expression in MSCs 10 days following treatment with 20nM BMP6 **(Table 1.3)**.

The activation of OSX, however, is not limited to BMP signaling, and there are conflicting reports suggesting that RUNX2 up-regulation may not be necessary for OSX activation. For example, investigators have successfully shown that Msh homeobox 2 (MSX2), a transcription factor up-regulated by BMP2 and thought to be important for osteogenic differentiation[107], is capable of inducing OSX expression in RUNX2 deficient

cells[106], while others argue that OSX is mainly regulated through DLX5[108]. In addition to BMP signaling, OSX is thought to be activated via the activities of IGF1[109] and the MAPK signaling cascade[110]. The combination of RUNX2 dependent and independent activation of OSX along with the information that, in addition to BMP signaling, OSX appears to be up-regulated by several pathways reveals a more complex picture of OSX regulation than originally thought.

While the details of OSX activation are beginning to emerge, other than the fact that OSX is required for bone formation, little is known about its functional roles. OSX encodes for a zinc fingered transcription factor from the SP family. It is thought to bind to CG rich sequences, known as SP binding sites, within the promoter regions of bone related transcripts. The increased expression of several genes has been associated with OSX, including type 1 collagen (Col1A1)[86,111], osteocalcin (OCN)[86], and osteopontin (OPN)[112]. Current reports regarding OSX's role in the regulation of cellular proliferation are conflicting. Fibroblasts over expressing OSX displayed increased proliferation[112], however, others argue that the OSX regulated activation of the Wnt signaling pathway antagonist, DKK1, results in decreased proliferation[113]. In addition to its roles in the modulation of cellular proliferation, OSX has also been shown to inhibit chondrogenesis, and although higher OSX expression levels are necessary for osteogenesis, low levels are sufficient enough to prevent cartilage differentiation[114].

In this work, MSCs derived from the bone marrow of three human donors were treated with siRNA to abrogate the expression of OSX. Following treatment with the bone inducing growth factor, BMP6, gene expression within OSX knockout (-OSX) and normal hMSCs was investigated using DNA microarray technology in an attempt to

identify individual genes and their associated biological processes which may be under the transcriptional control of OSX. The following analysis confirms a few of the existing reports on the transcriptional activities of OSX as well as introduces some novel functional roles for the bone regulating transcription factor.

DNA Microarray Analysis

An entirely different chip type, the Affymetrix Human Gene 1.0 Sense Transcript Genechip® array platform, was used for the OSX microarray analysis. In addition to cost savings, the HG 1.0 ST arrays have an advantage of whole transcript coverage. Each of the 28,869 well annotated genes represented on the chip contain multiple probes (~26) spread across their full lengths. In contrast, the HG-U133 Plus 2.0 arrays utilized for the BMP6 analysis contain probe sets solely concentrated to the 3' end of targets, leading to some shortcoming in detecting genes with alternative splicing, truncated transcripts, and/or nonpolyadenylated messages. Another key difference between the two chip types involves the nature of the target molecules; the 3' in vitro transcription arrays utilize biotinylated cRNA as opposed to biotinylated cDNA, which is used by the whole transcript arrays. The use of labeled cRNA targets results in increased cross hybridization, or the nonspecific binding of targets to unintended probes, and by using cDNA, investigators have shown reduced cross hybridization and better microarray performance[115]. Often times, the calculated PM-MM values can be negative, bringing the effectiveness of the MM probes into question. In response, PM-only arrays, including Affymetrix's Human Gene and Human Exon microarrays have been introduced.

OSX knockout and normal hMSCs were cultured within serum free conditions in the presence or absence of 10nM BMP6. Four days following BMP6 delivery, the mRNA

was extracted, processed, and distributed to the microarray core for processing. Twelve microarrays were used in this study, four per donor. The microarray summary information provided by dChip failed to detect sufficient outliers within any one array to indicate a faulty chip **(Table 2.1)**. The modeled expression value of OSX is shown along with the summary information, confirming the up-regulation of OSX in response to BMP6 treatment and the effective elimination of OSX within the knockout hMSCs. One noticeable difference between this microarray data and the previous BMP6 dose response data is the unnormalized median intensity of the arrays; the HG 1.0 ST had substantially lower median intensity values, resulting in adjusted dChip comparison criteria.

Table 2.1 - OSX Knockout Array Summary

Number	Individual	Array	Median Intensity (unnormalized)	% Array outlier	% Single outlier	OSX Expression
1	A	Control	68	0.183	0.082	25.67
2	A	Control + BMP6	67	0.271	0.123	349.02
3	A	OSX KO	85	0.093	0.06	16.29
4	A	OSX KO +BMP6	67	0.144	0.048	33.15
5	B	Control	66	0.211	0.098	23.73
6	B	Control + BMP6	74	0.195	0.072	207.91
7	B	OSX KO	76	0.117	0.057	21.88
8	B	OSX KO +BMP6	70	0.162	0.082	67.29
9	C	Control	59	1.245	0.581	27.26
10	C	Control + BMP6	61	0.295	0.129	656.53
11	C	OSX KO	65	0.304	0.159	23.04
12	C	OSX KO +BMP6	79	0.214	0.105	90.63

After visual inspection and evaluation of the summary information, the chips were deemed useable for microarray analysis. The DNA microarrays were normalized using dChip's invariant set normalization procedure, with the control array from individual A serving as the baseline array for normalization. Because the HG 1.0 ST arrays lack MM probes, the PM-MM model cannot be employed. Instead, the expression indices were obtained using dChip's PM-Only model[66]. The PM-Only model operates in much the same way as the PM-MM model with a few key differences. First, instead of using the

MM probes to subtract for nonspecific binding, the PM-Only model uses a background subtraction algorithm. Briefly, after normalization the microarrays are divided into 10 by 10 regions and the calculated 5th percentile of PM intensity values within each region is selected as the background. Once the background values are subtracted from all PM intensities within each region, the expression indices are obtained in a model very similar to the PM-MM model[66].

$$Y_{ij} = PM_{ij} = \theta_i \varphi_j + \varepsilon_{ij} \quad \sum_j \varphi_j^2 = J,\ \varepsilon_{ij} \sim N(0, \sigma^2)$$

Again, PM_{ij} is the perfect match intensity for the jth probe pair within the ith array, φ_j is the rate at which the jth probe pair increases in intensity after hybridization, also known as the probe sensitivity index, and θ_i is the resultant expression index for the ith array. εij is the random error associated with the model. Like the PM-MM model, the expression indices within the PM-Only model are obtained through an iterative least squares fitting procedure regarding one set of variables as known until the model converges on a single θ_i value for all of the probes within a gene's probe set.

Once model based expression values have been assigned to each gene, the chips can be compared for the purpose of identifying those which are differentially expressed. Similar to the previous analysis, genes of interest were filtered from the data. The filtering criteria was more lenient for the HG 1.0 ST arrays, because the lack of MM probes resulted in the loss of present/absent calls. Therefore, a filtered gene only needed to satisfy two criteria; it must have a coefficient of variation greater than or equal to 0.33, and it must have an expression value greater than 20 in at least 50% of the chips examined. In other words, the filtered genes of interest are those which have large differences in expression levels across arrays.

After modeling the data and isolating a list of filtered genes, the expression levels from the DNA microarrays were compared pair wise against one another to identify transcripts which may be under the transcriptional influence of OSX. Candidate genes for regulation by OSX were selected by isolating the BMP6 responsive genes which have significantly altered expression in the absence of OSX. BMP6 responsive genes were selected for by identifying the differentially expressed genes in response to 10nM BMP6 relative to the control hMSCs. Then, the expression levels of the BMP6 responsive genes were subsequently investigated by comparing the expression levels in hMSCs treated with BMP6 to -OSX hMSCs treated with BMP6. As an example, transcripts displaying an increase in expression following BMP6 treatment and a decrease in expression when comparing +BMP6 hMSCs to +BMP6 -OSX hMSCs are candidate genes likely to be activated by osterix.

The original microarray analysis included all three individuals and strict dChip comparison criteria. In order to be considered differentially expressed, a gene must have a |lower 90% C.I. of fold change| $\geq$ 1.5, a |difference in expression values| $\geq$ 25, and an unpaired t-test significance value of $p < 0.125$. The decrease observed in the |difference in expression value| criteria, from 100 in the BMP6 microarray analysis arises to 25 in the -OSX in the present analysis, arises due to the fact that the median intensity values for the HG 1.0 ST arrays are approximately one quarter of the median intensity values seen in the HG-U133 Plus 2.0 arrays. Additionally, the p-value cutoff was set higher than usual due to the small sample size number and the large spread in the expression level of osterix across individuals. Due to inefficient abrogation of OSX transcription in individual B, subsequent analyses focused solely on individuals A and C. Similar to the

previous microarray analysis, the DEG lists were provided to DAVID to examine for overrepresented biological processes which may be under osterix's transcriptional control. Additional details on the microarray analysis can be found within the results section.

Results

Microarray Analysis of All Three Donors

Bone-related transcripts up-regulated within hMSCs in response to 10nM BMP6 are similar to the differentially expressed genes seen in the previous 20nM BMP6 analysis, indicating osteogenic changes in gene expression occurring at one half of the BMP6 concentration. Up-regulation is observed in the transcription factors OSX, DLX5, and CBFB, as well as the bone marker KAZALD1. In addition, up-regulation was seen in the BMP antagonists NOG, GREM2, and SMAD7 **(Table 2.2)**.

Table 2.2 - Bone Related BMP6 Responsive Genes in All Three Donors

Probe Set	Gene	Accension	Control Mean	10nM BMP6 Mean	Fold Change	P-Value
Negative Regulators of BMP Signaling and Osteogenesis						
8008627	**NOG**	NM_005450	51.39	569.37	**11.08**	0.097
7925452	**GREM2**	NM_022469	104.18	502.09	**4.82**	0.001
8023220	**SMAD7**	NM_005904	70.55	133.09	**1.89**	0.002
Positive Markers and Potentiators of BMP Signaling and Osteogenesis						
7963664	**OSX**	NM_152860	25.38	404.46	**15.94**	0.102
7965873	**IGF1**	NM_001111283	53.48	296.75	**5.55**	0.086
8141140	**DLX5**	NM_005221	170.32	919.56	**5.4**	0.021
8061564	**ID1**	NM_181353	33.7	157.41	**4.67**	0.001
7929932	**KAZALD1**	NM_030929	107.35	399.34	**3.72**	0.028
7971015	**SMAD9**	NM_001127217	57.31	120.54	**2.1**	0.038
7996393	**CBFB**	NM_001755	791.99	1582.5	**2**	0.037

Of all the BMP6 responsive transcripts genome wide, only thirteen annotated genes satisfied the model criteria to be considered differentially expressed in response to the loss of OSX **(Table 2.3)**. The vast majority of genes, 12 out of 13, were down-regulated in the -OSX hMSCs provided with BMP6, implying that OSX plays a role in

their activation. Other than osteomodulin (OMD) none of the genes are clearly associated with bone formation, and they all appear to have separate, distinct roles. The DAVID functional annotation results reveal only 2 of the 13 genes, interleukin 7 receptor (IL7R) and vascular cell adhesion molecule (VCAM1) as associated with a common biological process, the regulation of the immune system. It is interesting that the only two process related genes, IL7R and VCAM1, appear to be oppositely regulated by OSX.

Table 2.3 - OSX Regulated Genes in All Three Donors

Probe Set	Gene	Accension	Control Mean	10nM BMP6 Mean	Fold Change	P-Value	10nM BMP6 Mean	10nM BMP6 -OSX Mean	Fold Change	P-Value
8145361	**NEFM**	NM_005382	138.45	1717.9	**12.41**	0.004	1717.9	267.82	**-6.41**	0.001
7963664	**OSX**	NM_152860	25.38	404.46	**15.94**	0.102	404.46	64.01	**-6.32**	0.121
8104901	**IL7R**	NM_002185	22.95	270.45	**11.78**	0.056	270.45	47.05	**-5.75**	0.066
8162388	**OMD**	NM_005014	21.93	638.78	**29.13**	0.057	638.78	143.55	**-4.45**	0.077
8105495	**PART1**	AF163475	29.14	100.66	**3.45**	0.107	100.66	27.1	**-3.71**	0.100
7972239	**SLITRK6**	NM_032229	23.45	144.72	**6.17**	0.049	144.72	44.64	**-3.24**	0.051
8016841	**TMEM100**	NM_001099640	19.35	156.03	**8.07**	0.016	156.03	50.39	**-3.1**	0.028
8045336	**GPR39**	NM_001508	120.67	775.84	**6.43**	0.003	775.84	298.98	**-2.59**	0.003
7974341	**GNG2**	NM_053064	59.27	498.64	**8.41**	0.028	498.64	195.32	**-2.55**	0.054
8055314	**LYPD1**	NM_144586	105.13	375.88	**3.58**	0.003	375.88	158.91	**-2.37**	0.003
7964687	**C12orf56**	NM_001099676	18.08	69.55	**3.85**	0.028	69.55	29.62	**-2.35**	0.032
8162908	**GRIN3A**	NM_133445	32.91	79.06	**2.4**	0.080	79.06	35.27	**-2.24**	0.085
7903358	**VCAM1**	NM_001078	640.47	198.38	**-3.23**	0.029	198.38	586.67	**2.96**	0.038

The expression of OSX, when plotted relative to the expression OMD, IL7R and guanine nucleotide binding protein (G protein), gamma 2 (GNG2), results in good linear fits (R^2>0.9). In contrast, when compared to the expression of a common housekeeping gene, beta actin (ACTB), the correlation is lost, further supporting the hypothesis that these genes are dependent on OSX for their expression **(Figure 2.1)**. Osteomodulin, also known as osteoadherin, is a proteoglycan found in bone and dentin and is thought to play a role in collagen matrix organization and biomineralization[116]. IL7R is implicated in the immune system, including aiding in T-cell maturation, and GNG2 encodes for a G

protein that has been found to be important in the inhibition of angiogenesis in zebrafish[117].

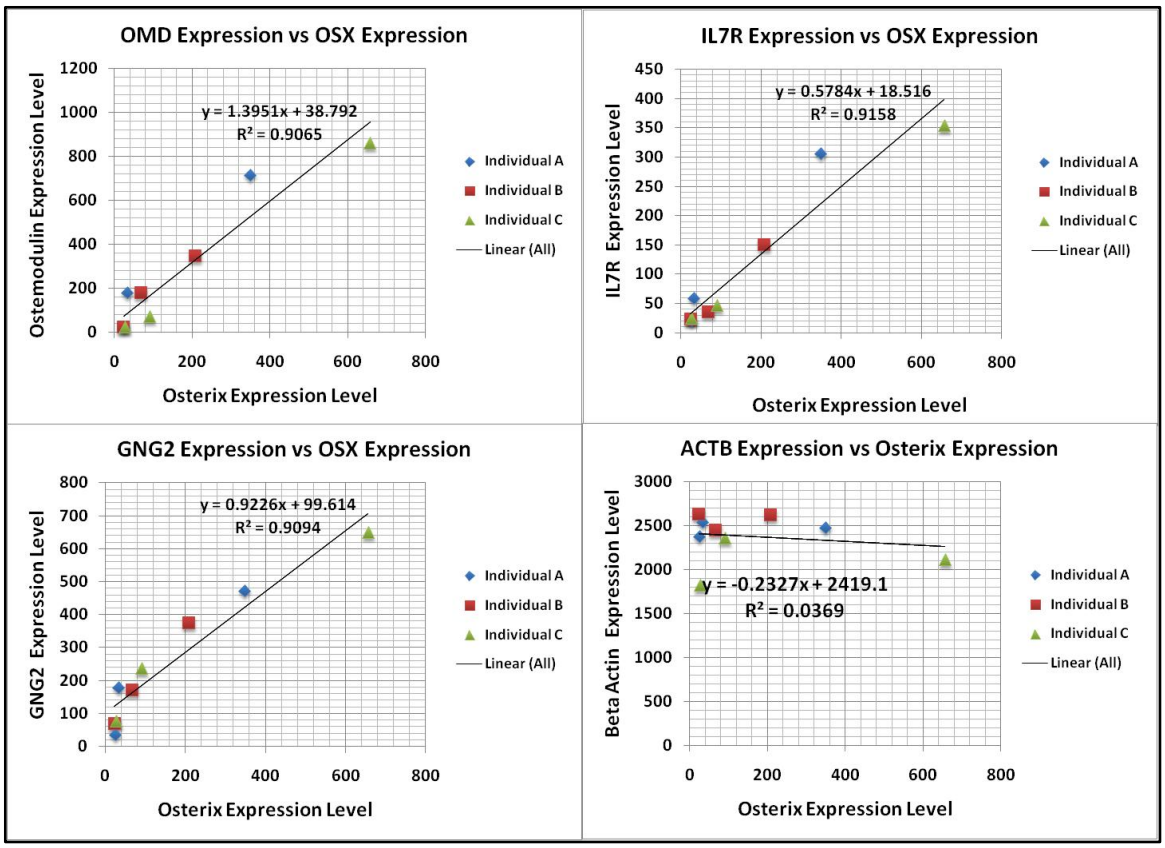

Figure 2.1 - OSX Expression Levels Vs Expression Levels of Proposed OSX Regulated Genes

By and large, there is no common biological theme in the BMP6 responsive genes which are differentially expressed following abrogation of OSX transcription in all three donors **(Table 2.3)**. One explanation may reside in the stringent comparison criteria requiring transcripts to satisfy a p-value cutoff with a sample size of 3. For instance, due to the differences in OSX expression, it wasn't even detected as differentially expressed in response to BMP6 nor was it seen as effectively silenced without increasing the p-value cutoff to 0.125. Elimination of the t-test requirement and replacing the |Lower 90% C.I. of Fold Change| >1.5 with |Fold Change| > 1.5 results in significantly more BMP6

responsive genes differentially expressed in response to the loss of OSX, including several genes important for skeletal system development **(Table 2.4)**.

Table 2.4 - Bone Related OSX Regulated Genes in All Three Donors Following Relaxation of Comparison Criteria

Probe Set	Gene	Accension	Control Mean	10nM BMP6 Mean	Fold Change	10nM BMP6 Mean	10nM BMP6 -OSX Mean	Fold Change
7898693	**ALPL**	NM_000478	62.73	251	**4**	251	48.63	**-5.16**
8162388	**OMD**	NM_005014	21.93	638.78	**29.13**	638.78	143.55	**-4.45**
8060850	**BMP2**	NM_001200	225.71	340.23	**1.51**	340.23	106.14	**-3.21**
8162394	**ASPN**	NM_017680	100.35	527.56	**5.26**	527.56	338.65	**-1.56**
8096301	**SPP1**	NM_001040058	392.8	716.05	**1.82**	716.05	463.99	**-1.54**

Bone related genes activated by OSX include; proteoglycans, OMD and asporin (ASPN), bone maker proteins, alkaline phosphatase (ALPL) and SPP1, and the osteoinducer, BMP2. Osteomodulin and asporin are both leucine-rich proteoglycan family members expressed in connective tissues. Osteomodulin, is restricted to mineralized tissues[118], and the overexpression of OMD results in the expression of markers of osteoblast differentiation, enhancing the bone maturation process[116]. Asporin is thought to contain a domain directly responsible for the mineralization of collagen[119] and has been shown to be increased in the subchondral bone of patients with osteoarthritis[120]. Another protein important for the mineralization of bone is alkaline phosphatase. ALPL has routinely been used as a marker for osteoblast activity, since it was originally shown to increase following bone fractures[121]. Even though its functions aren't entirely known, bone specific alkaline phosphatase is accepted to be a membrane anchored ectoprotein, which cleaves phosphate groups for use in mineralization[122]. Osteopontin is expressed by bone cells and is commonly used as a marker for osteoblast differentiation[123]. An important function of osteopontin is facilitating the binding of osteoblasts and osteoclasts to the extracellular matrix of developing bone[124]. Based upon

the microarray results, OSX is implicated in up-regulating proteins involved in mineralization and maturation of the extracellular environment. A complete list of the differentially expressed genes in response to BMP6 and OSX repression amongst all three donors can be found in **Appendix 2.1**.

A closer examination of the OSX expression levels within each donor **(Table 2.1)**, reveal them to vary substantially. For example, the expression of OSX increased ~13.5 fold and ~24 fold in hMSCs isolated from individuals A and C respectively, while only increasing ~8.75 fold in hMSCs from individual B when provided with 10nM BMP6. Further, following siRNA treatment, the expression of OSX in BMP6 treated hMSCs decreased ~95% and ~86% in individuals A and C respectively, while only decreasing by 68% in hMSCs from individual B. Provided with this information, a subsequent analysis was performed on donors A and C only, to determine if additional information can be gleaned from the microarray data.

Microarray Analysis of Donors A and C

Four arrays associated with hMSCs from donor B were eliminated from the microarray analysis and the dChip comparison criteria were relaxed. Because the sample size decreased to n=2, the t-test component was omitted from the comparison criteria. As a side not, even with a sample size of n=3, the t-test is really only beneficial for detecting very large differences in gene expression between samples. For the subsequent analysis, a differentially expressed gene must have a |fold change| > 1.5 and a |difference in expression value| > 25. The number of BMP6 responsive genes which were differentially expressed following OSX knockout increased. Interestingly, the removal of donor B resulted in the loss of BMP2 and SPP1 from the BMP6 responsive differentially

expressed gene list, likely due to large expression values from donor B skewing the group means. However, additional transcripts potentially under the influence of OSX were identified. BMP6 responsive transcripts down-regulated in the OSX knockout hMSCs are assumed to be activated by OSX. The bone related genes of interest include ALPL, aggrecan (ACAN), ASPN, DLX5, FRZB, KAZALD1, OMD, osteoglycin (OGN), and TNFRSF11B **(Table 2.5)**.

Table 2.5 - Bone Related OSX Regulated Genes in Two of Three Donors Following Relaxation of Comparison Criteria

Probe Set	Gene	Accension	Control Mean	10nM BMP6 Mean	Fold Change	10nM BMP6 Mean	10nM BMP6 -OSX Mean	Fold Change
8057506	**FRZB**	NM_001463	20.02	843.66	**42.13**	843.66	351.7	**-2.4**
8162388	**OMD**	NM_005014	21.92	786.15	**35.86**	786.15	125.36	**-6.27**
7963664	**OSX**	NM_152860	26.47	502.68	**18.99**	502.68	62.19	**-8.08**
7985786	**ACAN**	NM_013227	34.26	301.23	**8.79**	301.23	176.26	**-1.71**
8162394	**ASPN**	NM_017680	64.05	543.64	**8.49**	543.64	133.53	**-4.07**
7898693	**ALPL**	NM_000478	44.95	337.84	**7.52**	337.84	47.66	**-7.09**
8141140	**DLX5**	NM_005221	172.15	1021.05	**5.93**	1021.05	640.5	**-1.59**
8162373	**OGN**	NM_033014	19.34	90.92	**4.7**	90.92	36.57	**-2.49**
7929932	**KAZALD1**	NM_030929	106.19	449.93	**4.24**	449.93	278.94	**-1.61**
8152512	**TNFRSF11B**	NM_002546	653.06	81.2	**-8.04**	81.2	187.24	**2.31**

Compared to asporin and osteomodulin, little is known about the proteoglycan, osteoglycin. All the same, OGN has been shown to be expressed in human dentin and, like the other proteoglycans, plays a functional role in the extra cellular matrix. KAZALD1 is a gene expressed within matrix secreting osteoblasts[92], providing further credibility of OSX playing a functional role in extracellular matrix mineralization. According to the microarray data, OSX may also up-regulate the expression of an upstream transcription factor, DLX5, and another extracellular proteoglycan, ACAN, which is an important structural component of cartilage.

The only bone related gene which appears to be repressed by the expression of OSX encodes for osteoprotegerin (TNRFRSF11B/OPG), identifying a potential link between the differentiation of osteoblasts and osteoclasts. As mentioned previously, OPG encodes for a decoy receptor protein which functions by binding to RANKL, preventing differentiation of osteoclast precursors[95]. OPG knockout mice exhibited severe osteoporosis as a result of increased osteoclastogenesis and bone resorption[125]. The down-regulation of OPG in response to increased levels of osterix is indicative of the interplay between bone producing osteoblasts and bone destroying osteoclasts, and suggests that the master bone regulator, osterix, is important for active bone remodeling.

In addition to looking at the effects of OSX silencing on BMP6 responsive genes, those genes which were only differentially expressed within the BMP6 vs. BMP6 -OSX comparison were also investigated. Identified genes of interest include BMP2, matrix metalloproteinase 1 and 13 (MMP1, MMP13), alpha-2-macroglobulin (A2M), hyaluronan synthase 2 (HAS2), and hyaluronan and proteoglycan link protein 1 (HAPLN1) **(Table 2.6)**.

Table 2.6 - Additional Proposed OSX Regulated Genes of Interest in Two of Three Donors

Probe Set	Gene	Accension	10nM BMP6 Mean	10nM BMP6 -OSX Mean	Fold Change
7951271	**MMP1**	NM_002421	34.23	66.62	**1.95**
7951309	**MMP13**	NM_002427	22.03	48.51	**2.2**
8152617	**HAS2**	NM_005328	362.25	647.06	**1.79**
8112971	**HAPLN1**	NM_001884	281.94	472.61	**1.68**
7960947	**A2M**	NM_000014	103.05	46.01	**-2.24**
8060850	**BMP2**	NM_001200	340.82	125.22	**-2.72**

In the previous microarray analysis, BMP2 was shown to be up-regulated by the addition of 20nM BMP6 implying that it is BMP6 responsive. However, within the HG 1.0 ST arrays, only donor B showed strong activation of BMP2, suggesting that10nM

BMP6 isn't a sufficient concentration to activate BMP2 in all MSCs. OSX, however, does appear to play a role in the up-regulation of BMP2, as it was suppressed following the deactivation of OSX. Provided the microarray results from the two studies, it appears that there exists an interrelationship between osteogenic quantities of BMP6 and the activation of OSX and BMP2.

Two members of the matrix metalloproteinase family commonly expressed by chondrocytes, MMP13 and MMP1, and are responsible for the degradation of cartilage aggrecan[126]. The microarray data suggests that OSX is partially responsible for the inhibition of these proteinases. Recently, the loss of MMP13 has been attributed to a disruption of primary human articular chondrocyte terminal differentiation. MMP13 knockout chondrocytes experienced suppressed expression levels of RUNX2, VEGF, and the master chondrogenic transcription factor, SOX9[127]. Further, the expression of osterix was shown to inhibit chondrogenic differentiation of mesenchymal progenitor cells[114,128] by reducing expression levels of SOX9, although the mechanism by which osterix inhibits the expression of SOX9 is not very well understood. One possible explanation for osterix functioning as a switch, driving osteogenic differentiation and inhibiting chondrogenic differentiation, is through the repression of MMP13. Intriguingly, knocking out MMP13 results in increased expression of several osteogenic transcription factors, including OSX, suggesting that MMP13 may also have a regulatory role over OSX and bone regeneration[129]. The apparent OSX driven inhibition of the collagenases may not occur directly, as A2M, a proteinase inhibitor[130], appears to be up-regulated by OSX and may be responsible for the down-regulation of the MMPs. The microarray results

however, contrast with one study in which the long bones of OSX null mutants had decreased levels of MMP13 expression[131].

HAS2 and HAPLN1 are genes involved in the synthesis and regulation of hyaluronan, also known as hyaluronic acid (HA). HA is a major component of connective tissues, specifically cartilage, where one of its main functions is to increase the lubricity of joints. HAS2 is implicated in the synthesis of HA, and its up-regulation in the -OSX hMSCs indicates that OSX may function to reduce the production of HA. The inhibition of HAS2 has been linked to decreased production of HA, reduced cellular proliferation[132], and decreased expression and enzymatic activities of MMPs, specifically MMP7[133]. The 20nM BMP6 data also shows a decrease in HAS2 expression with a rise in OSX, however, both HAS1 and HAS3 have increased expression following addition of BMP6. Conversely, HAS1 and HAS3 do not appear to be up-regulated by 10nM BMP6, thus the relationship between OSX and HA production isn't clear. HAPLN1, also known as cartilage link protein 1 (CTRL1), is another important protein in cartilage, as CRTL1 null mice have reduced cartilage formation. While little is known about the regulation of CTRL1, it is thought to be partially under the control of SOX9[134]. Together, the microarray results suggest that one of the functions of OSX is to aid in the suppression of cartilage related proteins through the inhibition of the collagenases and HA associated genes. A complete list of the differentially expressed genes in response to BMP6 and OSX repression amongst donors A & C can be found in **Appendix 2.2**.

After manually searching through the differentially expressed gene lists for transcripts of interest, DAVID was once more used to determine if any biological processes were significantly overrepresented within the OSX regulated genes

(Figure 2.2). Two DEG lists were submitted, those genes which were down-regulated in response to a loss of OSX (OSX activated), and those which were up-regulated in response to a loss of OSX (OSX repressed). A total of 209 OSX activated genes were provided to DAVID and 148 were recognized and associated with a biological process. A large majority of genes, 155, were not used for the analysis, because they either were not associated with a biological process term, or they were the only gene associated with a term. Genes belonging to several biological processes appeared to be activated by OSX; 10 genes were associated with cellular morphogenesis, 14 with cell adhesion, and 3 with the negative regulation of Wnt receptor signaling.

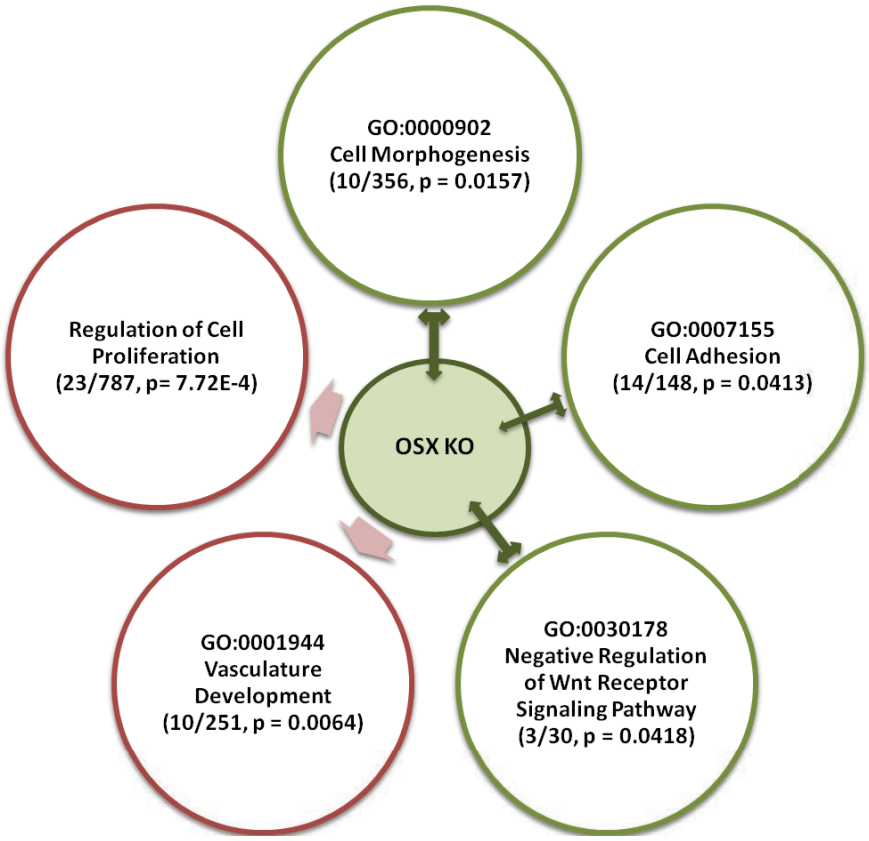

Figure 2.2 - Overrepresented Biological Processes within Significantly Up-Regulated and Down-Regulated Genes in OSX Null hMSCs

Overrepresented biological processes within the OSX repressed transcripts include the regulation of cellular proliferation and vasculature development. A total of

252 OSX repressed genes were provided to DAVID, and 181 of them were recognized and associated with a biological process. Again, a large majority of genes, 137, were either not associated with a Gene Ontology biological process term, or they were the only gene associated with their term, and thus were excluded from the DAVID analysis. Significantly enriched biological processes include 12 genes associated with regulation of proliferation and 10 genes associated with vasculature development Complete lists of differentially expressed genes associated with each significantly enriched biological process as well as other overrepresented biological processes not mentioned here can be found in **Appendices 2.3-2.4.**

Discussion

In this work, the functional roles of the osteogenic transcription factor, osterix, were explored using DNA microarray technology. Comparison of OSX null hMSCs with wildtype hMSCs in the presence of the osteoinducer, BMP6, revealed several classes of genes appearing to be regulated by OSX. When all three donor hMSCs were analyzed together under strict dChip comparison criteria, fewer than fifteen genes were differentially expressed. Those which were differentially expressed did not have any clear functional relationships, nor were they associated with any one particular biological process. One problem encountered when analyzing data from the limited number of human donors was the variability seen in the expression of transcripts across individuals, resulting in many transcripts failing to satisfy the two-sample t-test p-value cutoff, including OSX.

Relaxation of the comparison criteria provides some insights into the possible functions of OSX in the regulation of bone-related genes. Microarrays from all three

donors reveal OSX's role in the up-regulation of transcripts involved in the biomineralization process, including the proteoglycans osteomodulin and asporin, and two important bone marker proteins, osteopontin and alkaline phosphatase. The strong correlation between OSX and OMD expression in all three individuals is clear indication of OSX dependent activation of OMD, and this genetic relationship may prove very important to osteogenic differentiation of MSCs. A study has shown the over expression of OMD to result in an increase of osteoblast differentiation markers, such as increased alkaline phosphatase (ALP) activity and increased in vitro mineralization, as well as reduced proliferation and migration. Further, the concomitant activation of another proteoglycan, osteoglycin was observed when OMD was over expressed. On the contrary, repression of OMD expression resulted in increased cell proliferation and migration and the down-regulation of OGN[116].

The microarray data from all three donors also supports OSX's role in the activation of BMP2. In the previous BMP6 microarray analysis, BMP2 and OSX were found to be up-regulated in response to osteogenic concentrations of BMP6. However, when the expression of OSX is repressed, BMP2 expression levels also fall. Thus, it may be possible that BMP6 signaling reinforces the process of osteogenesis through the OSX regulated activation and production of autocrine and paracrine BMP2 signaling.

Due to the variability in the expression of BMP6 induced OSX and the inconsistent performance of the siRNA repression of OSX seen in donor B, the associated microarrays were removed from the analysis, resulting in the detection of additional genes which appear to be under the control of OSX. Besides OMD, ALPL, ASPN, and BMP2, the data suggests that OSX activates; a third proteoglycan involved in bone

mineralization, osteoglycin, a major ECM constituent of cartilage, aggrecan, the osteogenic transcription factor, DLX5, and an antagonist of Wnt signaling, FRZB. OSX has been postulated to inhibit cellular proliferation through suppression of the Wnt signaling pathway, specifically through the activation of the Wnt signaling inhibitor, DKK1 and the inhibition of β-catenin activity[113]. The microarray data reveals OSX's role in the inhibition of cellular proliferation on multiple fronts. Among the biological processes significantly enriched within the OSX activated genes is the negative regulation of Wnt receptor signaling pathway, including the genes, FRZB, DKK1, and TLE1 **(**see **Appendix 2.3)**. Additionally, one of the most overrepresented biological processes within OSX repressed transcripts was the regulation of cellular proliferation.

While the majority of bone-related genes appear to be down-regulated in response to OSX repression, several appear to be up-regulated, including osteoprotegerin, the matrix metalloproteinases MMP1 and MMP13, and several genes involved in the regulation of hyaluronic acid, HAS2 and HAPLN1. The up-regulation of these transcripts in OSX null hMSCs treated with osteogenic amounts of BMP6 suggests that they are repressed directly or indirectly by OSX. The OSX driven repression of OPG is indicative of the complex relationship between osteoblasts and osteoclasts; OPG's main role is to function as a decoy receptor for RANKL, also known as osteoclast differentiation factor, a signaling molecule responsible for promoting osteoclastogenesis. The OPG/RANKL ratio has been implicated in several bone disorders, including osteoporosis and osteopetrosis, as OPG deficient mice develop severe osteoporosis[125], while mice over expressing OPG suffer from too much bone formation[135]. Interestingly, the expression of OPG has been linked to the Wnt signaling pathway; specifically, it is activated by β-

catenin. Thus, one likely explanation of the OSX driven down-regulation of OPG may actually be a result of OSX's role in the suppression of Wnt signaling instead of a direct repression through OSX.

MMP1 and MMP13 are collagenases which function to degrade the aggrecan and collagen rich extracellular matrix found in cartilage. It is interesting to note the opposite trends seen in MMP and aggrecan expression in response to OSX, as the structural ECM component looks to be up-regulated by OSX, while the molecules responsible for its degradation are down-regulated. The expression of MMP13 is thought to be under the control of RUNX2, and is activated during the terminal stages of chondrocyte differentiation[123]. Following bone fracture, the expression of MMP13 is elevated, both in hypertrophic chondrocytes and immature osteoblasts, suggesting that MMP13 plays an important role in the rapid degradation of the cartilage matrix to make way for bone callus formation[136]. Very recently, the amount of MMP13 secreted in the urine has been proposed for use as a means to access fracture repair. The concentration of MMP13 in urine has been shown to peak by day 14 and then sharply declines following bone fractures[137]. Therefore, OSX may be a key player in signaling for an end to cartilage degradation and resorption, and the initialization the biomineralization process. Further, studies have pointed to OSX being a key trigger for directing osteogenesis and preventing chondrogenesis in RUNX2 expressing bi-potential hMSCs. MMP13 may contribute in this process, as the repression of MMP13 has resulted in the abrogation of chondrogenesis[127]. The inhibition of MMP13 is further supported by the OSX dependent activation of the MMP inhibitor, A2M.

The analysis of DNA microarray data from -OSX MSCs isolated from three human donors confirms existing reports on the functions of OSX in the literature and offers several novel roles for the osteogenic transcription factor. Firstly, it can be confirmed that OSX has a role in the inhibition of cell proliferation. In addition to the known activation of the Wnt antagonist DKK1[113], OSX also appears to up-regulate other Wnt signaling inhibitors, FRZB and TLE1. Further, among all the OSX repressed transcripts, a large number of them were associated with the regulation of proliferation. The OSX dependent down-regulation of OPG, and thus the activation of osteoclastogenesis may also be attributed to the inhibition of Wnt signaling[113,138]. Other novel roles of OSX include the down-regulation of matrix metalloproteinases responsible for the breakdown of the collagen matrix and the up-regulation of osteomodulin, osteoglycin, asporin, and alkaline phosphatase, all of which are important for bone mineralization. Further, positive feedback loops for OSX expression appear within the microarray data in the form of OSX dependent up-regulation of BMP2 and DLX5. It is interesting that one of the biological processes that appear to be down-regulated by OSX is vasculature development, as angiogenesis is integral for bone formation. The microarray data implies that this process may occur prior to OSX up-regulation, during the cartilage matrix digestion and resorption period of endochondral ossification. The microarray results establish a model of proposed OSX functions **(Figure 2.3)**.

Similar to the previous BMP6 microarray analysis, the OSK knockout study didn't take any statistics into account; a fold change in expression is not a statistically relevant term. Therefore, the two DNA microarray analyses are very qualitative in nature and necessitate further confirmation through additional experimentation.

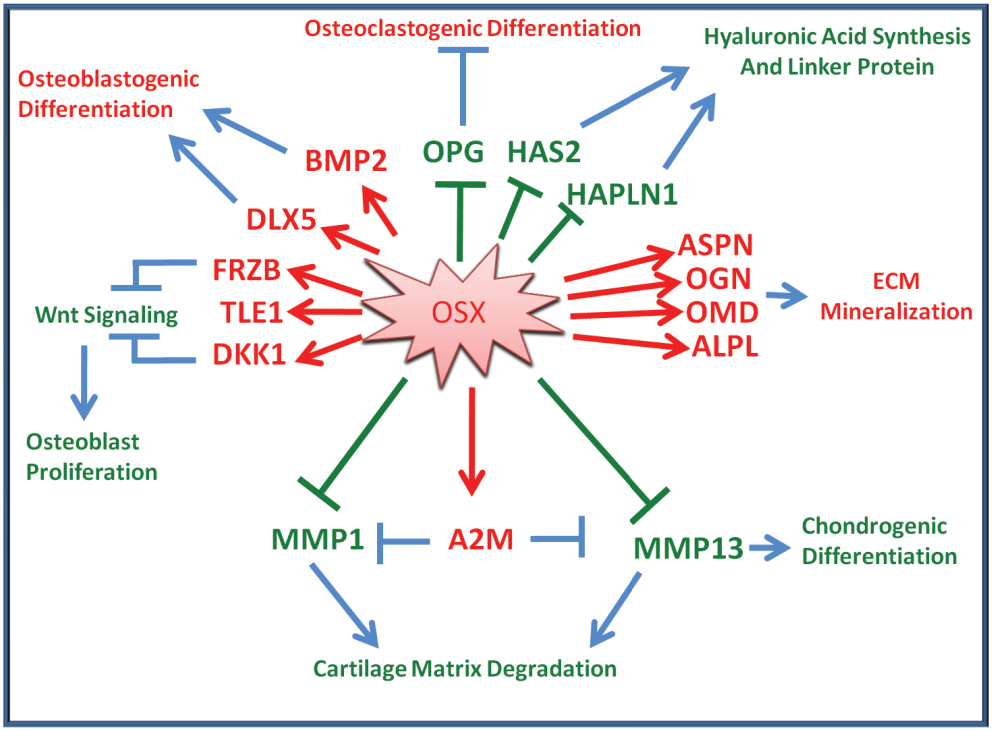

Figure 2.3 - Proposed Model of OSX Functions: Red (activating) and green (repressing) arrows are established by the -OSX microarray data, and the blue arrows are found throughout the literature.

Chapter 3: MSC Response to PCL Nanopillar and Nanofiber Surface Topographies

Motivation

Recently, MSCs have been demonstrated to differentiate into osteoblast-like cells without the use of bone differentiation media, by modifying the substrate nanotopography to contain nonordered nanopits or nanotubes approximately 100nm in diameter[60,61]. Differentiation occurs more readily on surface topographies which limit the amount of protein adsorption, thus forcing adhered cells to adopt highly stretched and stressed morphologies[61]. The ability to control MSC fate through their physical interactions with the underlying biomaterial surface topography is a very exciting field which has potential to significantly affect the future of tissue engineering.

To further our understanding of progenitor cell response to nanotopographical cues, poly(ε-caprolactone), a biocompatible, bioresorbable, FDA approved polymer, was used to fabricate nanopillar and nanofiber surfaces. The popularity of PCL has increased exponentially in the past decade, particularly within the field of electrospinning[139]. Electrospun PCL nanofiber scaffolds are designed to emulate the extracellular matrix of dense tissues, and they have been successful in increasing the osteogenic response of progenitor cells in the presence of bone differentiation media[140,56]. Likewise, gravimetrically extruded PCL nanopillars, are capable of enhancing bone protein production and mineralization in MSCs when osteogenic media is provided[55]. However,

the effect of either PCL nanofibers or nanopillars on differentiation in the absence of osteogenic cues has not hitherto been studied.

Here, plastic-adherent MSCs isolated from the bone marrow of Wistar and Sprague-Dawley rats[141] were cultured on PCL nanofiber and nanopillar topographies in normal growth media for a period of 28 days to determine the long-term effects imparted by nanotopography. Additionally, smooth PCL surfaces served as negative topographical controls, while polystyrene surfaces, containing seeded with MSCs cultured in bone differentiation media, served as positive controls for osteogenesis. Following four weeks of culture, MSCs on vertically oriented nanopillar surfaces acquire elongated morphologies and provide evidence of surface induced osteogenesis. While topography induced osteogenesis has been observed in MSCs on other biomaterials, this is the first documented case of PCL nanopillar induced differentiation. In contrast, horizontally oriented nanofibers do not drive osteogenic differentiation, but promote increased cellular adhesion and proliferation.

Materials and Methods

Fabrication of Smooth PCL Nanotopographies: Smooth PCL surfaces were prepared by melting 80 kDa PCL pellets on top of a glass plate at 160^{o}C for 15 minutes. To constrain the flow of polymer, the pellets were placed within 10mm diameter Teflon washers. Once the polymer becomes fluid, the center of the washer is filled entirely, and the surface facing the glass becomes exceptionally smooth, down to the nanoscale. The smooth PCL discs were removed from the oven and allowed to air cool before removal from the glass surface and surrounding washer material. Smooth PCL and standard tissue

culture polystyrene surfaces were viewed with the scanning electron microscope (SEM) to ensure surface smoothness **(Figure 3.1)**.

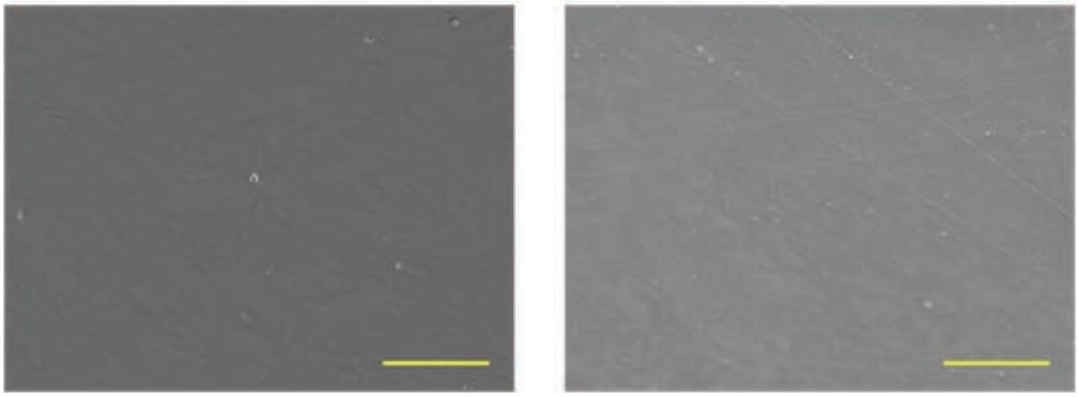

Figure 3.1 - SEM Images of Smooth PCL and Tissue Culture Polystyrene: SEM images (2,500x) verifying smoothness of PCL (left) and tissue culture polystyrene (right) samples. Scale bar = 10 μm.

PCL Nanopillar Fabrication: PCL nanopillars were fabricated based upon a previously described method of gravimetric extrusion[55]. Briefly, the fabricated smooth PCL discs are placed flat (smooth side down) on the top of porous aluminum oxide membranes, which have a pore size of approximately 100nm in diameter, and placed into a preheated oven to allow for the PCL to extrude down into the pores. Once the samples are removed from the oven and cooled, the aluminum oxide membranes are dissolved in a solution of 1N sodium hydroxide for 75 minutes. The nanopillar surfaces are then rinsed multiple times in DI water to remove any remaining membrane material. Finally samples are allowed to air dry and are stored in a desiccator until cell seeding.

The resultant nanopillar dimensions are dependent on several controllable parameters, including the molecular weight of the PCL, the temperature of the oven, and the time allotted for gravimetric extrusion. The molecular weight was fixed at 80 kDa and the temperature chosen for nanopillar extrusion was fixed at 160^{O}C. By altering the time spent in the oven by 30 second increments, it is possible to drastically alter nanopillar morphology, as observed by the SEM. PCL samples left in the oven for a short period of

time, 1 min, contained nanopillars which often appeared to form island-like clusters and had smaller aspect ratios. However, the insufficient extrusion times resulted in large areas of the samples, typically in the center, which were free of nanopillars. On the other hand, too long of a period in the oven, approximately 4 min, allowed individual nanopillars to melt together. An ideal nanopillar surface was generated by allowing an extrusion time of approximately 3min **(Figure 3.2)**.

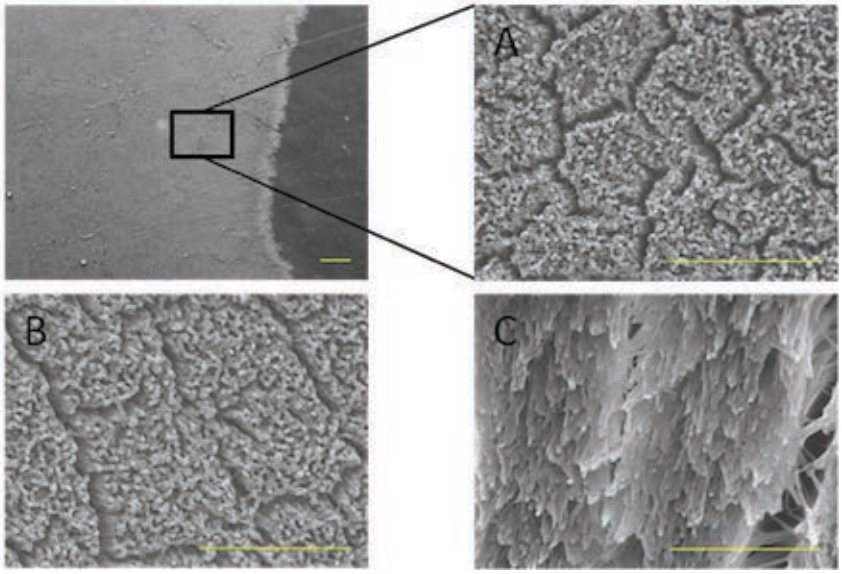

Figure 3.2 - SEM Images of PCL Nanopillars at Different Extrusion Times: SEM images (5,000x) A= 1.5 minutes, B = 3 minutes, C = 4 minutes Scale bar = 10 µm, (100 µm, upper left). The shaded area on right side of upper left image is free of nanopillars.

PCL Nanofiber Fabrication: PCL nanofibers were fabricated using a technique known as electrospinning. The apparatus consists of a polymer-filled, 10 ml glass syringe attached to a 20-gauge blunt tip catheter and placed within a syringe pump. A high-voltage power supply (Gamma High Voltage Research, ES30P-10W/DAM) is connected to the catheter tip by an alligator clip and the ground is connected to an aluminum foil collector. The PCL polymer solution is formulated as previously described[56]. In brief, the solution is composed of 80kDa PCL, oleic acid (OLA) (0.891g/mL), methanol and chloroform. To make 10 g of PCL polymer solution, 1.2 g of PCL pellets (12% PCL by

total weight) are dissolved in 5.2 mL chloroform, and 0.036 g OLA (3% OLA by PCL weight) is dissolved in 1.3 mL methanol. The two solutions are then mixed (4:1 chloroform:methanol volume ratio) to form the final product. Nanofiber morphology depends on several parameters including the volumetric flow rate, the applied voltage, and the distance from the catheter tip to the collector. For example, when the applied voltage was increased above 20kV, the nanofibers appeared to clump together, forming distinct honeycomb patterns, and when decreased below 12kV, beading was visible within the fiber structure (data not shown). Samples were originally fabricated using parameters previously established for PCL nanofibers[56]. However, the nanofibers appeared inconsistent in diameter and would often end abruptly. By increasing the flow rate and decreasing the applied voltage, nanofiber morphology markedly improved **(Figure 3.3)**. Due to electrical interference arcing across the syringe pump and shutting down the power, the applied voltage was decreased slightly for the fabrication of nanofibers to be seeded with rat MSCs. The final parameters for nanofiber fabrication included a flow rate of 10ml/hr, a tip-to-collector distance of 9cm, and an applied voltage of 17.5 kV. Individual samples were removed from the collector with a 10mm biopsy punch, and the OLA was leached out of the surfaces by soaking samples in methanol for 24h. Samples were air dried and stored in a desiccator until cell seeding.

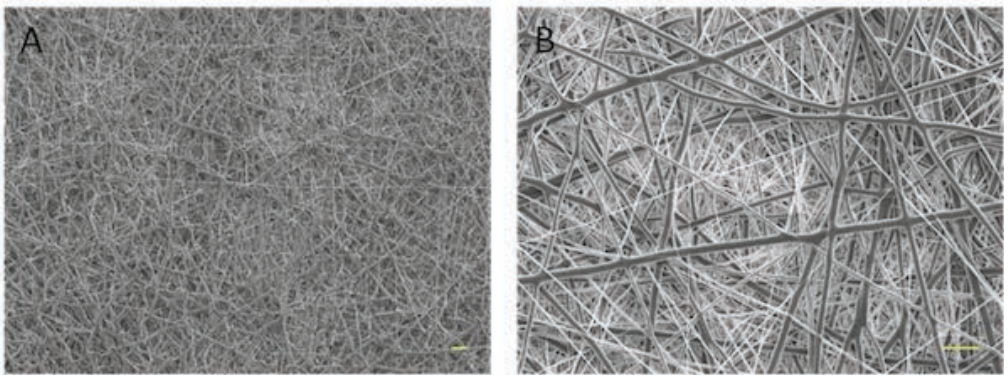

Figure 3.3 - SEM Images of PCL Nanofibers Electrospun at Different Parameters: A = Flow rate (2.8ml/hr), Voltage (20kV) Tip-to-Colletor (9cm)[56], B = Flow rate (10mL/hr), Voltage (20kV), Tip-to-Collector (9cm), Scale bar = 10 μm

Surface Characterization: Samples were sputter-coated with 10nm gold and imaged under a scanning electron microscope (JEOL JSM-6500F). Select images were measured with standard imaging software to determine nanofiber and nanopillar architecture.

Multipotent Mesenchymal Stromal Cell Isolation: With the approval of the Colorado State University Animal Care and Use Committee, MSCs were harvested from male Wistar and Sprague-Dawley rats (Rattus norvegicus). A plastic adherent selection method was used to isolate MSCs for this experiment[141]. In brief, limbs were aseptically removed from euthanized rats, and the bone marrow was repeatedly flushed through the long bones with complete culture media (CCM) (α-Minimal Essential Media (Fischer Scientific-Hyclone) supplemented w/ 2mM additional L-glutamine (Fisher Scientific-Hyclone), 10% fetal bovine serum (Atlanta Biologicals), and 1% penicillin/streptomycin (Fisher Scientific-Hyclone)) using a 10 ml syringe with 18 and 25 gauge needles. Cells were filtered through a 70um nylon filter into a clean 50mL centrifuge tube, counted with a hemocytometer, plated at high densities in a 75cm^2 culture flask containing CCM, and incubated at 37^oC and 5% CO_2. After 24h, non-adherent cells were washed away with PBS followed by biweekly PBS washes and media replacements. After the MSCs approached 40-50% confluence, they were passaged at low densities. The total time between passages was 9-11 days, and the typical cell yield was approximately 250,000 cells per 75 cm^2. MSCs were detached from the culture flask using 0.25% Trypsin/EDTA (Fischer Scientific-Hyclone) and seeded at a density of ~150 cells/cm^2 into new 75 cm^2 culture flasks containing pre-warmed CCM. This process was repeated several times until a sufficient amount of cells were collected for the study.

Sample Sterilization, Cell Seeding, and Culture: Samples were placed in 70% ethanol for 30 minutes, followed by three 5 minute PBS rinses and 30 minutes under UV light for sterilization. Prior to cell seeding, samples were conditioned in warm CCM within a 24-well plate for 1h. Passage 3 MSCs were centrifuged into a pellet and resuspended in CCM at a concentration of 25,000 cells/mL. Approximately 18,750 MSCs were seeded in each well by the addition of 0.75mL of cell solution, resulting in an estimated initial seeding density of 10,000 cells/cm^2. All surface topographies were seeded in triplicate (n=3) for each imaging assay. After 4 days of culture, half of the media was replaced in each well to allow time for cell adherence. On day 7, all of the media was replaced, and MSCs on polystyrene positive controls were switched over to bone differentiation media (CCM containing 10nM dexamethasone, 6mM β-glycerophosphate, and 50ug/ml L-ascorbic acid). Cell media was replaced every other day throughout the duration of the study.

Immunofluorescence of Actin, Vinculin, Osteopontin and Osteocalcin: MSCs were fixed in 3.7% formaldehyde for 15 minutes followed by three rinses in phosphate buffered saline (PBS). Cells were permeablilized with 1% triton x-100 for 3 minutes followed by an additional PBS rinse. All samples were then incubated in blocking solution (10% w/v bovine serum albumin (BSA) in PBS) for 20 minutes. Following aspiration, samples were incubated in primary antibody (FITC-conjugated mouse monoclonal anti-vinculin, Sigma F7053, mouse monoclonal anti-osteopontin, Santa Cruz sc-21742, goat polyclonal anti-osteocalcin, Santa Cruz sc-18319) solution (1:200 dilution in 1.5% w/v BSA in PBS) for 1 hour. In the case of osteocalcin (OCN) and osteopontin (OPN), primary antibodies were aspirated, and samples were rinsed with PBS followed

by incubation in a secondary antibody (chicken anti-mouse IgG-FITC, Santa Cruz sc-2989, donkey anti-goat IgG-FITC, Santa Cruz sc-2024) solution (1:200 dilution in 1.5% w/v BSA in PBS) for 45 minutes. Secondary antibodies were aspirated and rhodamine-phalloidin (PHDR1, The Protein Experts) was added (1:200 dilution in PBS (70nM)) for 20 minutes to stain for filamentous actin. During the last 5 minutes of actin staining, DAPI (Anaspec 83211 (300nM)) was added to stain for nuclei. Finally, samples were aspirated of stain and placed in PBS prior to imaging on an Axio Imager.A2 microscope. All surfaces were imaged three times at three different magnifications, 10x, 20x, and 50x, to provide nine representative images per sample.

MSC Fixation for Scanning Electron Microscopy: Cells were dehydrated and fixed on substrate surfaces. Samples were incubated in a solution of primary fixative (3% glutaraldehyde (Sigma), 0.1 M sodium cacodylate (Polysciences) and 0.1 M sucrose (Sigma)) for 45 min. Samples were then placed in secondary fixative (primary fixative without glutaraldehyde) for 10 min. Finally, the substrates were dehydrated by incubation in consecutive solutions of increasing ethanol concentration (35, 50, 70, 95 and 100%) for 10 min each. Further dehydration was accomplished by incubating the substrates in hexamethyldisilazane (HMDS) (Sigma) for 10 min. Samples were air dried and stored in a desiccator until imaging by SEM. The substrates were coated with a 10 nm layer of gold prior to being imaged.

Shape Factor and Cell Coverage Approximation: Individual MSCs adhered on smooth PCL and nanopillars with clearly defined borders were analyzed using the freely available imaging software, ImageJ[142], to obtain average shape factors and cell coverage areas. The cell shape factor is approximated by the ratio of cellular length to width.

Length is defined as the diameter of the smallest circle encompassing an entire cell (circumcircle), while width is defined as the diameter of the largest cirlce that will fit entirely within the cell (incircle). Using the elliptical drawing tool, circumcircles and incircles were fitted to selected cells to obtain approximate shape factors. Using the polygonal selction tool, cell outlines were traced to obtain coverage area approximations.

Cell Density Approximation: All immunofluorescently stained samples were imaged three times at the lowest magnification, resulting in nine images per surface condition. Using the DAPI layer and the thresholding tool in ImageJ, images were converted to binary representations of total nuclei. Grouped nuclei were partially resovled using ImageJ's watershed tool. The analyze particles tool was adjusted to recognize objects greater than 5 μm in diameter and with a circularity factor greater than 0.3. Once counted, cell numbers were averaged over sample type for each rat and divided by the total area of the image to obtain an approximation of cell density.

Statistical Analysis: Each experiment was replicated on three different samples (n=3) from two different cell populations. Samples sizes vary. For example, cell density calculations were based upon a sample size of n=9 (three 10x images per sample, three samples), whereas shape factor and area calculations were based upon the total number of cells analyzed (varied by surface type). Because variances were not assumed to be equal, quantitative results were analyzed using a Welch-Satterthwaite two sample t-test. Statistical significance was considered at $p < 0.05$.

Results and Discussion

Experimental PCL nanotopographies were characterized using scanning electron microscopy (SEM) **(Figure 3.4)**. Electrospun nanofibers used for this study were

fabricated with a median fiber diameter of 319 nm and a mean diameter of 415 ± 385 nm (mean ± SD, n=175). Occasional outlying fibers with diameters upwards of 3 μm were noticed and included in the statistical analysis, resulting in the large standard deviation. One possible explanation for the large variation in nanofiber diameters could reside with the syringe type. Prior to electrospinning the nanofibers for the experiment, the original glass syringe and metal plunger was replaced with an all-glass syringe to avoid electrical shorts. The seal between the glass plunger and syringe body wasn't as air tight as the metal/rubber plunger, resulting in slow solvent evaporation. Thus, the polymer solution viscosity may have increased over the course of electrospinning, resulting in inconsistent fiber diameters. Analysis of SEM images of PCL nanopillars showed that the average pillar diameter was 250 ± 37 nm (mean ± SD, n=200). Microchannels regularly appear on the nanopillar surfaces, forming canyon like structures attributed to the fabrication technique[55].

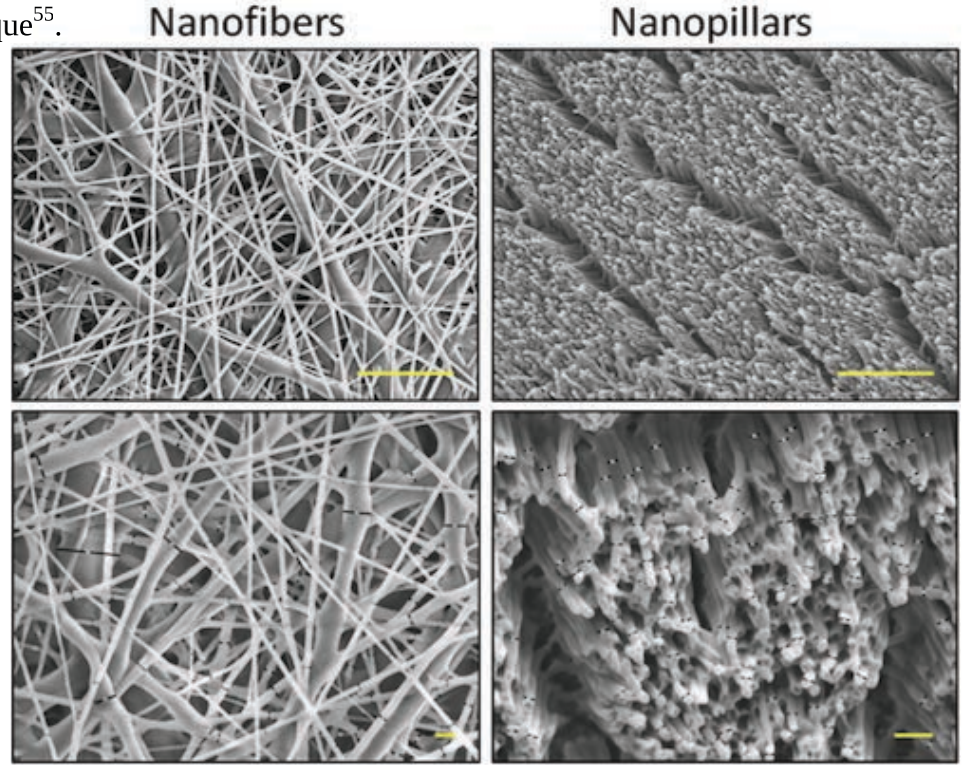

Figure 3.4 - Characterization of PCL Nanofiber and Nanopillar Surfaces: Top row- SEM images (2,500x), scale bar = 10 μm . Bottom row- SEM images showing nanofiber (5,000x) and nanopillar (10,000x) diameter distributions, scale bar =1 μm.

Third passage rat MSCs were seeded on standard tissue culture polystyrene and three fabricated PCL surfaces, smooth, nanofiber, and nanopillar, at low densities (~10,000 cells/cm^2) to provide optimal conditions for osteogenic differentiation[36]. Two and three weeks after initial cell seeding, MSC populations were assessed by immunofluorescent labeling of filamentous actin, nuclei and the focal adhesion protein, vinculin **(Figures 3.5-3.6)**. Progenitor cell response is clearly affected by surface nanotopography in terms of cell adherence, proliferation, and morphology. PCL nanofibers had the most pronounced effect on the number of adhered cells, with more MSCs residing on nanofibers than any other surface examined. After two weeks, nuclear counts reveal the average cell density to be ~80,000 cells/cm^2, which is significantly larger than the initial seeding density as well as MSC densities on other surfaces, suggesting increased adherence and proliferation on nanofiber topographies. In addition, cytoskeletal actin filaments of MSCs on nanofibers were less defined, more condensed, and difficult to bring into focus due to cell embedment within the three-dimensional surface topography. Conversely, PCL nanopillars resulted in significantly reduced attachment and proliferation, with an average two week cell density of ~5,500 cells/cm^2. Yet, PCL nanopillars appeared to have the greatest effect on cellular appearance, as MSCs often adopted highly elongated morphologies. The smooth control surfaces, PCL and polystyrene, induced MSCs to adopt uniformly spread morphologies with well-defined actin stress fibers, often aligning in a common direction. As expected, more cells adhered and proliferated on standard tissue culture polystyrene surfaces, ~28,000 cells/cm^2, than on hydrophobic smooth PCL surfaces, ~7,500 cells/cm^2 **(Figure 3.7)**.

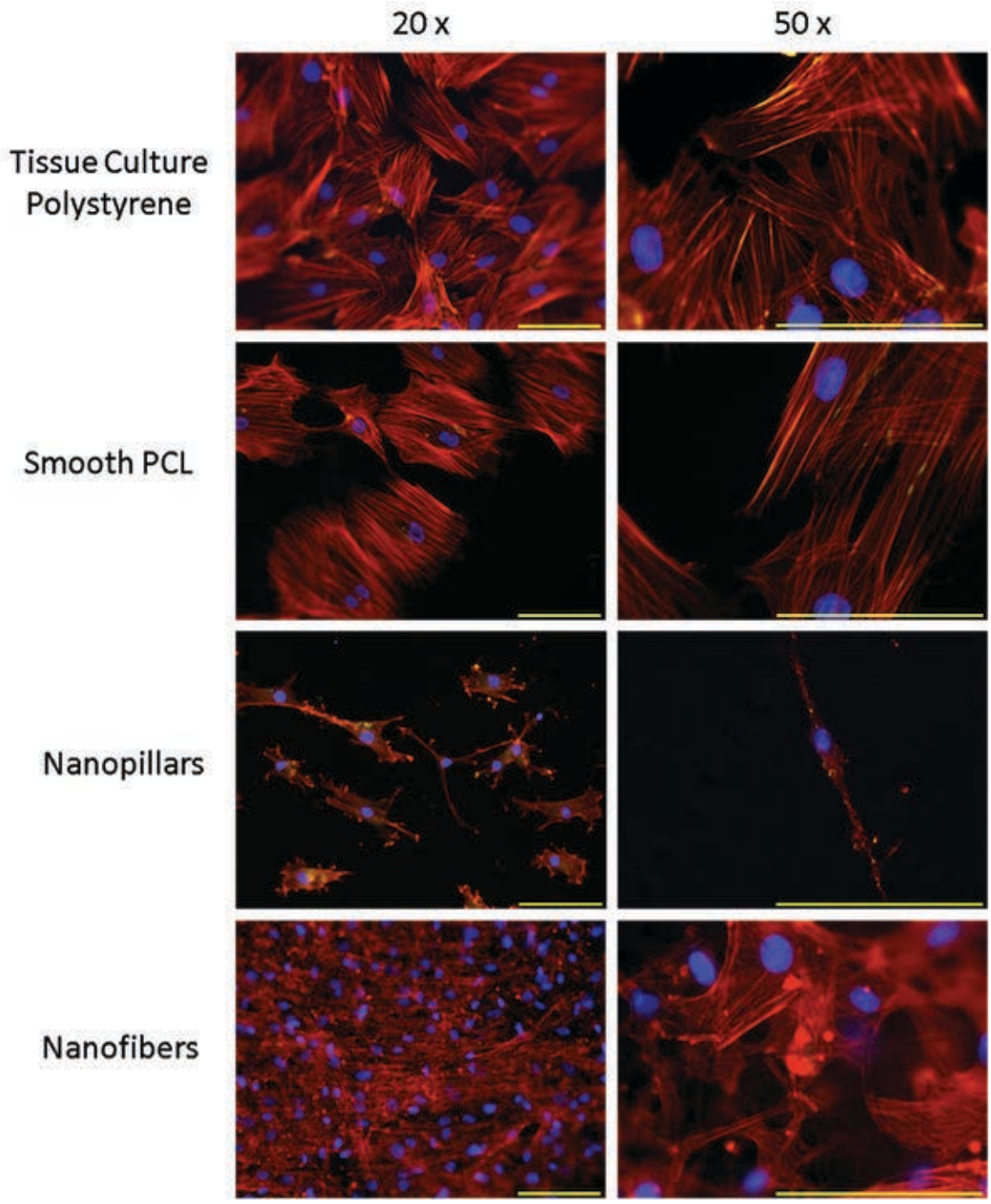

Figure 3.5 - Typical Response of Wistar MSCs after Two Weeks: Immunofluorescence images of MSC response to tissue culture polystyrene and smooth, nanopillar, and nanofiber PCL surfaces. Scale bar = 100 μm, blue = nucleus, red = actin filaments, green = vinculin**.**

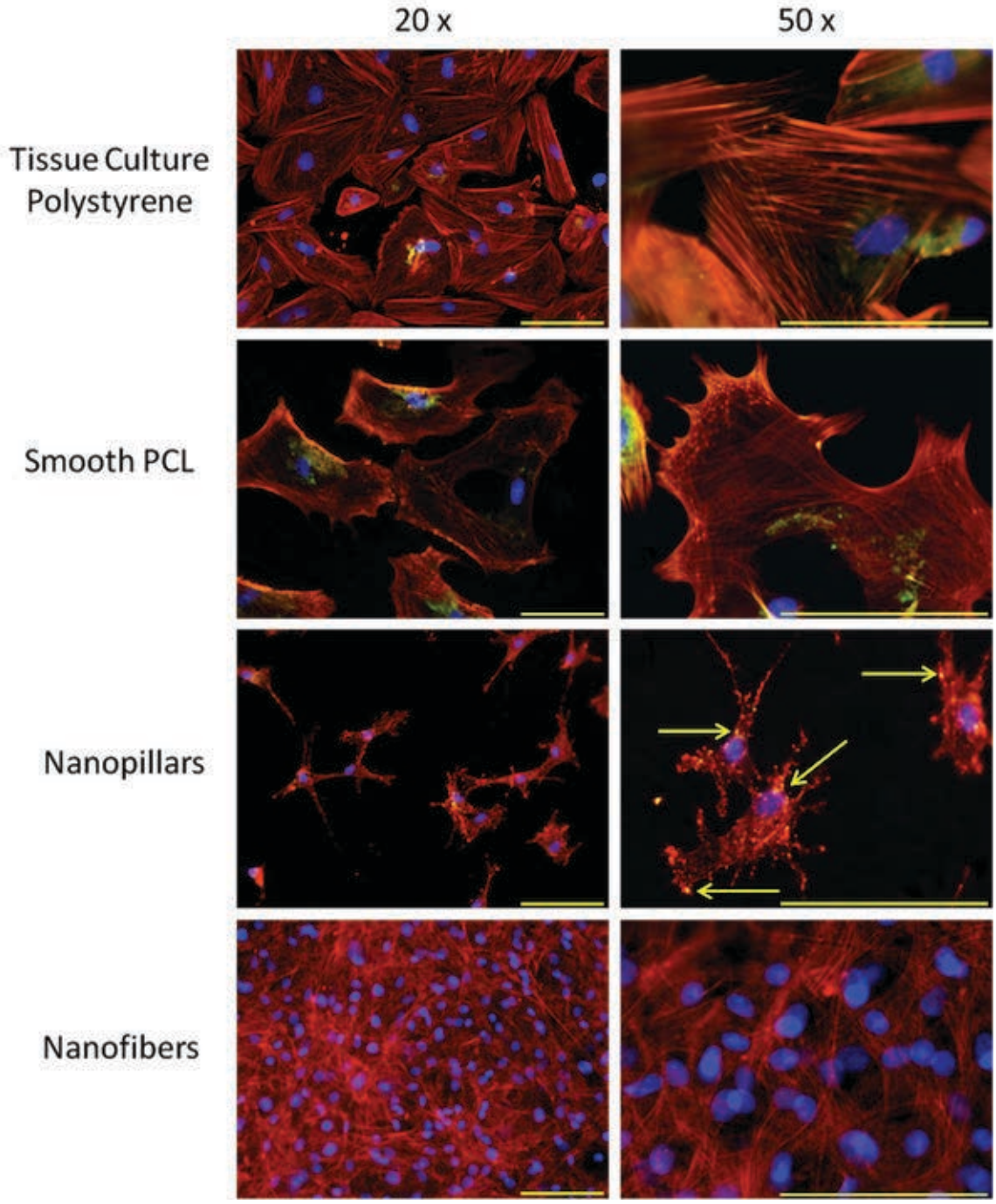

Figure 3.6 - Typical Response of Wistar MSCs after Three Weeks: Immunofluorescence images of MSC response to tissue culture polystyrene and smooth, nanopillar, and nanofiber PCL surfaces. Scale bar = 100 μm, blue = nucleus, red = actin filaments, green = vinculin. Arrows show focal adhesions on nanopillar surfaces.

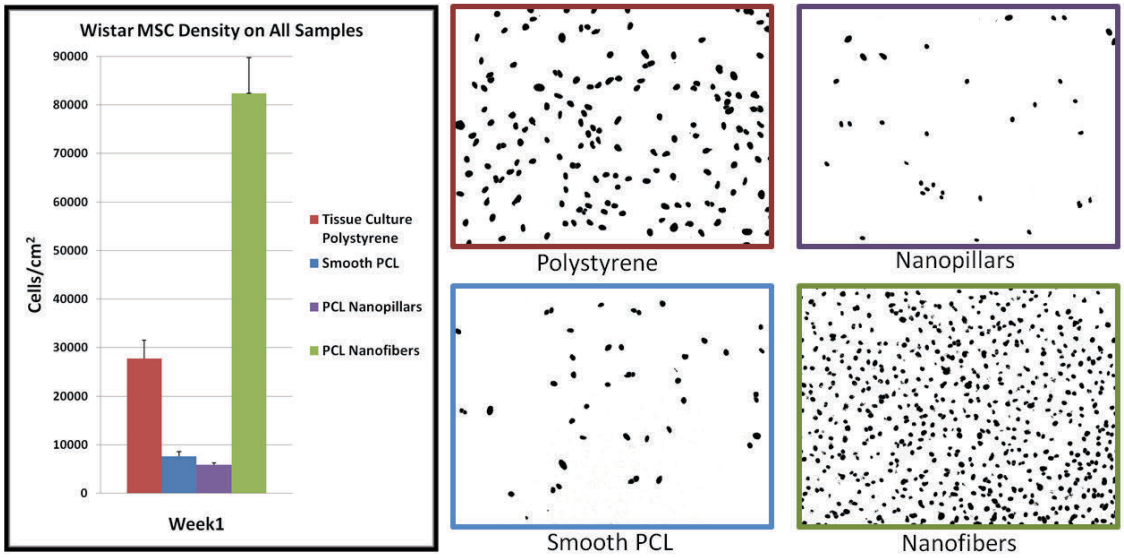

Figure 3.7 - Wistar MSC Density Following 2 Weeks of Culture: Representative images of nuclear counts, average ± standard error (n=9).

The contrasting morphologies of spread and elongated MSCs were further explored using standard imaging software to approximate cell coverage area and shape factors for individual cells on smooth and nanopillar PCL surfaces with clearly defined borders **(Fig. 3.8)**. MSCs on smooth PCL had significantly lower shape factors and significantly larger coverage areas compared to MSCs on nanopillars, a trend which was maintained over the course of the study. Smooth PCL consistently facilitated uniform spreading over large surface areas, whereas nanopillars promoted cellular elongation, covering smaller surface areas **(Table 3.1).** Due to high cell densities and poorly defined cellular borders, cell morphology was impossible to assess for MSCs on PCL nanofibers. While morphology remained fairly consistent on all samples between the second and third week of culture, cells on the nanopillars acquired additional cellular projections and became increasingly contracted in appearance, consistent with shape induced osteogenesis[37]. There were also some observable differences in vinculin staining over the course of the experiment. Very few MSCs had clearly defined green clusters, signifying a

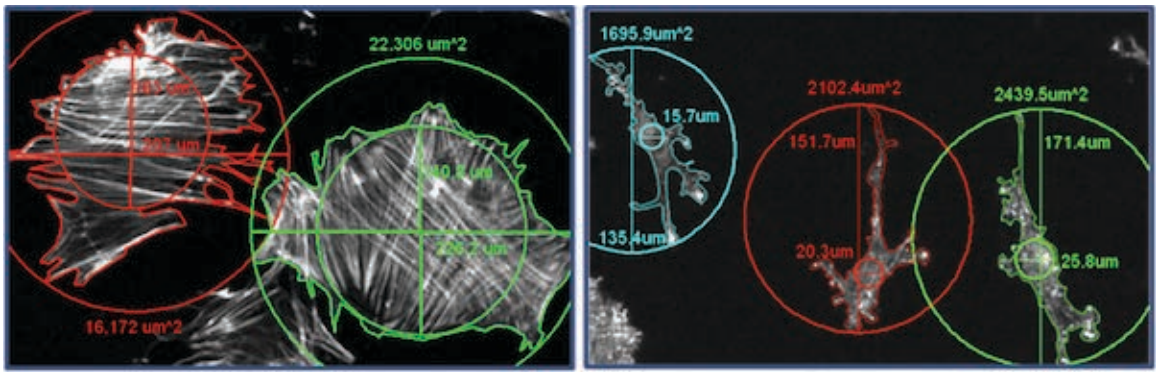

Figure 3.8 - Cellular Area and Shape Factor Approximation: Traced MSCs provide an idea of average cell coverage on and shape factors on Smooth PCL (left) & nanopillars (right). Shape factors were estimated by the ratio of cellular length to width.

lack of mature focal adhesions two weeks after cell seeding. After an additional week, MSCs on smooth control surfaces showed improved vinculin staining, with the majority observed surrounding the nuclear compartments. Small amounts of clustered vinculin were visible within MSCs cultured on nanopillar surfaces, forming speckled patterns consistent with small focal adhesions forming on pillar tops **(arrows in Figure 3.6).**

Table 3.1 - MSC Shape Factors and Coverage Areas of Wistar MSCs on Smooth PCL and Nanopillars: Values shown are arithmetic means ± standard deviations.

	Surface Type	Shape Factor (l/w)	Cell Area (μm^2)	Number of Cells
Week 2	Smooth PCL	1.84 ± 0.33	9,384 ± 5,475	29
Week 3	Smooth PCL	2.46 ± 0.41	10,753 ± 5,588	22
Week 4	Smooth PCL	1.79 ± 0.31	11,219 ± 4,205	27
Week 2	Nanopillar	6.84 ± 2.50	1,916 ± 792	29
Week 3	Nanopillar	7.07 ± 3.10	1,329 ± 483	24
Week 4	Nanopillar	7.50 ± 3.68	1,581 ± 815	43

The distinct morphologies seen in MSCs cultured on the different PCL surfaces results from the unique underlying nanotopographies. Cellular elongation on PCL nanopillars was commonly observed, and in some instances, MSCs would obtain lengths over twenty times their widths **(Figure 3.9)**. The porous nature of the PCL nanofibers allowed for MSCs to penetrate below the surface and underneath fibers. Fluorescence images revealed individual nanofibers surrounded by filamentous actin structures and

evidence of nanofibers crossing over the top of nuclei, suggesting cell embedment within the nano-structure **(Figure 3.10)**.

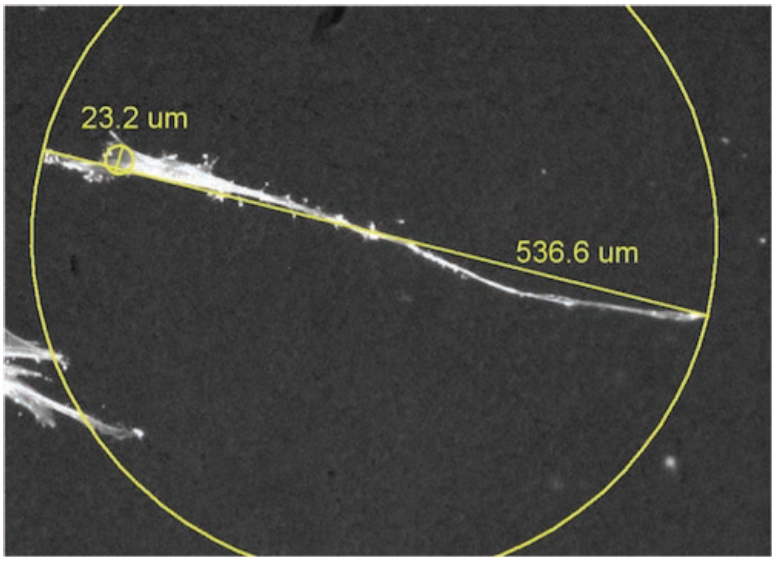

Figure 3.9 - Example of Exceptional Elongation in Response to PCL Nanopillars: A Sprague-Dawley MSC elongating over 20 times its width.

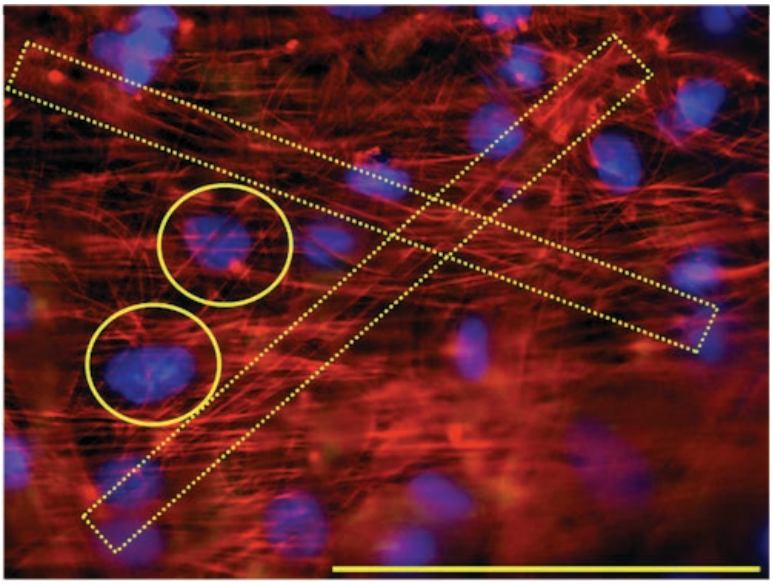

Figure 3.10 - Example of MSCs Embedded within PCL Nanofibers: Dotted boxes show F-actin surrounding nanofiber architecture. Nanofibers can be seen crossing over the top several nuclei (yellow circle). Scale bar=100 µm.

An interesting morphological response within a small percentage of MSCs seeded on the smooth PCL surfaces was the formation of actin cytoskeletal structures known as geodesic domes **(Figure 3.11)**. Geodesic domes, also called polygonal net formations, represent a structural network of polygonal elements, commonly seen in F-actin staining.

A study of rat fibroblasts revealed that geodesic domes do not form at cellular densities lower than 5,000 cells/cm2, and the introduction of groves and peaks onto the substrate surfaces significantly reduced the occurrence of dome formation[143]. Further, maintenance of geodesic domes requires intact actin cytoskeletons and cellular tension. Loss of structural isotropy is thought to lead to the collapse of the polygonal nets into the linear stress fibers, like those seen in the majority of cells on the smooth surfaces. The formation of geodesic domes within rat MSCs on smooth PCL and the lack of domes on PCL nanopillars are probably attributed to the underlying surface topography, as the pillar topography likely subjects the cells to anisotropic forces.

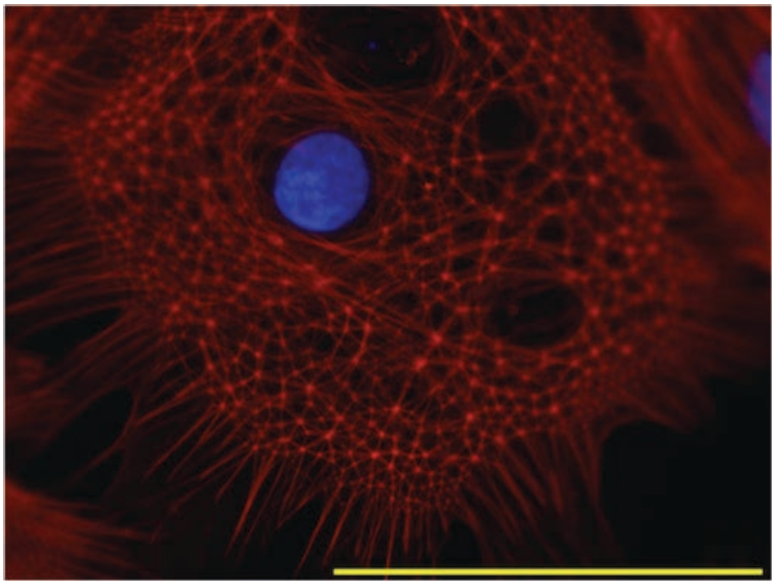

Figure 3.11 - Example of Geodesic Dome Cytoskeleton Structure Observed in a Small Percentage of MSCs on Smooth PCL: Scale bar = 100 μm.

MSC populations from the Wistar and Sprague-Dawley rats had similar shape factors, but covered different surface areas, with the Sprague-Dawley MSCs being the larger of the two cell types. A table of approximated shape factors and surfaces areas for MSCs from both rats can be found in **Appendix 3.1**. The difference in cell size is not surprising, provided the interspecies variability in MSC populations. While there were

measureable differences in MSC size, the morphological response to the separate PCL nanotopographies remained much the same.

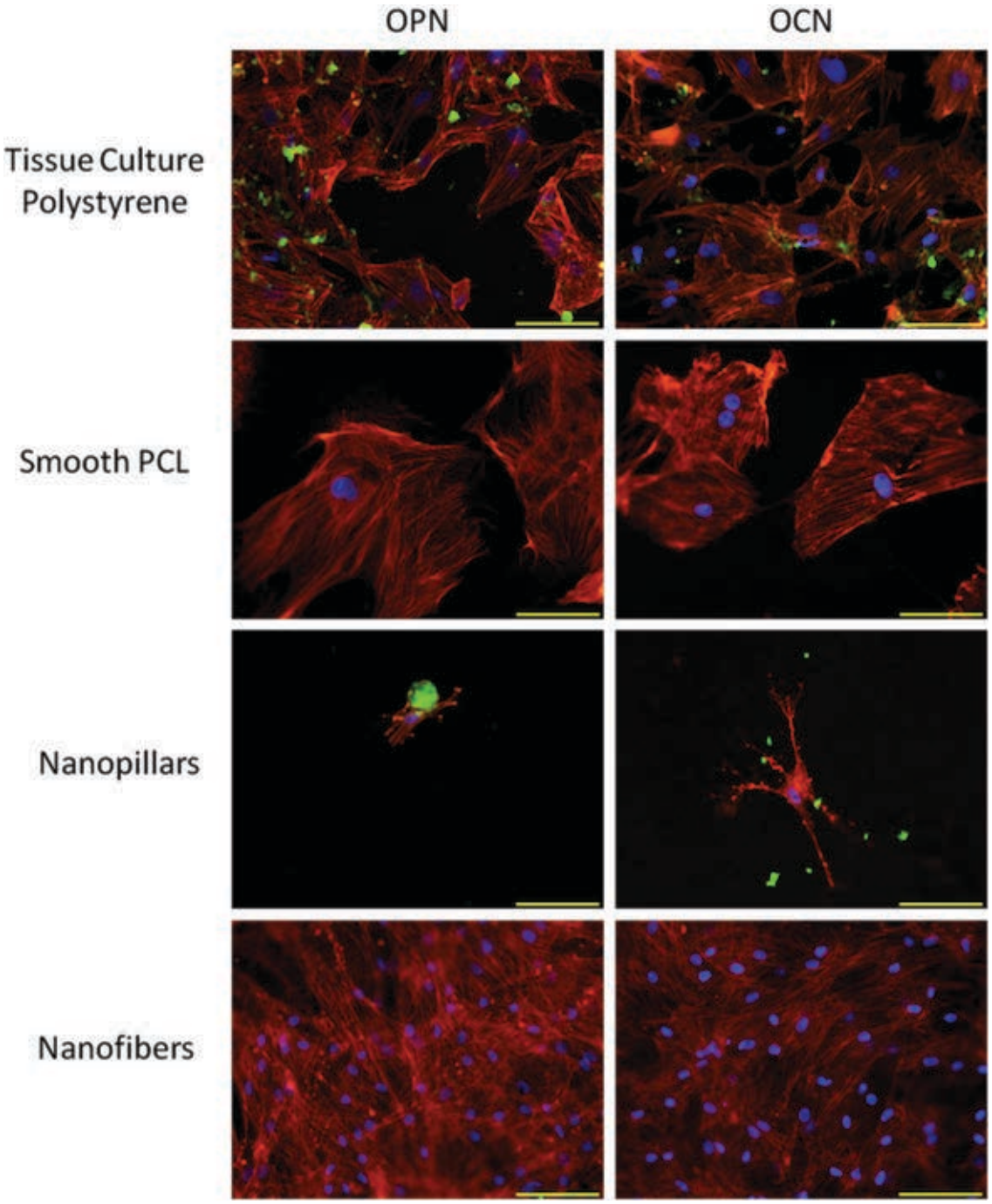

Figure 3.12 - Osteogenic Response of Sprague-Dawley MSCs after Four Weeks: Immunofluorescence images of MSCs after 4 weeks of culture on tissue culture polystyrene and smooth, nanopillar, and nanofiber PCL surfaces. Scale bar = 100 μm, blue = nucleus, red = actin filaments, geen = osteopontin/osteocalcin.

Following four weeks in culture, MSCs on the positive controls showed signs of osteogenic differentiation as a result of their production of two bone marker proteins, osteopontin and osteocalcin, detected by immunofluorescence. More importantly, MSCs on nanopillar surfaces also appeared to produce both osteocalcin and osteopontin, providing strong evidence for PCL nanopillar induced differentiation **(Figure 3.12)**. While the majority of osteocalcin and osteopontin observed on nanopillar samples appeared to be released and adsorbed onto the polymer surface, several cells were imaged containing internal osteopontin and osteocalcin, implying active protein production **(Figure 3.13)**. Further, the osteogenic response to nanopillars was not specific to one rat species, as MSCs from both rats positively stained for both bone proteins **(Figure 3.14)**. Neither MSCs on smooth PCL, nor those on nanofibers showed convincing signs of osteogenic differentiation in either rat species.

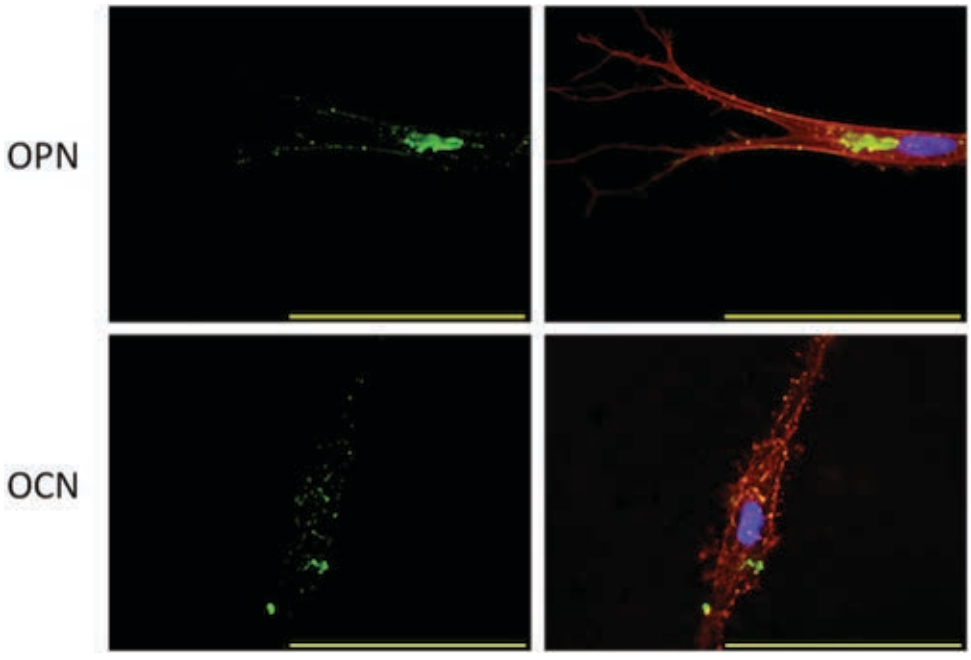

Figure 3.13 - Internal Bone Marker Production in Sprague-Dawley MSCs on PCL Nanopillars: Immunofluorescence images of MSCs after 4 weeks of culture on PCL nanopillar surfaces. Scale bar = 100 µm, blue = nucleus, red = actin filaments, geen = osteopontin/ osteocalcin

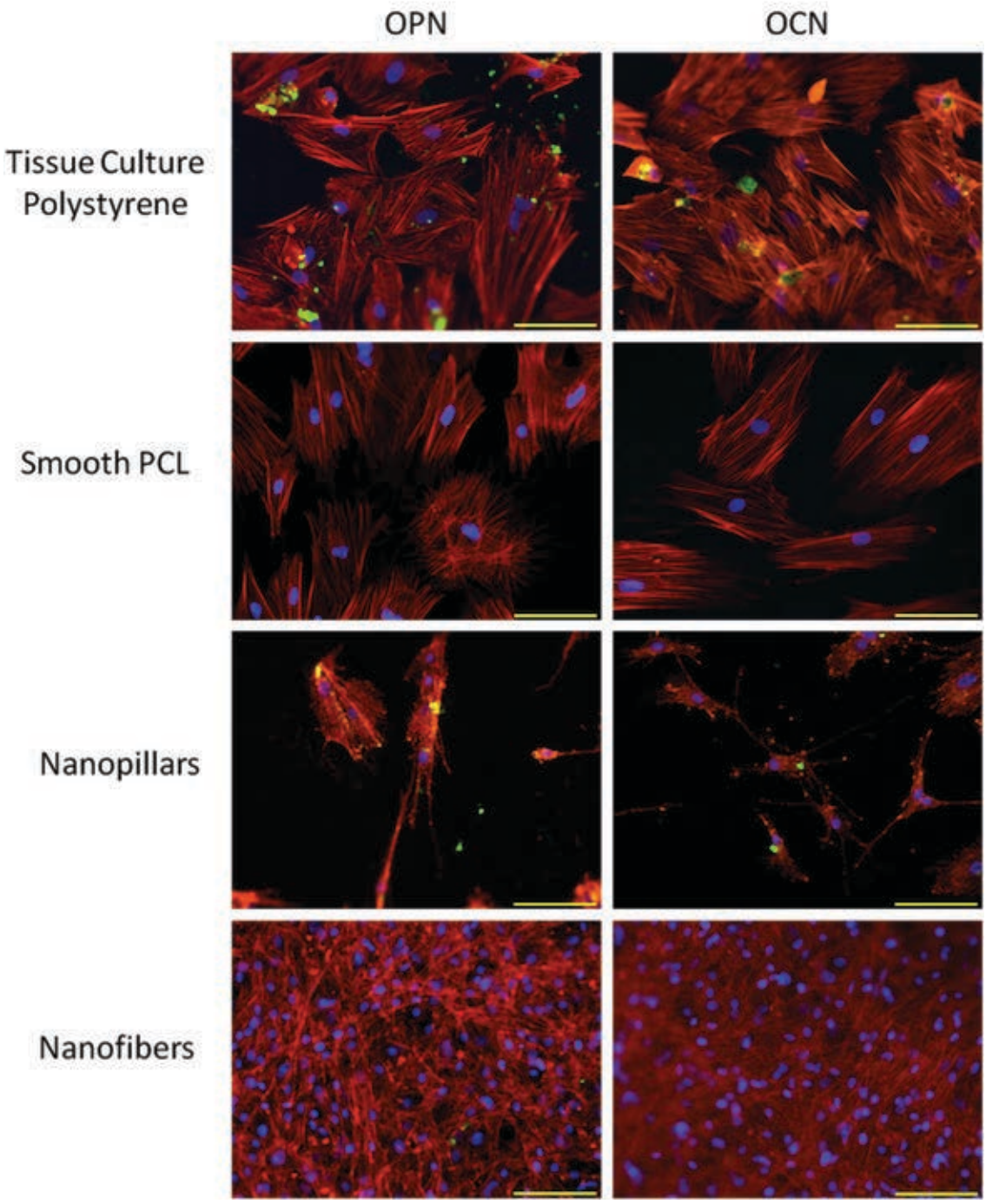

Figure 3.14 - Osteogenic Response of Wistar MSCs after Four Weeks: Immunofluorescence images of MSCs after 4 weeks of culture on tissue culture polystyrene and smooth, nanopillar, and nanofiber PCL surfaces. Scale bar = 100 μm, blue = nucleus, red = actin filaments, geen = osteopontin/osteocalcin.

SEM images of MSCs on nanopillar and nanofiber samples after four weeks offer an alternative to the immunofluorescent images. The contrasting cellular densities and

morphologies are clearly visible on the two different samples **(Figure 3.15)**. Elongation of MSCs on nanopillars is further evident in the SEM images, with higher magnifications revealing cellular projections interacting with individual nanopillars (see arrows). On the other hand, single MSCs are indistinguishable on nanofiber surfaces; the cells appear to form a consistent layer of dense tissue covering the majority of the surface. However, higher magnification images of breaks in the upper cell layer reveal a layer of MSCs underneath (see arrows). Further, confocal microscopy imaging of nanofiber samples revealed the penetration of MSCs to be on the order of 10 μm (data not shown).

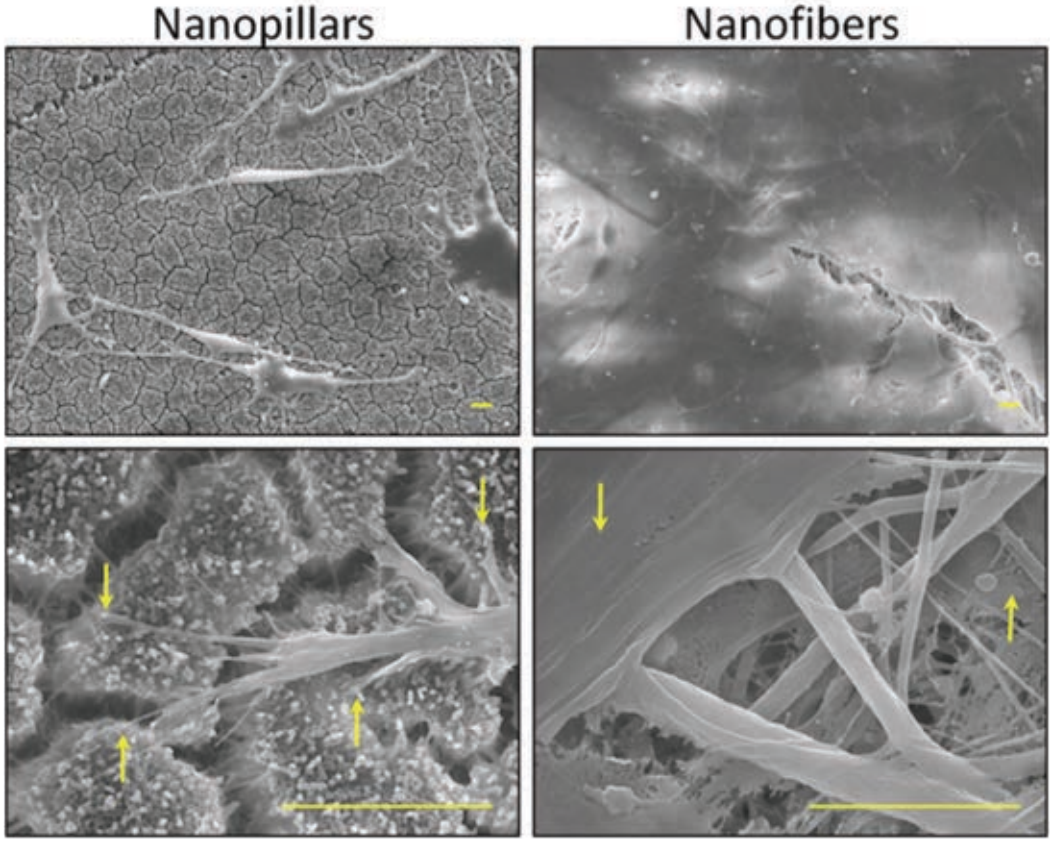

Figure 3.15 - Wistar MSCs after Four Weeks: Top Row- Low magnification SEM images of MSCs on PCL nanopillars and nanofibers (500x). **Bottom Row-** Higher magnification SEM images (5,000x) showing MSCs interacting with surface nanotopography. Scale bar = 10 μm.

Energy dispersive X-ray spectroscopy (EDX) was utilized in conjunction with the SEM to assess the degree of mineralization on the positive controls and PCL nanopillar

surfaces. SEM images revealed a substantial degree of mineralized cells on the positive control samples, and the EDX results from the positive controls revealed the presence of both calcium and phosphorous, the two primary components of hydroxyapatite, which comprises the inorganic portion of bone tissue **(Figure 3.16)**. Surprisingly, there was no evidence of mineralization on any of the PCL nanopillar surfaces. Following an additional six week study of rat MSCs on PCL nanopillars, calcium nor phosphorous was detected, raising some concerns (data not shown). The EDX data suggests that while PCL

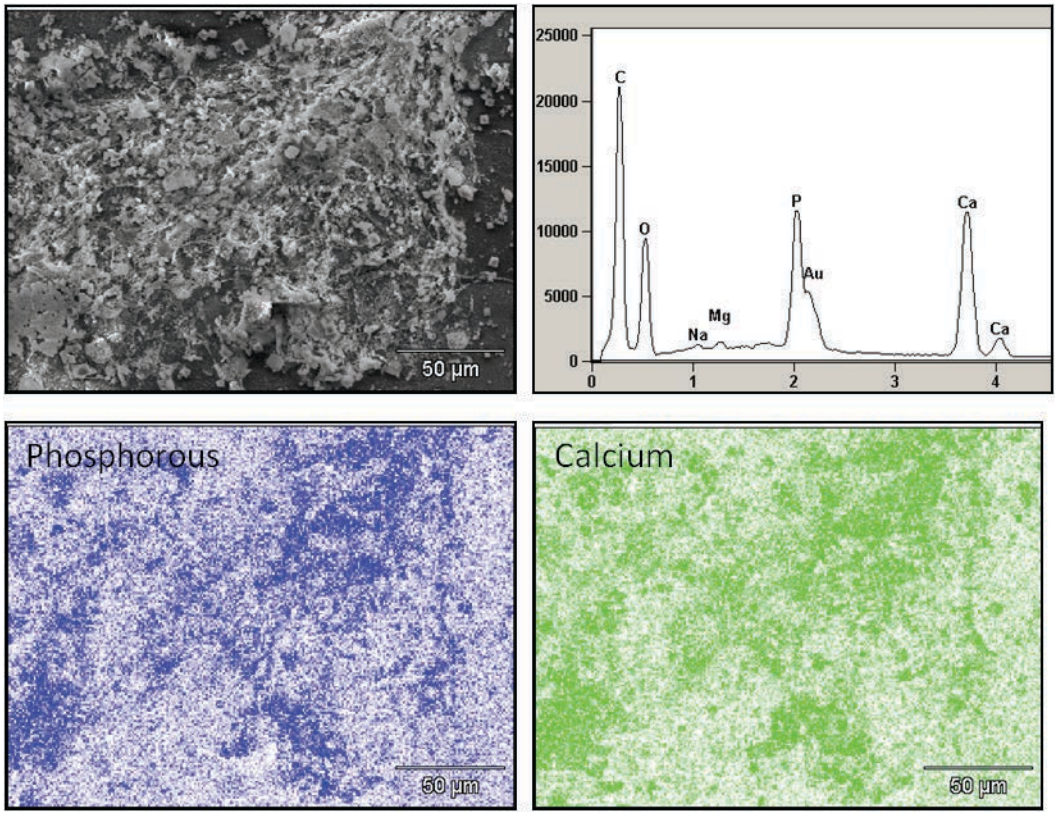

Figure 3.16 - EDX Results Showing Mineralization on Positive Control Samples

nanopillars cause MSCs to appear stretched and contracted in morphology and up-regulate two bone marker proteins, the surface is not sufficient enough to induce biomineralization. It is possible that the nanopillar topography is only capable of initiating one component of osteogenic differentiation, and the process of mineralization

requires additional signaling. Further, maybe the requisite amount of phosphate was not satisfied by the use of normal expansion media. For example, our collaborators report that ascorbic acid and β-glycerophosphate is required to form a hydroxyapatite-rich mineralized matrix in vitro[144].

This work provides the first known example of MSC differentiation into osteoblast-like cells induced solely by a non-ordered, non-rigid PCL nanopillar surface. Very recently, MSCs have shown signs of bone differentiation in the absence of differentiation media when seeded on PCL with a disordered nanopit topography[145]. Similar to this and other studies aimed at controlling progenitor cell fate using nanotopography, MSCs on PCL nanopillars adopt highly elongated and contracted appearances. While still in its infancy, the current hypothesis suggests that nanopillar surfaces on the order of 100-250 nm in diameter drive osteogenesis by subjecting MSCs to increased intracellular tension. Vinculin clustering at focal adhesion sites is correlated with increased myosin II tension in the cytoskeletal networks of these cells[146], and evidence of vinculin clustering on the tops of nanopillars and the contracted appearance of adhered MSCs supports this hypothesis. Further, it has been suggested that an extracellular matrix protein contained within fetal bovine serum, vitronectin, plays a pivotal role in the binding of MSCs to PCL surfaces[147]. Given vitronectin's role in inducing osteogenesis through the focal adhesion kinase (FAK) pathway[148] and the decreased protein adsorption seen on titania nanotubes >70nm, resulting in increased MSC elongation and osteogenesis[61], it is possible that a combination of both observations contribute to PCL nanopillar induced differentiation of rat MSCs into osteoblast-like cells. The nanopillar topography may result in limited locations for vitronectin

adsorption, requiring MSCs to stretch over long distances to adhere to the surface. The subsequent elongation and generation of intracellular tension/FAK signaling likely plays a major role in topography induced osteogenesis. Interestingly, this response was not observed on the nanofiber surfaces, implying that horizontally oriented topographies, while excellent for cellular proliferation and adherence, do not affect cell shape and thus cellular fate in a manner similar to nanopillars.

Conclusions and Suggestions for Future Work

The work presented in this thesis explores the differentiation of multipotent mesenchymal stromal cells into osteoblasts using a combination of bioinformatics and experimental methods. Affymetrix DNA microarrays, provided by our experimental collaborators from UPenn, were utilized on two separate fronts: to examine the genome wide changes that occur within marrow derived hMSCs in response to two different doses of BMP6, a suboptimal and osteogenic concentration, and to determine what effects the abrogation of the master transcription factor, osterix, has on transcripts which are actively involved in the differentiation process. Apart from the DNA microarray analyses, bench top experimental work involving the cellular response of rat MSCs to two very different polymer nanotopographies was conducted to determine if PCL nanopillars or nanofibers were capable of inducing osteogenesis in the absence of bone differentiation media.

The BMP6 DNA microarray analysis reveals a plausible explanation for the failed osteogenic differentiation of hMSCs in response to suboptimal concentrations (2nM) of BMP6. Novel findings within the microarray data support the notion that negative regulators of BMP signaling play a major role in the suppression of osteogenic signals at low BMP6 doses. For example the most up-regulated bone related transcripts in response to 2nM BMP6 were antagonists of the BMP signaling pathway and several of the significantly overrepresented biological processes within the up-regulated genes play negative roles in cellular differentiation and development. The genome wide changes in

expression support this hypothesis as more genes were affected at the earlier time point and the overall expression of the BMP6 responsive genes was drastically reduced by the later time point.

When hMSCs were provided with a ten-fold increase in BMP6 concentration (20nM), osteogenic differentiation was apparent. Transcription factors deemed vital to bone formation were activated, bone marker proteins were up-regulated, and the genome wide changes in gene expression suggest long-term genetic change. While many of the same negative regulators of BMP6 signaling were up-regulated, they were not up-regulated to the extent seen at the lower dose. Additionally, unlike the majority of bone related genes differentially expressed in response to 20nM BMP6, the negative regulators had smaller fold changes in expression at the later time point relative to the control samples. Taken together, this suggests that the negative regulators of BMP signaling may establish a threshold concentration for BMP, which must be surpassed to trigger a differentiation event. Further, the DNA microarray data also suggests that members of the Wnt receptor signaling pathway may play a major role in promoting osteogenesis, as many more Wnt related genes were differentially expressed in response to 20nM BMP6. This is not surprising, as recent work has discovered both BMP and Wnt transcription factor binding elements within the promoter regions of DLX5 and RUNX2[97], master regulators of osteogenesis upstream of OSX. The fact that DLX5 was up-regulated in response to 2nM BMP6 and not RUNX2 suggests that the BMP-Wnt crosstalk may be more important for RUNX2's activation.

Given the limited data, the response of MSCs to BMP6 needs to be explored in greater detail. There are several directions for future work which may be able to further

elucidate the response observed in the microarray data. It would be ideal to first determine if the observed response is seen across hMSCs form multiple individuals. This doesn't necessarily imply that additional DNA microarrays be performed, as the results from this analysis have provided ample transcripts of interest for detection using less expensive means. RT-PCR could be used to determine if the expression of negative regulators is consistent across several populations of MSCs, with disproportional activation at lowered BMP6 concentrations.

Another approach would utilize the construction and analysis of a computational model, based on a system of differential equations describing the reaction network involved in the transmission of signals from BMP ligands to the accumulation of transcription factors within the nucleus. The addition of negative feedback loops via the insertion of BMP antagonists into the model may help to assess the feasibility of our proposed hypothesis. Extracellular antagonists, such as gremlin, and intracellular inhibitory molecules, such as the I-Smads, could be introduced into the model to determine what type of negative regulation terminates the signal from the BMP ligands most efficiently. The ultimate goal of the modeling would be to show negative regulatory molecules to successfully abrogate BMP signaling at a baseline dose, yet fail to inhibit signaling with a ten-fold increase.

The negative feedback loop which has the greatest affect on dampening BMP signaling computationally could then be translated into the foundation for future experimental work. For example, if the external BMP antagonists were shown to have the greatest negative regulatory role in BMP signaling, they could be used as proposed targets for future knockout studies. The goal of such a study would be to compare

different BMP6 doses to determine if the knockout cells respond favorably to lower levels of BMP6.

DNA microarray data from the osterix knockout experiment confirmed some previously reported functions of the master bone regulator, as well as presents additional functional roles for OSX which have not yet been described. OSX's role in the activation of proteoglycans involved with biomineralization was recently reported by our collaborators. OSX over expression and knockout experiments up-regulated and down-regulated osteomodulin, osteoglycin, and asporin respectively[149]. The -OSX microarray data analyzed here supports that finding, with the additional OSX driven up-regulation of alkaline phosphatase. It has also been well established that OSX plays a role in the inhibition of cellular proliferation, both observed experimentally in cell proliferation assays[149] and linked to the inhibition of the Wnt receptor signaling pathway through the up-regulation of the Wnt antagonist DKK1[138]. Again, the -OSX microarray data supports these findings as OSX appeared to not only up-regulate DKK1, but other negative regulators of the Wnt pathway, including FRZB and TLE1. Further, the regulation of cellular proliferation was the most overrepresented biological process among the transcripts which were down-regulated in the knockout hMSCs.

Other functions of OSX which haven't been described include the down-regulation of matrix metalloproteinases responsible for cartilage breakdown, supporting the notion that one of OSX's main roles is the transition from a state of cartilage resorption to biomineralization. Therefore, the expression of OSX appears to be integrally involved in the complex process of endochondral ossification, as previously reported[128], whereby a cartilaginous precursor skeleton is broken down, remodeled, and

eventually mineralized to form bony tissue. OSX activation has also been shown to prevent chondrogenic differentiation of MSCs[128,114], and the repression of MMP13 could provide a plausible mechanism[127]. OSX induced repression of the collagenases may not occur in a direct manner, as the microarray data suggests that OSX activates an MMP inhibitor, alpha-2-macroglobulin, as well.

The -OSX microarray data also implicates OSX in the down-regulation of osteoprotegerin and genes involved in hyaluronic acid synthesis and regulation. The repression of OPG leads to an increase in osteoclastogenesis, and indicates that OSX may be important not only for anabolic bone activity, but catabolic activity as well. Again, it is unclear from the data if OPG is down-regulated directly by OSX, or if it occurs indirectly through the inhibition of the Wnt receptor signaling pathway[113] via DKK1[138]. Additionally, OSX may activate genes to reinforce its own expression through a series of positive feedback loops. Both BMP2 and DLX5, inducers of osteogenesis and OSX, appear to be up-regulated by OSX.

Reassuringly, many of the transcripts identified as being potential targets for activation and repression by OSX can be confirmed by looking at the 20nM BMP6 data. Case in point, OSX expression increases from 26-fold at day 4 to over 300-fold at day 10. During this period, the fold-changes relative to the control arrays of BMP2, DLX5, ASPN, OGN, ALPL, A2M, FRZB, TLE1, and DKK1 all increase, while they decrease amongst MMP1, MMP13, and OPG **(Table 4.1)**. Follow-up work regarding the functional roles of OSX should be conducted, specifically using RT-PCR to confirm the novel relationships between OSX and the observed differentially expressed genes within the microarray analysis.

Table 4.1 - 20nM BMP6 Microarray Data Confirms Majority of OSX Functional Roles Detected in the OSX Knockout Microarray Data

Probe Set	Gene	Accension	4 Day Control	4 Day 2nM BMP6	4 Day Fold Change	10 Day Control	10 Day 2nM BMP6	10 Day Fold Change
Osterix Expression								
1552340_at	**OSX**	NM_152860	35.92	945.41	**26.32**	13.26	4440.75	**334.92**
Involved in ECM Biomineralization								
224396_s_at	**ASPN**	AF316824	165.65	205.28	**1.24**	2507.84	11963.25	**4.77**
205908_s_at	**OMD**	NM_005014	22.89	2015.28	**88.05**	224.85	10297.54	**45.8**
218730_s_at	**OGN**	NM_014057	35.87	40.26	**1.12**	359.29	1587.04	**4.42**
215783_s_at	**ALPL**	X14174	325.8	606.48	**1.86**	543.02	3370.06	**6.21**
Involved with the Inhibiton of the Wnt Receptor Signaling Pathway								
203697_at	**FRZB**	U91903	96.42	171.7	**1.78**	126.45	639.92	**5.06**
204602_at	**DKK1**	NM_012242	2543.3	5093.18	**2**	1878.85	6050.36	**3.22**
228284_at	**TLE1**	BE302305	203.49	451.54	**2.22**	218.93	779.03	**3.56**
Involved with Collagen Matrix Degradation								
205959_at	**MMP13**	NM_002427	29.31	425.76	**14.53**	95.04	430.62	**4.53**
204475_at	**MMP1**	NM_002421	203.44	176.47	**-1.15**	490.94	230.37	**-2.13**
217757_at	**A2M**	NM_000014	214.83	211.29	**-1.02**	177.83	499.13	**2.81**
Potentiators of OSX Expression								
205289_at	**BMP2**	AA583044	47.66	195.41	**4.1**	159.95	778.19	**4.87**
213707_s_at	**DLX5**	NM_005221	311.68	2245.67	**7.2**	357.93	3037.97	**8.49**
Inhibition of Osteoclastogenesis								
204932_at	**OPG**	BF433902	10329.04	6030.78	**-1.71**	10241.18	1701.96	**-6.02**

Experimental work with MSCs resulted in some exciting findings. Nanotopography induced osteogenesis in the absence of bone differentiation media was investigated by seeding bone derived rat MSCs on two different PCL surfaces which have been previously shown to support increased osteoblastic activity when provided soluble osteoinducers[55,56]. PCL nanopillars and nanofibers supported very different cellular responses. MSCs on the vertically oriented nanopillars adhered poorly, but they adopted contracted and elongated cellular shapes; after four weeks of culture in normal growth media, MSCs showed positive signs of osteogenesis, including the production of two proteins indicative of bone formation, osteocalcin and osteopontin. This is the first known example of nanotopography induced osteogenesis on a PCL nanopillar surface. In contrast, PCL nanofibers did not appear to drive osteogenic differentiation. However,

MSCs seeded on nanofibers showed significantly enhanced proliferation and cellular embedment within the porous nanostructure. Smooth surfaces resulted in the uniform spreading of MSCs, covering large surface areas, but again, no osteogenesis was observed.

Options for future avenues of work related to this project are plentiful. While MSCs on PCL nanopillars produced bone marker proteins, there was no mineralization detected through EDX. Additional techniques used to substantiate mineralization by other researchers include the use of Alizarin red and Von Kossa staining to detect for calcium and phosphate. The use of mineral staining may prove more advantageous to EDX, which can be obscured by the elemental composition of the bulk material, and would aid in confirming the presence of lack of the inorganic bone constituents. It was shown that MSCs had the poorest adherence on nanopillars, thus future studies could examine why this is the case. It may be possible to alter the aspect ratio of the nanopillars to increase cellular adherence, while maintaining the osteogenic inducing properties of the surfaces.

Along those same lines, protein adsorption was never addressed in this study. The type, number, and distribution of surface bound proteins is very important, as cells do not bind directly to the surface, but adhere to the proteins which are adsorbed from the serum containing media. Surfaces which allow for increased overall protein adsorption tend to facilitate the uniform spreading of MSCs and are not supportive of osteogenesis[61]. It would be very interesting to see the protein adsorption patterns that different nanopillar topographies impart. Future work could isolate the most osteoinductive surface, within a broad range of nanopillar dimensions, and focus solely on the protein types and patterns that the surface pulls out of serum. By replicating the protein patterns observed on the

nanosurfaces, it may be possible to drive osteogenesis without the aid of nanotopography, solely based upon protein island size and distribution.

For example, the protein vitronectin is preferentially adsorbed onto PCL surfaces[147], and it has been shown to facilitate osteogenesis primarily through the FAK signaling pathway[148]. The FAK has been implicated in topography driven osteogenic differentiation, as it is associated with the activation of the Rho-ROCK signaling cascade and the downstream activation of RUNX2 via extracellular signal-related kinase (ERK)[150,151]. Hence, distinct protein patterning of vitronectin may allow for marked improvements in surface driven osteogenesis. The proliferative nature of PCL nanopillars is also worth further investigation. No conclusion can be drawn from the present study in terms of the increased proliferation rates, as the MSCs on standard tissue culture polystyrene were provided with bone differentiation media, which negatively affects proliferation. Future studies could determine if nanofiber topographies are capable of enhancing cellular proliferation over standard expansion methods.

Multipotent mesenchymal stromal cells have the potential to revolutionize modern medicine by supporting tissue regeneration. There will be a day in our future when the treatment of degenerative diseases with MSCs will be routine practice. The knowledge obtained from this present work may help to further elucidate the complex regulation of the genetic changes and surface environments required for successful differentiation of MSCs into fully functioning osteoblasts.

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LIST OF APPENDICES

Appendix 1.1 Up-Regulated Genes in Response to 2nM BMP6

Up-Regulated Genes at Both Days in Response to 2nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
208937_s_at	ID1: inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	D13889	121.29	4504.84	37.14	25.08	4383.56	*	267.43	3273.8	12.24	9.45	3006.37	*
214597_at	SSTR2: somatostatin receptor 2	BC000256	122.72	7.29	-16.84	-6.31	-115.44	*	12.71	121.85	9.59	4.02	109.15	*
224646_x_at	H19: H19, imprinted maternally expressed transcript (non-protein coding)	BF569051	92.72	1052.51	11.35	8.53	959.79	*	275.86	1958.8	7.1	6.17	1682.94	*
224997_x_at	H19: H19, imprinted maternally expressed transcript (non-protein coding)	AL575306	62.42	648.66	10.39	8.27	586.25	*	162.99	1037.65	6.37	5.47	874.66	*
205679_x_at	ACAN: aggrecan	NM_013227	628.14	3224.41	5.13	4.04	2596.27	*	504.84	2736.75	5.42	4.09	2231.91	*
207692_s_at	ACAN: aggrecan	NM_001135	610.85	2815.09	4.61	3.65	2204.24	*	485	2508.15	5.17	3.88	2023.15	*
223541_at	HAS3: hyaluronan synthase 3	AF232772	99.32	590.4	5.94	4.43	491.07	*	86.88	447.12	5.15	3.85	360.24	*
235504_at	GREM2: gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	BE786990	26.95	141.61	5.26	2.81	114.67	*	31.39	148.35	4.73	2.87	116.96	*
234880_x_at	KRTAP1-3: keratin associated protein 1-3	X63338	304.66	667.15	2.19	1.98	362.49	*	60.78	279.7	4.6	3.47	218.92	*
208650_s_at	CD24: CD24 molecule	BG327863	156.75	299.47	1.91	1.6	142.72	*	149.2	685.62	4.6	4.23	536.42	*
227307_at	TSPAN18: Tetraspanin 18	AL565381	71.08	230.86	3.25	2.71	159.78	*	109.23	482.14	4.41	3.89	372.91	*
240509_s_at	GREM2: gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	BF064262	15.32	118.49	7.73	4.49	103.17	*	46.36	192.53	4.15	3.18	146.17	*
220794_at	GREM2: gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	NM_022469	112.67	525.09	4.66	3.64	412.42	*	114.83	472.65	4.12	3.6	357.82	*
210881_s_at	IGF2 /// INS-IGF2: insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	M17863	93.74	590.55	6.3	4.77	496.82	*	132.89	537.53	4.04	3.35	404.63	*
228890_at	ATOH8: atonal homolog 8 (Drosophila)	BF434995	89.76	946.65	10.55	6.48	856.89	*	104.19	391.96	3.76	2.43	287.77	*
202410_x_at	IGF2 /// INS-IGF2: insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	NM_000612	188.67	1039.98	5.51	4.56	851.31	*	272.18	1013.31	3.72	3.12	741.13	*
213931_at	ID2 /// ID2B: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)	AI819238	188.07	749.22	3.98	3.51	561.15	*	70.14	240.29	3.43	2.7	170.15	*
209291_at	ID4: inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AW157094	611.75	2841.04	4.64	4.26	2229.29	*	455.18	1553.37	3.41	3.11	1098.19	*
207826_s_at	ID3: inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	NM_002167	1429.73	8519.96	5.96	5.03	7090.22	*	1717.39	5798.57	3.38	2.68	4081.18	*
209292_at	ID4: Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AL022726	105.74	499.47	4.72	3.97	393.73	*	86.67	285.2	3.29	2.79	198.53	*
205907_s_at	OMD: osteomodulin	AI765819	60.11	176.37	2.93	2.28	116.26	*	697.79	2243.46	3.22	2.85	1545.67	*
207147_at	DLX2: distal-less homeobox 2	NM_004405	87.03	432.98	4.98	3.73	345.95	*	61.22	196.37	3.21	2.31	135.15	*
219743_at	HEY2: hairy/enhancer-of-split related with YRPW motif 2	NM_012259	47.61	191.01	4.01	2.97	143.4	*	117.58	376.3	3.2	2.67	258.72	*
209293_x_at	ID4: inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	U16153	656.69	2883.31	4.39	4.01	2226.62	*	592.66	1695.55	2.86	2.55	1102.89	*
207388_s_at	PTGES: prostaglandin E synthase	NM_004878	65.04	283.63	4.36	2.91	218.58	*	92.24	238.99	2.59	2	146.75	*
221541_at	CRISPLD2: cysteine-rich secretory protein LCCL domain containing 2	AL136861	375.66	772.4	2.06	1.74	396.73	*	189.52	475.55	2.51	1.94	286.02	*
227719_at	SMAD9: SMAD family member 9	AA934610	328.57	1463.21	4.45	3.88	1134.64	*	404.8	963.66	2.38	2.14	558.86	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
207069_s_at	SMAD6: SMAD family member 6	NM_005585	298.92	920.71	3.08	2.49	621.78	*	355.81	809.88	2.28	1.93	454.07	*
213707_s_at	DLX5: distal-less homeobox 5	NM_005221	311.68	708.81	2.27	1.93	397.13	*	357.93	803.63	2.25	2.03	445.7	*
218353_at	RGS5: regulator of G-protein signaling 5	NM_025226	270.87	580.19	2.14	1.9	309.32	*	251	565.93	2.25	2.08	314.93	*
210367_s_at	PTGES: prostaglandin E synthase	AF010316	310.92	1099.52	3.54	3.06	788.59	*	514.64	1108.57	2.15	1.88	593.94	*
201565_s_at	ID2: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_002166	2551.34	8078.27	3.17	2.49	5526.92	*	2099.33	4516.89	2.15	1.7	2417.56	*
217511_at	KAZALD1: Kazal-type serine peptidase inhibitor domain 1	W28828	112.71	276.23	2.45	1.98	163.53	*	201.2	426.79	2.12	1.82	225.6	*
202409_at	IGF2 /// INS-IGF2: insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	X07868	1166.86	3465.76	2.97	2.43	2298.9	*	1796.4	3765.12	2.1	1.81	1968.72	*
209071_s_at	RGS5: regulator of G-protein signaling 5	AF159570	582.11	1243.4	2.14	1.99	661.29	*	474.59	972.39	2.05	1.76	497.8	*
218934_s_at	HSPB7: heat shock 27kDa protein family, member 7 (cardiovascular)	NM_014424	653.9	2132.46	3.26	3.01	1478.56	*	613.1	1249.14	2.04	1.82	636.05	*
230424_at	C5orf13: chromosome 5 open reading frame 13	AU144860	788.6	1293.45	1.64	1.54	504.85	*	289.08	580.94	2.01	1.8	291.86	*
235238_at	SHC4: SHC (Src homology 2 domain containing) family, member 4	BF676462	166.5	295.9	1.78	1.51	129.4	*	120.28	238.64	1.98	1.7	118.36	*
209070_s_at	RGS5: regulator of G-protein signaling 5	AI183997	462.99	918.23	1.98	1.79	455.24	*	422.68	830.28	1.96	1.74	407.6	*
201566_x_at	ID2: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	D13891	1403.48	4745.16	3.38	3.01	3341.67	*	1218.67	2350.05	1.93	1.75	1131.37	*
214767_s_at	HSPB6: heat shock protein, alpha-crystallin-related, B6	AL551046	299.12	1278.22	4.27	3.96	979.1	*	262.72	505.58	1.92	1.68	242.85	*
219729_at	PRRX2: paired related homeobox 2	NM_016307	427.89	1500.3	3.51	2.62	1072.41	*	816.16	1564.84	1.92	1.64	748.68	*
220976_s_at	KRTAP1-1: keratin associated protein 1-1	NM_030967	504.72	981.46	1.94	1.73	476.74	*	184.96	342.11	1.85	1.52	157.15	*
223321_s_at	FGFRL1: fibroblast growth factor receptor-like 1	AF312678	417.52	991.17	2.37	1.91	573.65	*	529.68	962.95	1.82	1.55	433.28	*
233533_at	KRTAP1-5: keratin associated protein 1-5	AJ406928	983.51	2060.08	2.09	2	1076.58	*	482.93	858.31	1.78	1.63	375.38	*
234951_s_at	COL12A1: collagen, type XII, alpha 1	AL080250	408.38	795.29	1.95	1.68	386.92	*	508.2	899.45	1.77	1.61	391.25	*
209167_at	GPM6B: glycoprotein M6B	AI419030	135.11	250.97	1.86	1.6	115.86	*	420.45	739.76	1.76	1.65	319.31	*
235944_at	HMCN1: hemicentin 1	BF446673	1949.78	3239.55	1.66	1.56	1289.77	*	1524.33	2683.85	1.76	1.64	1159.52	*
216269_s_at	ELN: elastin	M24782	69.99	216.87	3.1	2.7	146.88	*	475.65	829.99	1.74	1.66	354.34	*
203886_s_at	FBLN2: fibulin 2	NM_001998	319.35	1110.49	3.48	3.04	791.14	*	580.28	975.27	1.68	1.52	394.99	*
204223_at	PRELP: proline/arginine-rich end leucine-rich repeat protein	NM_002725	368.5	667.99	1.81	1.55	299.49	*	3263.61	5355.41	1.64	1.55	2091.81	*
206331_at	CALCRL: calcitonin receptor-like	NM_005795	208.24	365.09	1.75	1.53	156.84	*	494.2	805.36	1.63	1.53	311.15	*
230290_at	SCUBE3: signal peptide, CUB domain, EGF-like 3	BE674338	2075.47	3446.39	1.66	1.57	1370.92	*	1493.85	2427.22	1.62	1.52	933.36	*

Up-Regulated Genes at Day 4 in Response to 2nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
1558706_a_at	ATOH8: Atonal homolog 8 (Drosophila)	AL831857	15.89	131.96	8.3	4.37	116.07	*	17.12	58.97	3.44	1.58	41.85	
232133_at	ADAMTS10: ADAM metallopeptidase with thrombospondin type 1 motif, 10	AF163762	22.19	155.14	6.99	3.84	132.95	*	29.01	55.76	1.92	1.14	26.75	
215066_at	PTPRF: protein tyrosine phosphatase, receptor type, F	AU158443	20.12	133.35	6.63	3.21	113.24	*	7.19	17.3	2.41	0.7	10.11	
219058_x_at	TINAGL1: tubulointerstitial nephritis antigen-like 1	NM_022164	35.94	229.81	6.39	4.91	193.87	*	59.55	103.9	1.74	1.08	44.35	
231798_at	NOG: noggin	AL575177	46.78	290.9	6.22	2.83	244.12	*	32.47	34.09	1.05	0	1.61	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
230308_at	FAM120AOS: family with sequence similarity 120A opposite strand	AI091434	42.6	220.17	5.17	2.64	177.57	*	31.77	41.87	1.32	0.22	10.1	
229655_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	N66656	28.26	134.97	4.78	2.92	106.7	*	74.49	110.98	1.49	1.23	36.48	
226933_s_at	LOC100287917: hypothetical protein LOC100287917	AV646610	52.41	246.9	4.71	3.65	194.49	*	54.3	130.3	2.4	1.91	76	
1560477_a_at	SAMD11: sterile alpha motif domain containing 11	AK054643	97.33	371.92	3.82	2.34	274.59	*	90.13	147.41	1.64	1.03	57.28	
202077_at	NDUFAB1: NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	NM_005003	4694.08	17777.49	3.79	2.57	13083.41	*	4943.82	4478.99	-1.1	-0.59	-464.83	
221658_s_at	IL21R: interleukin 21 receptor	AF269133	47.9	175.01	3.65	2.71	127.11	*	40.57	81.12	2	1.36	40.55	
223316_at	CCDC3: coiled-coil domain containing 3	AL136562	68.34	227.94	3.34	2.57	159.59	*	146.89	167.32	1.14	0.82	20.43	
223648_s_at	FGFRL1: fibroblast growth factor receptor-like 1	AF279689	70.46	235.1	3.34	2.95	164.64	*	70.1	149.28	2.13	1.78	79.18	
210702_s_at	PTGIS: prostaglandin I2 (prostacyclin) synthase	D38145	137.43	454.19	3.3	2.63	316.76	*	57	92.73	1.63	0.96	35.73	
209652_s_at	PGF: placental growth factor	BC001422	337.4	1109.55	3.29	2.75	772.15	*	112.27	195.82	1.74	1.16	83.55	
205384_at	FXYD1: FXYD domain containing ion transport regulator 1	NM_005031	73.74	235.63	3.2	2.04	161.89	*	227.6	241.32	1.06	0.86	13.72	
1568598_at	KAZALD1: Kazal-type serine peptidase inhibitor domain 1	BF434771	59.27	189.44	3.2	1.99	130.17	*	76.74	129.75	1.69	1.15	53	
234068_s_at	AP2A1: adaptor-related protein complex 2, alpha 1 subunit	AC006942	129.05	411.27	3.19	2.62	282.22	*	112.63	126.21	1.12	0.81	13.59	
212670_at	ELN: elastin	AA479278	1195.75	3655.26	3.06	2.33	2459.5	*	4663.03	5261.71	1.13	1.03	598.68	
231680_at	Hs.15504.0	R95741	87.51	267.75	3.06	2.59	180.24	*	151.51	167.37	1.1	1	15.86	
208534_s_at	LOC100132214 /// RASA4 /// RASA4P: similar to calcium-promoted Ras inactivator /// RAS p21 protein activator 4 /// RAS p21 protein activator 4 pseudogene	NM_006989	104.08	315.93	3.04	2.62	211.85	*	105.45	146.28	1.39	1.16	40.83	
211453_s_at	AKT2: v-akt murine thymoma viral oncogene homolog 2	M77198	60.37	182.3	3.02	2.06	121.93	*	195.6	189.92	-1.03	-0.87	-5.68	
1562926_at	Hs2.382017.1	BC033846	53.62	155.96	2.91	2.35	102.34	*	36.44	67.46	1.85	1.13	31.02	
223627_at	MEX3B: mex-3 homolog B (C. elegans)	AL136778	427.41	1223.91	2.86	2.42	796.49	*	255.91	345.23	1.35	1.08	89.32	
1552804_a_at	TIRAP: toll-interleukin 1 receptor (TIR) domain containing adaptor protein	NM_148910	105.7	302.02	2.86	2.17	196.32	*	105.13	201.63	1.92	1.28	96.5	
240355_at	Hs.156924.0	AI332373	61.59	175.16	2.84	1.94	113.56	*	116.76	113.32	-1.03	-0.87	-3.44	
213942_at	MEGF6: multiple EGF-like-domains 6	AL134303	339.87	958.31	2.82	2.54	618.43	*	243.14	358.35	1.47	1.27	115.21	
221204_s_at	CRTAC1: cartilage acidic protein 1	NM_018058	139	385.02	2.77	2.41	246.02	*	65.49	62.87	-1.04	-0.71	-2.62	
218814_s_at	TMEM206: transmembrane protein 206	NM_018252	67.16	184.76	2.75	1.8	117.6	*	147.25	58.84	-2.5	-1.68	-88.41	
211340_s_at	MCAM: melanoma cell adhesion molecule	M28882	1168.9	3190.89	2.73	2.56	2021.99	*	1521.72	2396.55	1.57	1.46	874.82	
209087_x_at	MCAM: melanoma cell adhesion molecule	AF089868	1057.15	2854.82	2.7	2.44	1797.67	*	1371.31	2093.52	1.53	1.43	722.21	
244340_x_at	Hs.292663.0	AW975183	401.24	1084.78	2.7	2.07	683.54	*	246.73	296.58	1.2	0.91	49.84	
204999_s_at	ATF5: activating transcription factor 5	BC005174	188.39	507.6	2.69	2.44	319.21	*	39.42	41.49	1.05	0.51	2.07	
221991_at	NXPH3: neurexophilin 3	AI937333	114.21	302.71	2.65	1.98	188.5	*	287.41	465.89	1.62	1.44	178.48	
216352_x_at	PCDHGA3: protocadherin gamma subfamily A, 3	AF152509	206.3	545.4	2.64	2.3	339.11	*	340.59	452.48	1.33	1.25	111.89	
1557002_x_at	ESPNL: espin-like	BC042051	157.39	413.31	2.63	2.32	255.91	*	274.36	209.32	-1.31	-1.18	-65.04	
228210_at	NXPH3: neurexophilin 3	T10030	119.52	311.44	2.61	1.96	191.92	*	240.51	276.26	1.15	1	35.75	
206746_at	BFSP1: beaded filament structural protein 1, filensin	NM_001195	98.05	252.89	2.58	1.85	154.84	*	97.7	183.76	1.88	1.41	86.06	
229840_at	IQSEC2: IQ motif and Sec7 domain 2	AW026036	109.44	281.59	2.57	2.2	172.15	*	139.17	137.53	-1.01	-0.87	-1.63	
204794_at	DUSP2: dual specificity phosphatase 2	NM_004418	82.96	212.04	2.56	2.19	129.08	*	214.71	206.56	-1.04	-0.96	-8.14	
1556103_at	Hs2.323409.1	AI453268	231.6	592.18	2.56	2.31	360.57	*	238.45	199.85	-1.19	-1.09	-38.6	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
214021_x_at	ITGB5: Integrin, beta 5	AI335208	241.81	614.45	2.54	2.39	372.63	*	209.28	170.96	-1.22	-1	-38.31	
217066_s_at	DMPK: dystrophia myotonica-protein kinase	M87313	350.01	882.72	2.52	2.38	532.72	*	234.69	364.31	1.55	1.4	129.62	
203523_at	LSP1: lymphocyte-specific protein 1	NM_002339	422.38	1060.5	2.51	2.19	638.12	*	1300.72	1591.71	1.22	1.17	290.99	
203793_x_at	PCGF2: polycomb group ring finger 2	NM_007144	334.28	829.08	2.48	2.22	494.8	*	281.32	251.06	-1.12	-1.01	-30.26	
1565002_at	Hs2.383783.1	AK000236	93.57	228.96	2.45	2.21	135.39	*	102.6	107.19	1.04	0.85	4.59	
218010_x_at	PPDPF: pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	NM_024299	272.09	656.53	2.41	2.24	384.45	*	268.3	362.53	1.35	1.17	94.24	
225345_s_at	Hs.6630.0	AU155376	175.14	414.9	2.37	2	239.76	*	79.01	68.44	-1.15	-0.73	-10.57	
230933_at	DSTN: Destrin (actin depolymerizing factor)	AA458636	228.11	540.66	2.37	1.98	312.55	*	284.17	432.01	1.52	1.31	147.84	
212336_at	EPB41L1: erythrocyte membrane protein band 4.1-like 1	AA912711	74.98	177.28	2.36	1.92	102.3	*	81.31	119.19	1.47	1.11	37.88	
1555894_s_at	MTSS1L: metastasis suppressor 1-like	AA829283	171.34	404.36	2.36	2.13	233.02	*	252.02	251	-1	-0.89	-1.02	
219456_s_at	RIN3: Ras and Rab interactor 3	AW027923	129.31	304.42	2.35	2.18	175.11	*	39.88	55.58	1.39	0.39	15.7	
200884_at	CKB: creatine kinase, brain	NM_001823	390.34	912.33	2.34	1.96	521.99	*	1684.63	2536.96	1.51	1.42	852.33	
213606_s_at	ARHGDIA: Rho GDP dissociation inhibitor (GDI) alpha	AI571798	497.14	1162.01	2.34	2.2	664.87	*	722.97	828.15	1.15	1.07	105.18	
226869_at	MEGF6: multiple EGF-like-domains 6	AI655611	1158.55	2706.08	2.34	2.19	1547.52	*	607.59	795.82	1.31	1.17	188.23	
243358_at	IGF1R: insulin-like growth factor 1 receptor	BF347362	78.15	180.81	2.31	1.91	102.66	*	72.11	39.25	-1.84	-1.11	-32.86	
214454_at	ADAMTS2: ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_014244	790.8	1821.66	2.3	2.07	1030.86	*	1066.32	1362.79	1.28	1.19	296.47	
217849_s_at	CDC42BPB: CDC42 binding protein kinase beta (DMPK-like)	NM_006035	1005.65	2308.3	2.3	2.11	1302.66	*	916.97	833.17	-1.1	-1.02	-83.8	
224321_at	TMEFF2: transmembrane protein with EGF-like and two follistatin-like domains 2	AB004064	88.74	203.93	2.3	2.04	115.19	*	77.17	155.9	2.02	1.66	78.72	
231183_s_at	JAG1: Jagged 1 (Alagille syndrome)	AI457817	491.19	1129.59	2.3	2.15	638.4	*	602.15	762.8	1.27	1.17	160.66	
203394_s_at	HES1: hairy and enhancer of split 1, (Drosophila)	BE973687	469.74	1071.16	2.28	2.08	601.43	*	367.4	490.74	1.34	1.15	123.34	
208927_at	SPOP: speckle-type POZ protein	BF673888	1649.42	3767.54	2.28	2.17	2118.12	*	1576.03	1477.71	-1.07	-0.99	-98.32	
241578_x_at	Hs.302839.0	BG151692	332.81	757.96	2.28	2.14	425.15	*	592.38	418.4	-1.42	-1.38	-173.98	
214265_at	ITGA8: integrin, alpha 8	AI193623	198.11	450.11	2.27	1.93	251.99	*	38.71	41.82	1.08	0.69	3.11	
39966_at	CSPG5: chondroitin sulfate proteoglycan 5 (neuroglycan C)	AF059274	197.15	447.5	2.27	2.14	250.35	*	129.7	136.19	1.05	0.97	6.49	
214520_at	FOXC2: forkhead box C2 (MFH-1, mesenchyme forkhead 1)	NM_005251	239.12	537.2	2.25	2.03	298.08	*	163.36	149.94	-1.09	-0.86	-13.42	
227347_x_at	HES4: hairy and enhancer of split 4 (Drosophila)	NM_021170	256.36	576.37	2.25	1.95	320.01	*	349	573.21	1.64	1.47	224.21	
242365_at	Hs.222110.0	AA921687	83.77	188.14	2.25	1.81	104.37	*	59.75	82.12	1.37	0.89	22.37	
204452_s_at	FZD1: frizzled homolog 1 (Drosophila)	AF072872	178.79	400.49	2.24	1.95	221.69	*	274.99	398.49	1.45	1.31	123.5	
214535_s_at	ADAMTS2: ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_021599	432.08	968.38	2.24	1.95	536.3	*	469.57	484.14	1.03	0.96	14.57	
216246_at	Hs.8102.2	AF113008	322.28	720.48	2.24	2.01	398.19	*	282.04	271.96	-1.04	-0.89	-10.08	
244457_at	Hs.221024.0	BF724206	156.57	349.42	2.23	1.73	192.85	*	118.06	69.78	-1.69	-1.15	-48.28	
1569473_s_at	ZNF783: zinc finger family member 783	BC041610	885.03	1975.69	2.23	2.08	1090.67	*	1396.52	1229.56	-1.14	-1.06	-166.96	
203426_s_at	IGFBP5: insulin-like growth factor binding protein 5	M65062	98.26	218.16	2.22	1.86	119.9	*	355.83	457.79	1.29	1.18	101.97	
204986_s_at	TAOK2: TAO kinase 2	NM_016151	171.47	380.29	2.22	1.9	208.81	*	342.63	278.15	-1.23	-1.08	-64.48	
223635_s_at	SSBP3: single stranded DNA binding protein 3	BC003605	139.01	308.59	2.22	1.84	169.58	*	140.97	149.05	1.06	0.88	8.07	
205937_at	CGREF1: cell growth regulator with EF-hand domain 1	NM_006569	201.97	446.49	2.21	2.04	244.53	*	724.67	825.77	1.14	1.09	101.11	
37424_at	CCHCR1: coiled-coil alpha-helical rod protein 1	AB029343	162.79	360.32	2.21	1.74	197.54	*	323.27	272.83	-1.18	-1.05	-50.44	
1560095_s_at	Hs2.355371.1	CA311143	115.7	255.34	2.21	1.7	139.64	*	289.25	274.2	-1.05	-0.96	-15.05	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
228683_s_at	KCTD15: potassium channel tetramerisation domain containing 15	AI925361	144.44	317.38	2.2	1.82	172.94	*	143.2	188.77	1.32	1.23	45.57	
1554091_a_at	TIRAP: toll-interleukin 1 receptor (TIR) domain containing adaptor protein	BC032474	192.6	421.8	2.19	1.55	229.2	*	267.48	240.11	-1.11	-0.95	-27.37	
203989_x_at	F2R: coagulation factor II (thrombin) receptor	NM_001992	1051.45	2294.5	2.18	1.94	1243.05	*	1742.06	1796.72	1.03	0.95	54.66	
1560738_at	Hs2.162408.1	BC041933	104.31	227.73	2.18	2	123.42	*	110.36	118.62	1.07	0.95	8.26	
239309_at	DLX6: distal-less homeobox 6	T65128	159.55	345.51	2.17	1.81	185.96	*	137.54	226.79	1.65	1.42	89.26	
244171_at	MKLN1: muskelin 1, intracellular mediator containing kelch motifs	AW505004	97.23	210.91	2.17	1.92	113.68	*	75.85	97.1	1.28	1.07	21.25	
37462_i_at	SF3A2: splicing factor 3a, subunit 2, 66kDa	L21990	354.09	764.83	2.16	1.99	410.73	*	402.21	372.01	-1.08	-1.02	-30.2	
37996_s_at	DMPK: dystrophia myotonica-protein kinase	L08835	461.36	996.69	2.16	2	535.34	*	256.02	410.55	1.6	1.44	154.53	
209280_at	MRC2: mannose receptor, C type 2	U58856	192.78	414.57	2.15	1.66	221.79	*	157.05	212.14	1.35	1.05	55.09	
1562256_at	NLRP1: NLR family, pyrin domain containing 1	AL832400	155.06	333.85	2.15	1.9	178.79	*	189.24	199.5	1.05	0.97	10.26	
209098_s_at	JAG1: jagged 1 (Alagille syndrome)	U61276	933.45	1988.85	2.13	1.96	1055.4	*	1182.79	1605.23	1.36	1.27	422.44	
1557786_s_at	CHIC1: cysteine-rich hydrophobic domain 1	AA062610	266.3	564.5	2.12	1.96	298.2	*	160.58	163.1	1.02	0.69	2.51	
201654_s_at	HSPG2: heparan sulfate proteoglycan 2	AI991033	568.65	1200.33	2.11	1.97	631.67	*	284.71	372.37	1.31	1.14	87.66	
210869_s_at	MCAM: melanoma cell adhesion molecule	M29277	1400.82	2958.39	2.11	1.92	1557.58	*	1270.43	2017.82	1.59	1.5	747.39	
1566990_x_at	ARID1B: AT rich interactive domain 1B (SWI1-like)	Y08266	102.32	216.28	2.11	1.94	113.96	*	65.99	81.51	1.24	0.87	15.53	
212090_at	GRINA: glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	AL571424	1007.12	2119.48	2.1	1.99	1112.36	*	912.61	765.82	-1.19	-1.12	-146.79	
212909_at	LYPD1: LY6/PLAUR domain containing 1	AL567376	266.46	555.9	2.09	1.85	289.45	*	93.69	163.35	1.74	1.4	69.65	
214149_s_at	ATP6V0E1: ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	AI252582	126.68	263.48	2.08	1.8	136.8	*	116.52	117.45	1.01	0.82	0.93	
218045_x_at	PTMS: parathymosin	NM_002824	572.08	1191.03	2.08	1.94	618.95	*	993.99	1108.57	1.12	1.07	114.58	
224229_s_at	AKT3: v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AL117525	228.89	471.43	2.06	1.83	242.54	*	161.68	167.5	1.04	0.87	5.82	
231211_s_at	YIF1B: Yip1 interacting factor homolog B (S. cerevisiae)	AI254026	283.4	584.81	2.06	1.93	301.41	*	145.57	149.35	1.03	0.83	3.78	
1569106_s_at	SETD5: SET domain containing 5	BI087313	368.67	758.38	2.06	1.9	389.71	*	357.98	328.77	-1.09	-1.02	-29.22	
210100_s_at	ABCA2: ATP-binding cassette, sub-family A (ABC1), member 2	AF327657	129.01	265	2.05	1.79	135.99	*	114.05	115.97	1.02	0.86	1.92	
211958_at	IGFBP5: insulin-like growth factor binding protein 5	R73554	1329.22	2727.27	2.05	1.75	1398.05	*	4741.24	6617.75	1.4	1.31	1876.51	
213765_at	MFAP5: microfibrillar associated protein 5	AW665892	1298.93	2668.39	2.05	1.8	1369.46	*	5326.06	5870.33	1.1	1.04	544.27	
214041_x_at	RPL37A: Ribosomal protein L37a	BE857772	544.62	1115.37	2.05	1.93	570.75	*	494.21	475.99	-1.04	-0.98	-18.22	
220703_at	C10orf110: chromosome 10 open reading frame 110	NM_018470	132.38	271.2	2.05	1.69	138.83	*	95.79	195.36	2.04	1.41	99.57	
226559_at	IER5L: immediate early response 5-like	AL555612	495.08	1010.12	2.04	1.95	515.04	*	344.01	350.77	1.02	0.91	6.77	
241084_x_at	DYNC1H1: dynein, cytoplasmic 1, heavy chain 1	BF062339	295.42	602.19	2.04	1.75	306.76	*	184.49	206.83	1.12	1	22.34	
209462_at	APLP1: amyloid beta (A4) precursor-like protein 1	U48437	363.82	739.65	2.03	1.77	375.84	*	513.39	825.51	1.61	1.46	312.11	
1555471_a_at	FMN2: formin 2	BC014364	497.15	1003.38	2.02	1.76	506.22	*	388.47	514.47	1.32	1.18	125.99	
207061_at	ERN1: endoplasmic reticulum to nucleus signaling 1	NM_001433	104.69	210.81	2.01	1.61	106.13	*	182.02	289.25	1.59	1.42	107.23	
224673_at	LENG8: leukocyte receptor cluster (LRC) member 8	AI613244	485.96	977.92	2.01	1.91	491.97	*	216.67	264.01	1.22	1.01	47.34	
207788_s_at	SORBS3: sorbin and SH3 domain containing 3	NM_005775	474.04	949.77	2	1.9	475.73	*	629.2	599.67	-1.05	-0.98	-29.52	
211892_s_at	PTGIS: prostaglandin I2 (prostacyclin) synthase	AF297052	245.33	489.65	2	1.83	244.32	*	126.13	128.92	1.02	0.87	2.79	
201203_s_at	RRBP1: ribosome binding protein 1 homolog 180kDa (dog)	AI921320	768.62	1525.81	1.99	1.85	757.19	*	980.85	891.12	-1.1	-1.03	-89.72	
1552652_at	HPS4: Hermansky-Pudlak syndrome 4	NM_152843	196.35	391.36	1.99	1.78	195.01	*	39.06	54.71	1.4	0.32	15.65	
1552914_a_at	CD276: CD276 molecule	NM_025240	172.27	343.66	1.99	1.66	171.39	*	311.53	436.69	1.4	1.29	125.16	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
209086_x_at	MCAM: melanoma cell adhesion molecule	BE964361	659.4	1303.75	1.98	1.8	644.35	*	719.74	999.48	1.39	1.27	279.75	
227023_at	GLI4 /// ZFP41: GLI family zinc finger 4 /// zinc finger protein 41 homolog (mouse)	AI570458	134.54	265.51	1.97	1.78	130.96	*	115.2	137.07	1.19	1.01	21.86	
214794_at	PA2G4: proliferation-associated 2G4, 38kDa	BF669264	730.38	1434.73	1.96	1.85	704.35	*	702.96	551.42	-1.27	-1.16	-151.54	
220975_s_at	C1QTNF1: C1q and tumor necrosis factor related protein 1	NM_030968	314.41	617.46	1.96	1.73	303.04	*	399.82	348.14	-1.15	-1.02	-51.68	
236901_at	Hs.17733.0	AA035730	298.52	586.3	1.96	1.79	287.78	*	517.22	518.93	1	0.93	1.71	
243590_at	Hs.258395.0	AA860184	139.89	274.78	1.96	1.6	134.9	*	155.65	130.69	-1.19	-1.03	-24.96	
202718_at	IGFBP2: insulin-like growth factor binding protein 2, 36kDa	NM_000597	2632.75	5134.76	1.95	1.86	2502.01	*	2610.28	3240.66	1.24	1.16	630.38	
206029_at	ANKRD1: ankyrin repeat domain 1 (cardiac muscle)	NM_014391	702.74	1368.21	1.95	1.8	665.47	*	464.74	358.09	-1.3	-1.23	-106.65	
216949_s_at	PKD1: polycystic kidney disease 1 (autosomal dominant)	L39891	171.75	334.36	1.95	1.63	162.61	*	115.04	175.19	1.52	1.27	60.16	
242986_at	Hs.297680.0	BF513384	148.12	288.58	1.95	1.75	140.45	*	80.11	83.78	1.05	0.78	3.67	
1558828_s_at	LOC728264: Hypothetical LOC728264	AL703532	750.86	1460.67	1.95	1.8	709.81	*	122.95	210.93	1.72	1.28	87.98	
208033_s_at	ZFHX3: zinc finger homeobox 3	NM_006885	428.86	833.26	1.94	1.84	404.4	*	380.61	307.29	-1.24	-1.12	-73.32	
215068_s_at	FBXL18: F-box and leucine-rich repeat protein 18	BC004228	340.2	659.69	1.94	1.84	319.5	*	335.81	283.8	-1.18	-1.05	-52.01	
212962_at	SYDE1: synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	AK023573	244.64	473.03	1.93	1.82	228.39	*	176.58	230.54	1.31	1.15	53.96	
218995_s_at	EDN1: endothelin 1	NM_001955	223.8	432.15	1.93	1.7	208.35	*	70.82	102.93	1.45	1.06	32.11	
221172_at	C7orf69: chromosome 7 open reading frame 69	NM_025031	222.2	428	1.93	1.68	205.8	*	28.84	25.92	-1.11	-0.02	-2.92	
203571_s_at	C10orf116: chromosome 10 open reading frame 116	NM_006829	1235.84	2372.46	1.92	1.69	1136.62	*	3363.15	5064.1	1.51	1.45	1700.96	
204529_s_at	TOX: thymocyte selection-associated high mobility group box	AI961231	118.16	227.25	1.92	1.59	109.09	*	343.43	552	1.61	1.45	208.57	
206996_x_at	CACNB1: calcium channel, voltage-dependent, beta 1 subunit	NM_000723	133.89	256.54	1.92	1.69	122.65	*	179.93	245.93	1.37	1.28	65.99	
226288_s_at	NLGN2: neuroligin 2	AI951319	349.9	671.72	1.92	1.76	321.83	*	330.75	353.24	1.07	0.94	22.49	
214660_at	PELO: Pelota homolog (Drosophila)	X68742	390.66	745.38	1.91	1.79	354.72	*	616.04	723.79	1.17	1.12	107.75	
200879_s_at	EPAS1: endothelial PAS domain protein 1	NM_001430	1262.57	2404.38	1.9	1.82	1141.81	*	867.92	974.95	1.12	1.03	107.02	
213764_s_at	MFAP5: microfibrillar associated protein 5	AW665892	898.37	1705.23	1.9	1.72	806.86	*	3558.3	3934.01	1.11	1.05	375.71	
221643_s_at	RERE: arginine-glutamic acid dipeptide (RE) repeats	AF016005	264.96	502.3	1.9	1.77	237.33	*	213.48	199.73	-1.07	-0.96	-13.75	
231974_at	MLL2: myeloid/lymphoid or mixed-lineage leukemia 2	AI742164	259.97	494.39	1.9	1.75	234.42	*	146.92	175.41	1.19	0.99	28.49	
241473_at	Hs.174870.0	AI624440	504.78	961.48	1.9	1.79	456.7	*	56.72	96.02	1.69	1.18	39.29	
1554195_a_at	C5orf46: chromosome 5 open reading frame 46	BC021680	887.1	1684.4	1.9	1.75	797.3	*	334.61	365.19	1.09	0.91	30.57	
235243_at	CLIP3: CAP-GLY domain containing linker protein 3	R24970	186.83	354.09	1.9	1.74	167.25	*	159.74	171.68	1.07	0.92	11.94	
1487_at	ESRRA: estrogen-related receptor alpha	L38487	626.12	1184.07	1.89	1.75	557.95	*	499.03	535.99	1.07	0.97	36.97	
235666_at	Hs.153717.0	AA903473	496.85	938.14	1.89	1.7	441.3	*	125.05	197.09	1.58	1.31	72.04	
242138_at	DLX1: distal-less homeobox 1	BF060783	188.03	355.23	1.89	1.62	167.2	*	252	324.14	1.29	1.15	72.13	
202648_at	Hs.298262.0	BC000023	135.79	254.73	1.88	1.65	118.94	*	95.68	102.87	1.08	0.81	7.2	
212325_at	LIMCH1: LIM and calponin homology domains 1	AK027231	339.07	635.88	1.88	1.57	296.81	*	463.48	558.87	1.21	1.07	95.4	
1555480_a_at	FBLIM1: filamin binding LIM protein 1	AF459643	1952.19	3677.09	1.88	1.8	1724.9	*	1187.23	1168.54	-1.02	-0.93	-18.69	
1566989_at	ARID1B: AT rich interactive domain 1B (SWI1-like)	Y08266	733.31	1381.17	1.88	1.81	647.86	*	424.96	441.77	1.04	0.96	16.81	
203395_s_at	HES1: hairy and enhancer of split 1, (Drosophila)	NM_005524	595.99	1116.47	1.87	1.66	520.48	*	596.93	665.45	1.11	1.03	68.52	
227006_at	PPP1R14A: protein phosphatase 1, regulatory (inhibitor) subunit 14A	AA156998	944.76	1767.93	1.87	1.71	823.17	*	715.07	1158.68	1.62	1.47	443.61	
234106_s_at	FLYWCH1: FLYWCH-type zinc finger 1	BC001973	332.17	621.56	1.87	1.7	289.4	*	242.82	265.11	1.09	0.93	22.29	
205341_at	EHD2: EH-domain containing 2	NM_014601	606.14	1130.3	1.86	1.79	524.16	*	670.45	622.36	-1.08	-1.02	-48.09	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
213125_at	OLFML2B: olfactomedin-like 2B	AW007573	922.02	1715.55	1.86	1.6	793.53	*	3540.38	3482.83	-1.02	-0.94	-57.55	
202046_s_at	GRLF1: glucocorticoid receptor DNA binding factor 1	NM_004491	222.61	411.89	1.85	1.72	189.28	*	113.13	130.34	1.15	0.88	17.21	
205856_at	SLC14A1: solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	NM_015865	671.38	1238.12	1.84	1.78	566.74	*	218.46	305.29	1.4	1.27	86.82	
201461_s_at	MAPKAPK2: mitogen-activated protein kinase-activated protein kinase 2	NM_004759	453.82	829.93	1.83	1.71	376.12	*	541.91	525.63	-1.03	-0.96	-16.28	
204657_s_at	SHB: Src homology 2 domain containing adaptor protein B	NM_003028	242.86	444.88	1.83	1.67	202.02	*	202.76	195.55	-1.04	-0.91	-7.2	
207661_s_at	SH3PXD2A: SH3 and PX domains 2A	NM_014631	255.19	466.83	1.83	1.71	211.64	*	195.32	213.49	1.09	0.99	18.17	
222650_s_at	SLC2A4RG: SLC2A4 regulator	BE898559	443.39	813	1.83	1.73	369.61	*	558.2	549.24	-1.02	-0.95	-8.96	
231851_at	RAVER2: ribonucleoprotein, PTB-binding 2	AL359613	236.64	433.8	1.83	1.61	197.16	*	175.9	232.85	1.32	1.14	56.95	
1555784_s_at	IRAK1: interleukin-1 receptor-associated kinase 1	AF346607	297.73	544.63	1.83	1.66	246.9	*	312.96	310.47	-1.01	-0.92	-2.48	
204420_at	FOSL1: FOS-like antigen 1	BG251266	237.16	432.71	1.82	1.59	195.55	*	320.17	214.9	-1.49	-1.27	-105.27	
214023_x_at	TUBB2B: tubulin, beta 2B	AL533838	180.85	329.64	1.82	1.63	148.8	*	213.2	263.22	1.23	1.08	50.02	
231735_s_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	NM_014086	1201.48	2187.43	1.82	1.64	985.96	*	639.9	944.18	1.48	1.21	304.28	
1557749_at	EHBP1L1: EH domain binding protein 1-like 1	AK092750	771.57	1403.67	1.82	1.75	632.1	*	759.31	822.57	1.08	1.05	63.26	
203683_s_at	VEGFB: vascular endothelial growth factor B	NM_003377	900.75	1632.13	1.81	1.76	731.39	*	1209.73	1119.22	-1.08	-1.02	-90.51	
205713_s_at	COMP: cartilage oligomeric matrix protein	NM_000095	1183.05	2138.37	1.81	1.68	955.32	*	2561.63	3907.31	1.53	1.47	1345.68	
215138_s_at	RP1-21O18.1: kazrin	AB015329	225.85	408.45	1.81	1.62	182.6	*	272.11	221.2	-1.23	-1.02	-50.9	
215535_s_at	AGPAT1: 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	AF007145	1316.15	2377.76	1.81	1.7	1061.61	*	1395.64	1198.52	-1.16	-1.08	-197.12	
49049_at	DTX3: deltex homolog 3 (Drosophila)	N92708	184.35	333.02	1.81	1.59	148.67	*	176.15	176.84	1	0.89	0.69	
232859_s_at	MAGI1: membrane associated guanylate kinase, WW and PDZ domain containing 1	AL110296	536.06	971.7	1.81	1.7	435.64	*	368.1	314.38	-1.17	-1.05	-53.72	
1555483_x_at	FBLIM1: filamin binding LIM protein 1	AF459643	1036.48	1878.26	1.81	1.74	841.78	*	601.75	692.06	1.15	1.06	90.31	
226966_at	PRPF40B: PRP40 pre-mRNA processing factor 40 homolog B (S. cerevisiae)	BF108696	147.25	264.79	1.8	1.62	117.53	*	115.29	110.64	-1.04	-0.8	-4.65	
209322_s_at	SH2B1: SH2B adaptor protein 1	AF227968	178.58	319.85	1.79	1.54	141.27	*	137.03	149.51	1.09	0.89	12.48	
221350_at	HOXC8: homeobox C8	NM_022658	500.78	896.49	1.79	1.65	395.71	*	318.79	293.78	-1.09	-0.93	-25.01	
1559583_at	CD276: CD276 molecule	AK074849	174.68	312.4	1.79	1.64	137.72	*	143.72	153.54	1.07	0.93	9.83	
205425_at	HIP1: huntingtin interacting protein 1	NM_005338	605.64	1082.98	1.79	1.67	477.34	*	330.6	394.98	1.19	1.08	64.38	
208871_at	ATN1: atrophin 1	D31840	172.92	307.01	1.78	1.62	134.09	*	114.56	89.08	-1.29	-1.06	-25.49	
211356_x_at	LEPR: leptin receptor	U66495	435.05	772.8	1.78	1.59	337.75	*	877.37	1211.66	1.38	1.29	334.29	
215260_s_at	TCF3: transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	X52078	166.06	296.17	1.78	1.5	130.11	*	130.89	139.7	1.07	0.84	8.81	
202896_s_at	SIRPA: signal-regulatory protein alpha	NM_004648	353.14	626.27	1.77	1.6	273.13	*	422.04	352.07	-1.2	-1.08	-69.97	
217856_at	RBM8A: RNA binding motif protein 8A	AF182415	323.07	572.8	1.77	1.6	249.74	*	210.27	257.84	1.23	0.99	47.57	
227299_at	CCNI: Cyclin I	AA020986	156.5	276.23	1.77	1.51	119.74	*	134.51	170.65	1.27	1.13	36.14	
232330_at	C7orf44: Chromosome 7 open reading frame 44	AK024861	143.49	254.53	1.77	1.52	111.04	*	30.18	46.41	1.54	0.82	16.22	
206070_s_at	EPHA3: EPH receptor A3	AF213459	745.31	1309.2	1.76	1.59	563.89	*	1525.08	2424.2	1.59	1.44	899.12	
229151_at	SLC14A1: solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	BE673587	496.21	875.47	1.76	1.62	379.26	*	217.68	235.26	1.08	0.94	17.58	
201309_x_at	C5orf13: chromosome 5 open reading frame 13	U36189	3212.98	5611.57	1.75	1.52	2398.58	*	7707.64	9758.26	1.27	1.2	2050.62	
201806_s_at	ATXN2L: ataxin 2-like	NM_007245	238.09	417.03	1.75	1.57	178.94	*	106.07	147.31	1.39	1.08	41.23	
203239_s_at	CNOT3: CCR4-NOT transcription complex, subunit 3	NM_014516	303.97	530.61	1.75	1.63	226.63	*	250.49	264.77	1.06	0.97	14.28	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
228360_at	LYPD6B: LY6/PLAUR domain containing 6B	BF060747	560.86	981.69	1.75	1.59	420.84	*	331.51	485.64	1.46	1.19	154.13	
214443_at	PVR: poliovirus receptor	NM_006505	276.6	480.58	1.74	1.58	203.98	*	196.68	217.91	1.11	0.96	21.23	
217937_s_at	HDAC7: histone deacetylase 7	NM_016596	364.31	632.17	1.74	1.6	267.86	*	304.03	305.54	1	0.87	1.52	
207511_s_at	C2orf24: chromosome 2 open reading frame 24	NM_015680	438.13	759.54	1.73	1.65	321.42	*	498.07	449.67	-1.11	-1.04	-48.4	
226731_at	PELO: Pelota homolog (Drosophila)	AA156873	297.62	516.14	1.73	1.57	218.52	*	537.91	590.71	1.1	1.02	52.8	
204396_s_at	GRK5: G protein-coupled receptor kinase 5	NM_005308	464.44	799.58	1.72	1.55	335.15	*	636.98	526.46	-1.21	-1.1	-110.52	
204790_at	SMAD7: SMAD family member 7	NM_005904	2713.04	4678.29	1.72	1.6	1965.25	*	2241.18	2850.26	1.27	1.18	609.08	
214001_x_at	Hs.76230.2	AW302047	242.74	416.74	1.72	1.55	173.99	*	162.17	224.67	1.39	1.24	62.5	
216155_at	Hs.306686.0	AK024543	164.07	282.27	1.72	1.5	118.2	*	67.49	76.39	1.13	0.65	8.9	
209016_s_at	KRT7: keratin 7	BC002700	1482.51	2536.06	1.71	1.62	1053.54	*	1150.71	1128.01	-1.02	-0.95	-22.71	
216971_s_at	PLEC1: plectin 1, intermediate filament binding protein 500kDa	Z54367	1089.7	1866.52	1.71	1.63	776.82	*	1083.52	986.9	-1.1	-1.04	-96.62	
209675_s_at	HNRNPUL1: heterogeneous nuclear ribonucleoprotein U-like 1	BC004242	590.33	1001.22	1.7	1.57	410.89	*	419.44	459.26	1.09	0.99	39.82	
221994_at	PDLIM5: PDZ and LIM domain 5	AA196325	360.79	614.42	1.7	1.54	253.63	*	262.51	296.62	1.13	0.97	34.11	
227410_at	FAM43A: family with sequence similarity 43, member A	AW264102	805.54	1369.93	1.7	1.52	564.39	*	297.48	346.11	1.16	1.02	48.63	
236653_at	LOC148189: Hypothetical LOC148189	AA629075	312.45	532.1	1.7	1.58	219.65	*	220.11	259.56	1.18	1.1	39.45	
1557586_s_at	ATP6V1H: ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	AW468382	229.88	389.85	1.7	1.51	159.97	*	223.32	164.99	-1.35	-1.17	-58.33	
207390_s_at	SMTN: smoothelin	NM_006932	665.78	1123.3	1.69	1.54	457.53	*	1575.17	1708.94	1.08	1.04	133.76	
210649_s_at	ARID1A: AT rich interactive domain 1A (SWI-like)	AF231056	758.38	1279.41	1.69	1.62	521.03	*	481.18	484.29	1.01	0.9	3.11	
211355_x_at	LEPR: leptin receptor	U52914	413.6	698.77	1.69	1.53	285.17	*	833.61	1123.85	1.35	1.28	290.25	
1559397_s_at	PRR14: proline rich 14	BE788667	256.25	433.02	1.69	1.51	176.77	*	213.43	219.64	1.03	0.86	6.21	
203254_s_at	TLN1: talin 1	NM_006289	2056.67	3460.96	1.68	1.58	1404.29	*	1594.79	1675.85	1.05	0.95	81.06	
203289_s_at	C16orf35: chromosome 16 open reading frame 35	BE791629	236.33	397.26	1.68	1.54	160.94	*	224.65	175.28	-1.28	-1.1	-49.38	
235281_x_at	AHNAK: AHNAK nucleoprotein	AA523289	242.39	406.89	1.68	1.51	164.5	*	197.88	166.57	-1.19	-0.99	-31.31	
223618_at	FMN2: formin 2	AF225426	618.17	1038.37	1.68	1.57	420.2	*	470.97	610.42	1.3	1.2	139.45	
232710_at	Hs.288988.0	AK021477	244.87	408.56	1.67	1.53	163.69	*	35.09	30.62	-1.15	-0.47	-4.47	
212662_at	PVR: poliovirus receptor	BE615277	493.79	819.29	1.66	1.55	325.5	*	248.92	287.26	1.15	1.02	38.34	
228074_at	ITPRIPL2: inositol 1,4,5-triphosphate receptor interacting protein-like 2	BF112168	196.18	326.53	1.66	1.54	130.35	*	170.3	156.91	-1.09	-0.92	-13.4	
241957_x_at	LIN7B: lin-7 homolog B (C. elegans)	AI686521	274.96	456.09	1.66	1.51	181.14	*	302.4	388.83	1.29	1.12	86.43	
1554761_a_at	HEATR2: HEAT repeat containing 2	BC010850	370.19	615.89	1.66	1.55	245.7	*	340.75	302.98	-1.12	-1.01	-37.76	
206724_at	CBX4: chromobox homolog 4 (Pc class homolog, Drosophila)	NM_003655	462.86	763.75	1.65	1.56	300.9	*	298.24	310.88	1.04	0.93	12.64	
218522_s_at	MAP1S: microtubule-associated protein 1S	NM_018174	420.43	692.22	1.65	1.54	271.8	*	362.45	338.62	-1.07	-0.97	-23.82	
201228_s_at	ARIH2: ariadne homolog 2 (Drosophila)	AW074830	518.79	850.85	1.64	1.55	332.06	*	435.74	433.77	-1	-0.92	-1.97	
204926_at	INHBA: inhibin, beta A	NM_002192	1065.24	1734.12	1.63	1.52	668.88	*	524.89	557.64	1.06	0.97	32.75	
224766_at	RPL37: Ribosomal protein L37	AW008221	371.54	600.65	1.62	1.51	229.11	*	134.25	133.48	-1.01	-0.77	-0.78	
203448_s_at	TERF1: telomeric repeat binding factor (NIMA-interacting) 1	AI347136	1010.74	1629.01	1.61	1.55	618.27	*	664.11	572.2	-1.16	-1.06	-91.91	
202775_s_at	SFRS8: splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	NM_004592	590.9	946.28	1.6	1.51	355.38	*	340.86	341.39	1	0.85	0.53	

Up-Regulated Genes at Day 10 in Response to 2nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
204379_s_at	FGFR3: fibroblast growth factor receptor 3	NM_000142	29.68	80.27	2.7	1.83	50.58		15.79	258.05	16.34	7.92	242.26	*
210115_at	RPL39L: ribosomal protein L39-like	L05096	1008.03	971.35	-1.04	-0.99	-36.68		1192.68	14419.45	12.09	6.28	13226.77	*
213488_at	SNED1: sushi, nidogen and EGF-like domains 1	N73970	664.77	455.08	-1.46	-1.3	-209.68		1053.65	10863.78	10.31	4.27	9810.13	*
222375_at	Hs.291839.0	AW970944	238.76	236.98	-1.01	-0.95	-1.78		29.35	175.67	5.99	3.12	146.32	*
209771_x_at	CD24: CD24 molecule	AA761181	488.35	701.25	1.44	1.22	212.9		397.45	1846.46	4.65	4.12	1449.01	*
242076_at	Hs.293348.0	AA761055	13.53	17.89	1.32	0	4.36		37.7	172.43	4.57	3.08	134.73	*
212586_at	CAST: calpastatin	AA195244	3522.09	3703.03	1.05	0.54	180.93		3225.36	14405.43	4.47	3	11180.08	*
228819_at	TSPAN18: tetraspanin 18	AI161133	54.48	90.84	1.67	1.07	36.36		45.87	200.28	4.37	3.35	154.41	*
216379_x_at	CD24: CD24 molecule	AK000168	472.85	639.95	1.35	1.18	167.1		431.88	1777.74	4.12	3.85	1345.86	*
227933_at	LINGO1: leucine rich repeat and Ig domain containing 1	AI193252	23.28	32.84	1.41	0.18	9.56		42.83	176.36	4.12	3.29	133.54	*
208651_x_at	CD24: CD24 molecule	M58664	265.31	402.54	1.52	1.42	137.22		240.88	912.15	3.79	3.5	671.27	*
205908_s_at	OMD: osteomodulin	NM_005014	22.89	43.65	1.91	1.27	20.76		224.85	812.95	3.62	3.18	588.09	*
238745_at	Hs.308708.0	AA114990	96.46	133.59	1.38	1.15	37.13		45.08	158.52	3.52	2.24	113.44	*
239126_at	C19orf23: chromosome 19 open reading frame 23	AA012950	20.25	48.37	2.39	0.97	28.12		57.29	201.12	3.51	2.83	143.83	*
239070_at	Hs.164259.0	AI434790	67.46	90.66	1.34	0.94	23.2		45.42	158.85	3.5	2.06	113.43	*
266_s_at	CD24: CD24 molecule	L33930	359.73	446.03	1.24	1.13	86.3		273.3	952.74	3.49	3.2	679.44	*
225142_at	JHDM1D: jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	AW294022	113.74	102.77	-1.11	-0.87	-10.98		48.44	160.78	3.32	2.09	112.34	*
233109_at	COL12A1: Collagen, type XII, alpha 1	AU146651	490.07	690.4	1.41	1.31	200.32		74.67	217.81	2.92	2.36	143.14	*
222921_s_at	HEY2: hairy/enhancer-of-split related with YRPW motif 2	AF232238	52.96	152.38	2.88	2.15	99.42		100.4	270.05	2.69	2.25	169.65	*
219478_at	WFDC1: WAP four-disulfide core domain 1	NM_021197	90.82	118.21	1.3	0.73	27.39		121.38	309.78	2.55	2.14	188.4	*
209921_at	SLC7A11: solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AB040875	5153.74	4823.58	-1.07	-1.03	-330.15		881.28	2159.93	2.45	2.01	1278.65	*
217678_at	SLC7A11: solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AA488687	3659.02	4298.51	1.17	1.13	639.49		619.89	1497.93	2.42	2.22	878.04	*
234976_x_at	SLC4A5: Solute carrier family 4, sodium bicarbonate cotransporter, member 5	BG324504	834.15	946.81	1.14	1.08	112.66		139.98	332.98	2.38	1.86	193	*
209772_s_at	CD24: CD24 molecule	X69397	268.29	236.52	-1.13	-0.94	-31.77		247.06	574.67	2.33	2.02	327.61	*
213040_s_at	NPTXR: neuronal pentraxin receptor	AL008583	243.07	293.8	1.21	0.99	50.73		478.2	1113.03	2.33	2.12	634.82	*
227480_at	SUSD2: sushi domain containing 2	Z92546	61.17	81	1.32	0.78	19.83		135.98	313.71	2.31	2.04	177.74	*
242669_at	UFM1: Ubiquitin-fold modifier 1	BF514975	562.9	543.03	-1.04	-0.97	-19.87		102.96	236.88	2.3	1.87	133.92	*
203438_at	STC2: stanniocalcin 2	AI435828	5945.36	6888.55	1.16	1.1	943.19		819.61	1852.29	2.26	1.98	1032.68	*
239517_at	ITGB6: Integrin, beta 6	AA609987	31.07	34.15	1.1	0.02	3.08		81.07	182.6	2.25	1.76	101.53	*
235911_at	Hs.184727.0	AI885815	839.27	541.54	-1.55	-1.37	-297.73		348.19	775.3	2.23	2.01	427.1	*
213909_at	LRRC15: leucine rich repeat containing 15	AU147799	236.76	200.14	-1.18	-0.73	-36.62		783.85	1732.48	2.21	1.94	948.63	*
203378_at	PCF11: PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	AB020631	924.93	1336.35	1.44	1.33	411.42		561.31	1192.85	2.13	1.88	631.54	*
202887_s_at	DDIT4: DNA-damage-inducible transcript 4	NM_019058	7836.23	7104.5	-1.1	-1.06	-731.72		1001.73	2088.29	2.08	1.72	1086.56	*
219270_at	CHAC1: ChaC, cation transport regulator homolog 1 (E. coli)	NM_024111	4032.27	3206.08	-1.26	-1.14	-826.19		521.1	1062.77	2.04	1.76	541.67	*
225540_at	MAP2: microtubule-associated protein 2	BF342661	132.54	219.42	1.66	1.37	86.88		98.13	200.63	2.04	1.73	102.49	*
221000_s_at	KAZALD1: Kazal-type serine peptidase inhibitor domain 1	NM_030929	213.37	416.34	1.95	1.45	202.96		277.13	561.44	2.03	1.64	284.31	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
231688_at	MMP8: matrix metallopeptidase 8 (neutrophil collagenase)	AW337833	15.23	4.03	-3.78	-1.32	-11.21		141.71	284.54	2.01	1.68	142.83	*
209465_x_at	PTN: pleiotrophin	AL565812	299.71	377.16	1.26	1.06	77.45		768.03	1531.5	1.99	1.75	763.47	*
218484_at	NDUFA4L2: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	NM_020142	859.56	1088.96	1.27	1.18	229.4		575.03	1139.51	1.98	1.78	564.48	*
228481_at	Hs.163443.0	BG541187	1832.62	2567.64	1.4	1.31	735.02		620.08	1220.83	1.97	1.7	600.75	*
202803_s_at	ITGB2: integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	NM_000211	300.48	159.58	-1.88	-1.42	-140.9		336.27	660.33	1.96	1.82	324.05	*
209343_at	EFHD1: EF-hand domain family, member D1	BC002449	248.44	281.77	1.13	0.98	33.33		169.21	331.77	1.96	1.6	162.56	*
213791_at	PENK: proenkephalin	NM_006211	362.96	387.83	1.07	0.88	24.87		885.25	1728.22	1.95	1.75	842.97	*
204537_s_at	GABRE: gamma-aminobutyric acid (GABA) A receptor, epsilon	NM_004961	592.67	692.18	1.17	1.1	99.51		184.98	358.18	1.94	1.78	173.2	*
209466_x_at	PTN: pleiotrophin	M57399	316.74	436.19	1.38	1.04	119.45		460.16	894.24	1.94	1.7	434.07	*
211737_x_at	PTN: pleiotrophin	BC005916	369.16	494.36	1.34	1.14	125.2		659.21	1281.41	1.94	1.71	622.2	*
219310_at	TMEM90B: transmembrane protein 90B	NM_024893	371.54	540.18	1.45	1.27	168.65		288.23	559.11	1.94	1.69	270.88	*
224375_at	LOC100293563: DC48	AF271776	438.26	219.55	-2	-1.42	-218.71		282.2	543.29	1.93	1.7	261.09	*
224579_at	SLC38A1: solute carrier family 38, member 1	BF247552	2313.54	2146.59	-1.08	-1.04	-166.95		741.58	1422.56	1.92	1.79	680.97	*
205404_at	HSD11B1: hydroxysteroid (11-beta) dehydrogenase 1	NM_005525	103.84	89.21	-1.16	-0.68	-14.63		272.79	521.84	1.91	1.68	249.05	*
217966_s_at	FAM129A: family with sequence similarity 129, member A	NM_022083	2447.88	2382.05	-1.03	-0.96	-65.84		251.33	477.64	1.9	1.61	226.3	*
241355_at	HR: hairless homolog (mouse)	BF528433	205.7	256.19	1.25	0.93	50.5		200.2	380.02	1.9	1.63	179.82	*
213645_at	ENOSF1: enolase superfamily member 1	AF305057	747.59	575.17	-1.3	-1.23	-172.41		141.01	266.32	1.89	1.6	125.31	*
221577_x_at	GDF15 /// LOC100292463: growth differentiation factor 15 /// similar to growth differentiation factor 15	AF003934	4321.58	5395.7	1.25	1.2	1074.12		739.64	1400.29	1.89	1.56	660.65	*
235595_at	ARHGEF2: Rho/Rac guanine nucleotide exchange factor (GEF) 2	AW299534	1339.23	1381.85	1.03	1	42.62		114.81	216.38	1.88	1.5	101.56	*
202847_at	PCK2: phosphoenolpyruvate carboxykinase 2 (mitochondrial)	NM_004563	5854.48	5157.47	-1.14	-1.08	-697.01		1193.38	2229.5	1.87	1.65	1036.12	*
205047_s_at	ASNS: asparagine synthetase	NM_001673	9962.13	9374.43	-1.06	-1.03	-587.69		2197.01	4092.97	1.86	1.58	1895.96	*
224559_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AF001540	8643.56	8626.34	-1	-0.95	-17.22		2107.31	3891.5	1.85	1.58	1784.19	*
220892_s_at	PSAT1: phosphoserine aminotransferase 1	NM_021154	9404.88	8602.67	-1.09	-1.06	-802.22		3031.42	5544.57	1.83	1.65	2513.15	*
230546_at	VASH1: vasohibin 1	AA142893	107.54	129.29	1.2	0.92	21.75		150.29	274.73	1.83	1.73	124.44	*
242482_at	PRKAR1A: protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	AI682905	412.36	362.65	-1.14	-1.05	-49.7		141.07	258.16	1.83	1.65	117.09	*
1555860_x_at	LOC440944: hypothetical LOC440944	CA430188	496.54	539.35	1.09	1.01	42.8		165.36	303.31	1.83	1.64	137.96	*
203222_s_at	TLE1: transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	NM_005077	129.74	120.03	-1.08	-0.84	-9.7		141.87	257.23	1.81	1.53	115.35	*
207148_x_at	MYOZ2: myozenin 2	NM_016599	213.98	243.91	1.14	0.98	29.93		155.45	281.99	1.81	1.6	126.54	*
230142_s_at	CIRBP: cold inducible RNA binding protein	AW088030	987.07	1184.95	1.2	1.12	197.88		251.12	455.49	1.81	1.53	204.37	*
235716_at	Hs.194258.0	AW157450	1180.34	1314.89	1.11	1.06	134.56		191.37	344.51	1.8	1.63	153.14	*
210815_s_at	CALCRL: calcitonin receptor-like	U17473	158.6	232.17	1.46	1.19	73.56		386.4	690.06	1.79	1.65	303.66	*
220988_s_at	AMACR /// C1QTNF3: alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	NM_030945	136.84	199.04	1.45	0.67	62.21		1076.75	1895.78	1.76	1.61	819.03	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
227188_at	C21orf63: chromosome 21 open reading frame 63	AI744591	307.33	329.61	1.07	0.98	22.28		184.16	324.82	1.76	1.65	140.66	*
228582_x_at	Hs.6975.3	AI475544	1944.41	2368.75	1.22	1.15	424.34		522.19	919.6	1.76	1.6	397.4	*
200924_s_at	SLC3A2: solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	NM_002394	4018.3	4082.31	1.02	0.96	64.01		1031.38	1803.8	1.75	1.55	772.43	*
218665_at	FZD4: frizzled homolog 4 (Drosophila)	NM_012193	341.85	530.4	1.55	1.41	188.56		361.07	632.46	1.75	1.58	271.39	*
203638_s_at	FGFR2: fibroblast growth factor receptor 2	NM_022969	392.41	414.07	1.06	0.91	21.66		572.36	988.33	1.73	1.6	415.97	*
238320_at	NEAT1: nuclear paraspeckle assembly transcript 1 (non-protein coding)	AV659198	1901.14	2447.93	1.29	1.22	546.79		416.57	722.13	1.73	1.52	305.56	*
206315_at	CRLF1: cytokine receptor-like factor 1	NM_004750	1405.19	2290.41	1.63	1.38	885.22		1220.9	2101.27	1.72	1.56	880.38	*
206480_at	LTC4S: leukotriene C4 synthase	NM_000897	132.78	129.54	-1.02	-0.79	-3.24		165.13	282.14	1.71	1.55	117.01	*
218237_s_at	SLC38A1: solute carrier family 38, member 1	NM_030674	2141.87	2178.71	1.02	0.97	36.83		743.28	1253.71	1.69	1.54	510.42	*
228224_at	PRELP: proline/arginine-rich end leucine-rich repeat protein	AA573140	210.89	327.33	1.55	1.35	116.44		1631.1	2752.07	1.69	1.61	1120.97	*
219093_at	PID1: phosphotyrosine interaction domain containing 1	NM_017933	2894.8	3494.82	1.21	1.12	600.02		2153.89	3598.01	1.67	1.52	1444.12	*
224558_s_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AI446756	5042.96	4893.56	-1.03	-0.99	-149.4		1516.43	2529.8	1.67	1.55	1013.38	*
241400_at	Hs.160316.0	AI860360	3098.03	3924.49	1.27	1.25	826.46		188.1	314.21	1.67	1.5	126.11	*
202980_s_at	SIAH1: seven in absentia homolog 1 (Drosophila)	AI953523	1096.86	1371.4	1.25	1.18	274.53		736.4	1219.9	1.66	1.55	483.51	*
229795_at	Hs.48945.0	AI701591	628.21	894.26	1.42	1.26	266.05		559.2	929.02	1.66	1.53	369.82	*
234996_at	CALCRL: calcitonin receptor-like	AI478743	119.97	152.21	1.27	1.14	32.25		293.66	485.5	1.65	1.55	191.83	*
212649_at	DHX29: DEAH (Asp-Glu-Ala-His) box polypeptide 29	AL079292	266.2	119.31	-2.23	-1.82	-146.89		173.6	285.67	1.65	1.52	112.07	*
37022_at	PRELP: proline/arginine-rich end leucine-rich repeat protein	U41344	246.95	338.34	1.37	0.95	91.38		2006.02	3244.75	1.62	1.55	1238.72	*
226534_at	KITLG: KIT ligand	AI446414	1504.5	1593.81	1.06	0.99	89.32		1529.73	2452.2	1.6	1.52	922.47	*
205743_at	STAC: SH3 and cysteine rich domain	NM_003149	895.98	1132.2	1.26	1.2	236.22		484.53	772.51	1.59	1.5	287.98	*

Appendix 1.2 Down-Regulated Genes in Response to 2nM BMP6

Down-Regulated Genes at Both Days in Response to 2nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
229580_at	Hs.7413.0	R71596	251.83	15.8	-15.94	-8.4	-236.02	*	450.01	20.24	-22.24	-14.02	-429.77	*
203716_s_at	DPP4: dipeptidyl-peptidase 4	M80536	862.03	64.81	-13.3	-8.93	-797.22	*	594.15	107.67	-5.52	-4.01	-486.48	*
221898_at	PDPN: podoplanin	AU154455	361.63	110.9	-3.26	-2.73	-250.73	*	381.23	71.35	-5.34	-4.18	-309.88	*
211518_s_at	BMP4: bone morphogenetic protein 4	D30751	1146.8	131.27	-8.74	-6.63	-1015.53	*	2341.4	440.52	-5.32	-4.85	-1900.88	*
204879_at	PDPN: podoplanin	NM_006474	583.49	128.08	-4.56	-3.74	-455.41	*	611.9	131.93	-4.64	-3.73	-479.98	*
221371_at	TNFSF18: tumor necrosis factor (ligand) superfamily, member 18	NM_005092	183.46	46.77	-3.92	-2.94	-136.69	*	306.26	77.15	-3.97	-2.93	-229.1	*
208075_s_at	CCL7: chemokine (C-C motif) ligand 7	NM_006273	456.89	57.01	-8.01	-5.93	-399.88	*	1176.14	299.35	-3.93	-3.69	-876.8	*
232102_at	METTL6: methyltransferase like 6	AK027185	168.9	50.89	-3.32	-1.88	-118	*	194.61	50.51	-3.85	-2.17	-144.09	*
218723_s_at	C13orf15: chromosome 13 open reading frame 15	NM_014059	195.41	21.36	-9.15	-5.27	-174.05	*	489.11	128.63	-3.8	-3.31	-360.48	*
211478_s_at	DPP4: dipeptidyl-peptidase 4	M74777	1080.68	185.49	-5.83	-5.32	-895.19	*	736.96	200.01	-3.68	-3.33	-536.95	*
203717_at	DPP4: dipeptidyl-peptidase 4	NM_001935	1993.17	419.01	-4.76	-4.38	-1574.16	*	1320.15	413.9	-3.19	-2.97	-906.25	*
230121_at	C1orf133: chromosome 1 open reading frame 133	BF508679	281.99	76.21	-3.7	-2.87	-205.78	*	868.4	274.6	-3.16	-2.91	-593.8	*
238778_at	MPP7: membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	AI244661	282.34	90.56	-3.12	-2.72	-191.79	*	371.05	123.38	-3.01	-2.66	-247.67	*
230660_at	SERTAD4: SERTA domain containing 4	AU146709	254.07	35.59	-7.14	-4.45	-218.48	*	625.34	209.91	-2.98	-2.68	-415.43	*
203434_s_at	MME: membrane metallo-endopeptidase	AI433463	253.37	39.7	-6.38	-4.55	-213.67	*	601.06	206.84	-2.91	-2.65	-394.22	*
235337_at	Hs.88143.0	AI276403	384.64	175.47	-2.19	-2.05	-209.16	*	926.96	323.97	-2.86	-2.79	-602.99	*
203435_s_at	MME: membrane metallo-endopeptidase	NM_007287	246.04	4.01	-61.33	-20.09	-242.03	*	476.47	166.95	-2.85	-2.74	-309.52	*
211067_s_at	GAS7: growth arrest-specific 7	BC006454	481.95	136.08	-3.54	-3.15	-345.87	*	354.96	129.09	-2.75	-2.43	-225.87	*
206614_at	GDF5: growth differentiation factor 5	NM_000557	623.98	161.31	-3.87	-3.35	-462.67	*	899.84	330.03	-2.73	-2.61	-569.81	*
222717_at	SDPR: serum deprivation response (phosphatidylserine binding protein)	BF982174	324.34	94.79	-3.42	-2.7	-229.55	*	554.72	206.5	-2.69	-2.44	-348.22	*
37512_at	HSD17B6: hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	U89281	901.48	246.79	-3.65	-3.29	-654.69	*	1160.67	446.18	-2.6	-2.43	-714.5	*
229674_at	SERTAD4: SERTA domain containing 4	AL035414	615	195.8	-3.14	-2.76	-419.2	*	1257.43	489.26	-2.57	-2.35	-768.17	*
226804_at	FAM20A: family with sequence similarity 20, member A	AI632223	547.67	83.92	-6.53	-4.75	-463.75	*	542.83	211.57	-2.57	-2.19	-331.26	*
205302_at	IGFBP1: insulin-like growth factor binding protein 1	NM_000596	831.51	264.44	-3.14	-2.95	-567.07	*	180.98	71.22	-2.54	-2.07	-109.76	*
209277_at	TFPI2: tissue factor pathway inhibitor 2	AL574096	738.09	268.02	-2.75	-2.53	-470.08	*	261.81	105.12	-2.49	-2.04	-156.69	*
202912_at	ADM: adrenomedullin	NM_001124	3820.54	1022.25	-3.74	-3.36	-2798.29	*	2165.9	884.43	-2.45	-2.29	-1281.46	*
227394_at	NCAM1: neural cell adhesion molecule 1	W94001	1560.11	325.69	-4.79	-4.08	-1234.42	*	657.8	275.14	-2.39	-2.11	-382.65	*
238125_at	ADAMTS16: ADAM metallopeptidase with thrombospondin type 1 motif, 16	AI740544	289.34	121.13	-2.39	-2.11	-168.22	*	571.91	241.8	-2.37	-2.15	-330.11	*
209278_s_at	TFPI2: tissue factor pathway inhibitor 2	L27624	1717.9	746.2	-2.3	-2.05	-971.7	*	520.01	224.88	-2.31	-1.95	-295.13	*
210078_s_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	L39833	2036.38	802.43	-2.54	-2.32	-1233.94	*	2163.88	938.26	-2.31	-2.17	-1225.62	*
202688_at	TNFSF10: tumor necrosis factor (ligand) superfamily, member 10	NM_003810	428.24	121.62	-3.52	-2.83	-306.61	*	383	165.92	-2.31	-1.97	-217.08	*
210121_at	B3GALT2: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	AF288390	825.45	289.94	-2.85	-2.66	-535.5	*	467.94	203.47	-2.3	-2.02	-264.46	*
228335_at	CLDN11: claudin 11	AW264204	3595.88	2236	-1.61	-1.5	-1359.89	*	2140.45	934.36	-2.29	-2.07	-1206.09	*
209496_at	RARRES2: retinoic acid receptor responder (tazarotene induced) 2	BC000069	1237.61	296.9	-4.17	-3.21	-940.71	*	2392.06	1045.11	-2.29	-2.15	-1346.95	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
218451_at	CDCP1: CUB domain containing protein 1	NM_022842	813.62	404.92	-2.01	-1.91	-408.7	*	496.73	217.63	-2.28	-1.97	-279.1	*
219213_at	JAM2: junctional adhesion molecule 2	NM_021219	322.09	165.11	-1.95	-1.68	-156.98	*	471.46	208.59	-2.26	-2.05	-262.88	*
212843_at	NCAM1: neural cell adhesion molecule 1	AA126505	950.33	190.15	-5	-4.49	-760.18	*	358.92	158.87	-2.26	-1.93	-200.06	*
217452_s_at	B3GALT2: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	Y15014	855.57	412.89	-2.07	-1.91	-442.69	*	561.58	250.08	-2.25	-2.03	-311.5	*
227749_at	Hs.15085.0	AI703496	415.25	193.36	-2.15	-1.88	-221.89	*	471.75	210.95	-2.24	-2.07	-260.8	*
210471_s_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	U33428	1140.47	374.29	-3.05	-2.78	-766.18	*	1236.37	563.8	-2.19	-2.02	-672.57	*
205700_at	HSD17B6: hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	NM_003725	1468.33	474.28	-3.1	-2.74	-994.05	*	1862.58	855.97	-2.18	-1.97	-1006.61	*
205249_at	EGR2: early growth response 2	NM_000399	1436.25	550.53	-2.61	-2.41	-885.72	*	754.08	349.11	-2.16	-1.92	-404.96	*
230831_at	FRMD5: FERM domain containing 5	AW294986	237.68	121.7	-1.95	-1.64	-115.99	*	271.85	126.76	-2.14	-1.92	-145.08	*
219501_at	ENOX1: ecto-NOX disulfide-thiol exchanger 1	NM_017993	1380.14	498.62	-2.77	-2.51	-881.52	*	892.86	417.3	-2.14	-1.85	-475.56	*
202687_s_at	TNFSF10: tumor necrosis factor (ligand) superfamily, member 10	U57059	260	35.69	-7.29	-5.05	-224.31	*	235.18	110.09	-2.14	-1.77	-125.1	*
204105_s_at	NRCAM: neuronal cell adhesion molecule	NM_005010	217.81	78.27	-2.78	-2.23	-139.55	*	327.5	154.11	-2.13	-1.91	-173.39	*
214111_at	OPCML: opioid binding protein/cell adhesion molecule-like	AF070577	291.91	141.82	-2.06	-1.72	-150.09	*	238.26	112.18	-2.12	-1.71	-126.08	*
205240_at	GPSM2: G-protein signaling modulator 2 (AGS3-like, C. elegans)	NM_013296	260.49	126.91	-2.05	-1.52	-133.58	*	942.77	446.67	-2.11	-1.94	-496.11	*
225817_at	CGNL1: cingulin-like 1	AB051536	540.05	132.78	-4.07	-3.04	-407.27	*	1757.89	837.66	-2.1	-1.95	-920.23	*
229116_at	CNKSR2: connector enhancer of kinase suppressor of Ras 2	AI670947	901.94	194.07	-4.65	-3.85	-707.87	*	498.02	238.49	-2.09	-1.8	-259.53	*
221019_s_at	COLEC12: collectin sub-family member 12	NM_030781	370.49	152.53	-2.43	-2.02	-217.95	*	429.18	207.6	-2.07	-1.87	-221.58	*
209211_at	KLF5: Kruppel-like factor 5 (intestinal)	AF132818	639.86	209.4	-3.06	-2.77	-430.46	*	504.21	243.34	-2.07	-1.94	-260.87	*
213338_at	TMEM158: transmembrane protein 158	BF062629	3390.81	1365.62	-2.48	-2.2	-2025.19	*	3447.02	1675.38	-2.06	-1.88	-1771.64	*
211596_s_at	LRIG1: leucine-rich repeats and immunoglobulin-like domains 1	AB050468	871.29	302.87	-2.88	-2.52	-568.42	*	1219.34	591.65	-2.06	-1.94	-627.69	*
209369_at	ANXA3: annexin A3	M63310	446.68	182.12	-2.45	-2.15	-264.56	*	351.36	171.89	-2.04	-1.8	-179.47	*
228885_at	MAMDC2: MAM domain containing 2	AI862120	1214.75	687.73	-1.77	-1.62	-527.01	*	2010.72	1000.63	-2.01	-1.85	-1010.08	*
220639_at	TM4SF20: transmembrane 4 L six family member 20	NM_024795	245.96	96.03	-2.56	-2.16	-149.93	*	254.19	128.38	-1.98	-1.68	-125.81	*
228780_at	Hs.47448.0	AW149422	493.18	130.1	-3.79	-3.23	-363.08	*	351.22	177.39	-1.98	-1.74	-173.83	*
214797_s_at	PCTK3: PCTAIRE protein kinase 3	BC000281	228.64	83.11	-2.75	-2.29	-145.53	*	221.35	112.32	-1.97	-1.72	-109.03	*
217999_s_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	NM_007350	1264.1	637.04	-1.98	-1.82	-627.06	*	603.93	307.84	-1.96	-1.77	-296.09	*
209850_s_at	CDC42EP2: CDC42 effector protein (Rho GTPase binding) 2	BC005406	376.89	166.96	-2.26	-1.85	-209.94	*	363.85	186.38	-1.95	-1.62	-177.46	*
241981_at	FAM20A: family with sequence similarity 20, member A	AW291369	393.68	89.84	-4.38	-3.83	-303.84	*	317.36	163.02	-1.95	-1.79	-154.34	*
228937_at	C13orf31: chromosome 13 open reading frame 31	AI659800	3092.13	1587.04	-1.95	-1.84	-1505.09	*	1487.46	766.74	-1.94	-1.81	-720.72	*
209212_s_at	KLF5: Kruppel-like factor 5 (intestinal)	AB030824	717.43	273.07	-2.63	-2.39	-444.35	*	564.46	291.87	-1.93	-1.8	-272.59	*
232914_s_at	SYTL2: synaptotagmin-like 2	AB046817	1089.57	421.25	-2.59	-2.31	-668.32	*	2171.68	1146.37	-1.89	-1.8	-1025.31	*
205381_at	LRRC17: leucine rich repeat containing 17	NM_005824	1295.09	692.93	-1.87	-1.66	-602.16	*	3959.58	2112.46	-1.87	-1.82	-1847.12	*
225496_s_at	SYTL2: synaptotagmin-like 2	N21426	866.91	290.7	-2.98	-2.38	-576.21	*	1710.55	913.25	-1.87	-1.74	-797.3	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
217998_at	LOC100289208 /// PHLDA1: hypothetical protein LOC100289208 /// pleckstrin homology-like domain, family A, member 1	NM_007350	1203.33	712.26	-1.69	-1.52	-491.07	*	781.17	423.02	-1.85	-1.64	-358.16	*
210261_at	KCNK2: potassium channel, subfamily K, member 2	AF004711	1412.66	696.45	-2.03	-1.82	-716.21	*	2664.52	1438.64	-1.85	-1.75	-1225.88	*
236028_at	IBSP: integrin-binding sialoprotein	BE466675	3607.92	627.32	-5.75	-5.13	-2980.6	*	1681.29	918.81	-1.83	-1.62	-762.48	*
202986_at	ARNT2: aryl-hydrocarbon receptor nuclear translocator 2	NM_014862	975.41	455.35	-2.14	-2	-520.06	*	1128.23	619.6	-1.82	-1.74	-508.62	*
203185_at	RASSF2: Ras association (RalGDS/AF-6) domain family member 2	NM_014737	222.11	82.32	-2.7	-1.79	-139.8	*	390.57	215.35	-1.81	-1.62	-175.22	*
213506_at	F2RL1: coagulation factor II (thrombin) receptor-like 1	BE965369	432.43	195.38	-2.21	-1.93	-237.05	*	386.33	217.46	-1.78	-1.61	-168.87	*
1553147_at	RANBP3L: RAN binding protein 3-like	NM_145000	367.28	210	-1.75	-1.58	-157.27	*	579.29	329.6	-1.76	-1.65	-249.69	*
239582_at	PML: promyelocytic leukemia	AW514654	360.92	198.65	-1.82	-1.61	-162.27	*	358.33	205.53	-1.74	-1.6	-152.8	*
217767_at	C3: complement component 3	NM_000064	1329.19	682.59	-1.95	-1.67	-646.6	*	3862.5	2219.26	-1.74	-1.67	-1643.24	*
228654_at	SPIN4: spindlin family, member 4	AU145277	540.07	303.53	-1.78	-1.56	-236.55	*	1139.6	660.46	-1.73	-1.6	-479.14	*
203407_at	PPL: periplakin	NM_002705	346.03	56.97	-6.07	-4.69	-289.05	*	874.14	504.13	-1.73	-1.64	-370.02	*
206932_at	CH25H: cholesterol 25-hydroxylase	NM_003956	455.9	222.57	-2.05	-1.62	-233.32	*	775.71	450.73	-1.72	-1.63	-324.98	*
218501_at	ARHGEF3: Rho guanine nucleotide exchange factor (GEF) 3	NM_019555	899.46	390.41	-2.3	-2.01	-509.05	*	521.52	304.96	-1.71	-1.57	-216.55	*
243221_at	FAM20A: family with sequence similarity 20, member A	AA579773	235.54	72.2	-3.26	-2.8	-163.34	*	270.47	157.76	-1.71	-1.52	-112.71	*
214772_at	C11orf41: chromosome 11 open reading frame 41	H08993	515.2	290.68	-1.77	-1.6	-224.52	*	528.04	310.14	-1.7	-1.6	-217.89	*
229942_at	BNC2: basonuclin 2	AW024890	933.08	530.19	-1.76	-1.64	-402.88	*	792.32	475.85	-1.67	-1.56	-316.47	*
218815_s_at	TMEM51: transmembrane protein 51	NM_018022	326.89	171.9	-1.9	-1.75	-154.99	*	421.37	258.88	-1.63	-1.53	-162.49	*
213071_at	DPT: dermatopontin	AL049798	212.36	44.52	-4.77	-3.11	-167.84	*	1817.27	1121.38	-1.62	-1.55	-695.89	*
227145_at	LOXL4: lysyl oxidase-like 4	AW190565	4331.77	2173.72	-1.99	-1.84	-2158.05	*	3297.9	2110.54	-1.56	-1.51	-1187.35	*
218975_at	COL5A3: collagen, type V, alpha 3	NM_015719	667	274.05	-2.43	-1.93	-392.94	*	2271.13	1452.5	-1.56	-1.53	-818.64	*
212649_at	DHX29: DEAH (Asp-Glu-Ala-His) box polypeptide 29	AL079292	266.2	119.31	-2.23	-1.82	-146.89	*	173.6	285.67	1.65	1.52	112.07	*
214597_at	SSTR2: somatostatin receptor 2	BC000256	122.72	7.29	-16.84	-6.31	-115.44	*	12.71	121.85	9.59	4.02	109.15	*

Down-Regulated Genes at Day 4 in Response to 2nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
207977_s_at	DPT: dermatopontin	NM_001937	246.34	34.11	-7.22	-4.24	-212.23	*	2213.96	1536.9	-1.44	-1.37	-677.06	
207370_at	IBSP: integrin-binding sialoprotein	NM_004967	990.26	143.27	-6.91	-5.62	-846.99	*	398.45	230.35	-1.73	-1.32	-168.1	
202086_at	MX1: myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	NM_002462	586.34	90	-6.51	-4.22	-496.34	*	733.2	987.88	1.35	1.3	254.68	
234681_s_at	CHD6: chromodomain helicase DNA binding protein 6	AK026022	156.11	24.5	-6.37	-3.43	-131.62	*	36.77	30.56	-1.2	-0.2	-6.22	
210587_at	INHBE: inhibin, beta E	BC005161	871.17	160.75	-5.42	-4.66	-710.42	*	10.92	11.15	1.02	0.39	0.24	
203423_at	RBP1: retinol binding protein 1, cellular	NM_002899	436.92	84.35	-5.18	-4.15	-352.58	*	87.85	44.85	-1.96	-1.47	-43	
213068_at	DPT: dermatopontin	AI146848	199.35	42.33	-4.71	-2.96	-157.02	*	2183.86	1378.6	-1.58	-1.5	-805.26	
235335_at	ABCA9: ATP-binding cassette, sub-family A (ABC1), member 9	AI446543	161.2	36.12	-4.46	-3.37	-125.08	*	81.14	26.69	-3.04	-2.54	-54.45	
215813_s_at	PTGS1: prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	S36219	159.87	37.74	-4.24	-3.19	-122.13	*	50.13	42.9	-1.17	-0.82	-7.23	
232455_x_at	LOC340085: hypothetical protein LOC340085	AU145408	134.05	32.5	-4.12	-1.8	-101.55	*	34.19	54.66	1.6	1.09	20.47	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
217465_at	NCKAP1: NCK-associated protein 1	AK001291	173.63	42.33	-4.1	-2.64	-131.3	*	203.21	274.93	1.35	1.24	71.72	
204439_at	IFI44L: interferon-induced protein 44-like	NM_006820	500.23	125.73	-3.98	-3.03	-374.5	*	842.83	978.13	1.16	1.11	135.3	
222561_at	LANCL2: LanC lantibiotic synthetase component C-like 2 (bacterial)	AJ278245	919.03	242.49	-3.79	-3.14	-676.54	*	483.52	306.26	-1.58	-1.35	-177.26	
204774_at	EVI2A: ecotropic viral integration site 2A	NM_014210	643.11	177.52	-3.62	-3.01	-465.59	*	964.36	721.63	-1.34	-1.26	-242.72	
216554_s_at	Hs.254105.1	U88968	468.33	133.99	-3.5	-2.47	-334.34	*	523.14	666.72	1.27	1.22	143.57	
236029_at	FAT3: FAT tumor suppressor homolog 3 (Drosophila)	AI283093	163.93	46.84	-3.5	-2.31	-117.09	*	179.57	164.44	-1.09	-0.92	-15.13	
240148_at	MSH6: MutS homolog 6 (E. coli)	AA814800	226.3	64.86	-3.49	-2.42	-161.44	*	225.12	153.2	-1.47	-1.29	-71.92	
210872_x_at	GAS7: growth arrest-specific 7	BC001152	193.13	56.11	-3.44	-2.71	-137.02	*	146.57	50.53	-2.9	-2.35	-96.05	
242943_at	ST8SIA4: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	AA352113	150.86	43.84	-3.44	-2.22	-107.02	*	98.85	77.57	-1.27	-0.99	-21.28	
205128_x_at	PTGS1: prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_000962	167.47	49.11	-3.41	-2.41	-118.35	*	88.58	69.5	-1.27	-0.88	-19.08	
219825_at	CYP26B1: cytochrome P450, family 26, subfamily B, polypeptide 1	NM_019885	155.16	46.65	-3.33	-2.16	-108.51	*	37.32	28.11	-1.33	-0.79	-9.2	
206914_at	CRTAM: cytotoxic and regulatory T cell molecule	NM_019604	262.93	80.7	-3.26	-2.77	-182.22	*	185.15	101.41	-1.83	-1.58	-83.74	
204994_at	MX2: myxovirus (influenza virus) resistance 2 (mouse)	NM_002463	245.53	75.69	-3.24	-2.63	-169.84	*	282.52	294.96	1.04	0.96	12.44	
228610_at	TM9SF3: Transmembrane 9 superfamily member 3	AI040432	167.38	51.92	-3.22	-2.27	-115.46	*	210.56	254.14	1.21	1.12	43.57	
209541_at	IGF1: insulin-like growth factor 1 (somatomedin C)	AI972496	248.8	77.88	-3.19	-2.32	-170.92	*	1233.07	790.05	-1.56	-1.47	-443.02	
227487_s_at	SERPINE2: Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	AI359165	648.36	203.33	-3.19	-2.73	-445.02	*	561.13	782.84	1.4	1.35	221.71	
1561064_a_at	Hs2.286666.1	BC015159	233.81	76.21	-3.07	-2.67	-157.6	*	139.22	64.48	-2.16	-1.75	-74.74	
207571_x_at	C1orf38: chromosome 1 open reading frame 38	NM_004848	274.23	90.01	-3.05	-2.54	-184.22	*	221.58	145.4	-1.52	-1.33	-76.18	
242794_at	MAML3: mastermind-like 3 (Drosophila)	AI569476	180.26	60.38	-2.99	-2.39	-119.87	*	120.25	73.57	-1.63	-1.21	-46.68	
223044_at	SLC40A1: solute carrier family 40 (iron-regulated transporter), member 1	AL136944	199.62	67.32	-2.97	-2.3	-132.3	*	658.48	417.47	-1.58	-1.41	-241.01	
201171_at	ATP6V0E1: ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	NM_003945	336.92	113.95	-2.96	-2.32	-222.97	*	474.91	530.14	1.12	1.04	55.23	
239879_at	LOC284998: hypothetical protein LOC284998	N63566	162.56	54.86	-2.96	-2.39	-107.69	*	107.39	60.47	-1.78	-1.32	-46.93	
218219_s_at	LANCL2: LanC lantibiotic synthetase component C-like 2 (bacterial)	NM_018697	1585.49	542.5	-2.92	-2.68	-1042.99	*	976.73	650.72	-1.5	-1.4	-326.01	
225564_at	C1QTNF9 /// SPATA13: C1q and tumor necrosis factor related protein 9 /// spermatogenesis associated 13	AW269397	1346.33	460.98	-2.92	-2.47	-885.35	*	2181.93	1556.68	-1.4	-1.32	-625.26	
1566342_at	SOD2: Superoxide dismutase 2, mitochondrial	R34841	862.08	302.8	-2.85	-2.21	-559.27	*	1025.52	1231.61	1.2	1.14	206.09	
213247_at	SVEP1: sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	AA716107	1259.81	443.31	-2.84	-2.35	-816.5	*	1169.16	733.29	-1.59	-1.48	-435.87	
1569807_at	Hs2.382123.1	BC031234	179.66	63.25	-2.84	-2.05	-116.41	*	209.52	128.85	-1.63	-1.42	-80.67	
216598_s_at	CCL2: chemokine (C-C motif) ligand 2	S69738	6526.2	2307.52	-2.83	-2.49	-4218.68	*	9508.03	6646.73	-1.43	-1.34	-2861.3	
221922_at	GPSM2: G-protein signaling modulator 2 (AGS3-like, C. elegans)	AW195581	379.12	134.61	-2.82	-2.04	-244.5	*	1067.79	752.82	-1.42	-1.34	-314.97	
1553141_at	C13orf31: chromosome 13 open reading frame 31	BC035749	902.33	325.71	-2.77	-2.5	-576.62	*	339.66	214.29	-1.59	-1.4	-125.36	
239979_at	Hs.201875.0	BE645480	264.19	96	-2.75	-2.34	-168.19	*	27.66	46.11	1.67	0.88	18.44	
205767_at	EREG: epiregulin	NM_001432	339.83	124.23	-2.74	-2.43	-215.6	*	145.93	75.74	-1.93	-1.6	-70.19	
221960_s_at	RAB2A: RAB2A, member RAS oncogene family	AI189609	507.54	186.78	-2.72	-2.36	-320.76	*	548.86	702.69	1.28	1.23	153.83	
1555904_at	Hs2.380934.1	BM975756	481.93	179.17	-2.69	-2.5	-302.76	*	413.51	310.02	-1.33	-1.27	-103.49	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
212801_at	CIT: citron (rho-interacting, serine/threonine kinase 21)	AI861788	184.54	68.8	-2.68	-1.74	-115.74	*	459.56	326.52	-1.41	-1.32	-133.05	
230418_s_at	GALNTL1: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	AI097463	362.54	135.06	-2.68	-2.06	-227.47	*	1722.56	1281.63	-1.34	-1.31	-440.92	
204967_at	SHROOM2: shroom family member 2	NM_001649	1302.09	500.96	-2.6	-2.34	-801.13	*	1024.65	897.22	-1.14	-1.06	-127.43	
223551_at	PKIB: protein kinase (cAMP-dependent, catalytic) inhibitor beta	AF225513	217.09	83.51	-2.6	-2.1	-133.58	*	81.08	34.21	-2.37	-1.59	-46.87	
232649_at	GLDN: gliomedin	AU157510	254.62	98.74	-2.58	-2.15	-155.88	*	129	151.4	1.17	1	22.4	
228728_at	C7orf58: chromosome 7 open reading frame 58	BF724137	732.75	286.86	-2.55	-2.25	-445.89	*	978.28	627.42	-1.56	-1.46	-350.86	
234464_s_at	EME1: essential meiotic endonuclease 1 homolog 1 (S. pombe)	AK021607	462.64	183.01	-2.53	-1.8	-279.64	*	631.37	809.14	1.28	1.19	177.77	
212977_at	CXCR7: chemokine (C-X-C motif) receptor 7	AI817041	396	157.51	-2.51	-2.24	-238.49	*	514.87	406.3	-1.27	-1.16	-108.57	
219773_at	NOX4: NADPH oxidase 4	NM_016931	254.56	102.39	-2.49	-2.09	-152.17	*	169.6	126.78	-1.34	-1.15	-42.82	
214257_s_at	Hs.50785.1	AA890010	17976.61	7281.79	-2.47	-1.9	-10694.82	*	6829.71	6949.12	1.02	0.77	119.41	
235486_at	C11orf41: chromosome 11 open reading frame 41	AI879661	579.1	234.5	-2.47	-2.14	-344.6	*	382.3	253.5	-1.51	-1.37	-128.81	
238617_at	Hs.143134.0	AW207243	560.72	226.99	-2.47	-2.21	-333.73	*	190.86	127.41	-1.5	-1.31	-63.45	
205479_s_at	PLAU: plasminogen activator, urokinase	NM_002658	3162.35	1285.14	-2.46	-2.15	-1877.22	*	5446.96	3934.14	-1.38	-1.3	-1512.83	
229121_at	CMKLR1: chemokine-like receptor 1	BE857553	1724.64	700.25	-2.46	-2.28	-1024.38	*	2407.61	1778.22	-1.35	-1.31	-629.39	
209031_at	CADM1: cell adhesion molecule 1	AL519710	1625.38	673.52	-2.41	-2.12	-951.85	*	1039.67	1287.48	1.24	1.18	247.81	
231559_at	NNMT: Nicotinamide N-methyltransferase	AV650983	205.24	85.3	-2.41	-1.77	-119.94	*	242.29	276.87	1.14	1.07	34.58	
242541_at	ABCA9: ATP-binding cassette, sub-family A (ABC1), member 9	AV692159	238.64	98.98	-2.41	-2.09	-139.66	*	99.86	42	-2.38	-1.69	-57.86	
204972_at	OAS2: 2'-5'-oligoadenylate synthetase 2, 69/71kDa	NM_016817	299.66	125.04	-2.4	-1.81	-174.62	*	440.59	423.69	-1.04	-0.98	-16.9	
209193_at	PIM1: pim-1 oncogene	M24779	1197.76	499.99	-2.4	-2.14	-697.77	*	765.41	536.06	-1.43	-1.32	-229.35	
206090_s_at	DISC1: disrupted in schizophrenia 1	NM_018662	285.11	119.38	-2.39	-2.04	-165.73	*	321.95	250.15	-1.29	-1.2	-71.8	
228309_at	Hs.22391.2	AA130982	297.44	125.7	-2.37	-1.63	-171.74	*	290.84	324.71	1.12	1.06	33.87	
227550_at	GFRA1: GDNF family receptor alpha 1	AW242720	422.49	178.86	-2.36	-2.02	-243.63	*	755.31	530.56	-1.42	-1.35	-224.75	
221211_s_at	C21orf7: chromosome 21 open reading frame 7	NM_020152	3537.36	1505.13	-2.35	-2.2	-2032.23	*	4069.16	3653.76	-1.11	-1.07	-415.4	
240259_at	FLRT2: Fibronectin leucine rich transmembrane protein 2	AI188161	217.86	93.68	-2.33	-1.91	-124.18	*	121.14	104.57	-1.16	-0.96	-16.57	
219334_s_at	OBFC2A: oligonucleotide/oligosaccharide-binding fold containing 2A	NM_022837	283.21	122.26	-2.32	-2.01	-160.95	*	106.91	110.75	1.04	0.87	3.84	
225328_at	Hs.6630.0	N21643	364.41	156.77	-2.32	-1.95	-207.65	*	147.86	153.53	1.04	0.78	5.67	
223925_s_at	MTPN: myotrophin	AF130088	255.33	111.32	-2.29	-1.68	-144.01	*	279.71	310.66	1.11	1.04	30.95	
207375_s_at	IL15RA: interleukin 15 receptor, alpha	NM_002189	206.74	90.49	-2.28	-1.83	-116.25	*	176.74	112.93	-1.57	-1.33	-63.81	
1561394_s_at	KIAA1755: KIAA1755	AW014122	361.59	158.66	-2.28	-2.03	-202.93	*	89.14	88.33	-1.01	-0.69	-0.82	
218974_at	SOBP: sine oculis binding protein homolog (Drosophila)	NM_018013	274.13	120.69	-2.27	-1.88	-153.44	*	444.05	384.52	-1.15	-1.09	-59.54	
208078_s_at	SIK1: salt-inducible kinase 1	NM_030751	665.83	297.05	-2.24	-1.96	-368.78	*	279.82	191.39	-1.46	-1.28	-88.43	
210785_s_at	C1orf38: chromosome 1 open reading frame 38	AB035482	313.87	140.22	-2.24	-1.95	-173.65	*	246.28	191.93	-1.28	-1.15	-54.35	
228235_at	MGC16121: hypothetical protein MGC16121	BE048571	520.04	232.48	-2.24	-1.98	-287.55	*	270.24	190.66	-1.42	-1.19	-79.58	
235236_at	LOC100131897: Uncharacterized protein LOC100131897	AI991459	437.4	194.97	-2.24	-2.01	-242.43	*	143.07	143.37	1	0.9	0.3	
204802_at	RRAD: Ras-related associated with diabetes	NM_004165	833.96	374	-2.23	-2.1	-459.97	*	334.38	328.21	-1.02	-0.92	-6.18	
227051_at	Hs.43047.0	AU157716	4069.64	1826.25	-2.23	-2.1	-2243.39	*	3666.04	3019.51	-1.21	-1.14	-646.54	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
228325_at	KIAA0146: KIAA0146	AI363213	239.84	108.17	-2.22	-1.79	-131.67	*	124.99	105.01	-1.19	-0.95	-19.97	
210538_s_at	BIRC3: baculoviral IAP repeat-containing 3	U37546	351.21	158.64	-2.21	-1.95	-192.57	*	190.19	151.18	-1.26	-1.09	-39.01	
210818_s_at	BACH1: BTB and CNC homology 1, basic leucine zipper transcription factor 1	AF026199	420.85	190.18	-2.21	-1.88	-230.67	*	367.17	313.8	-1.17	-1.07	-53.37	
202668_at	EFNB2: ephrin-B2	BF001670	1104.13	502.5	-2.2	-1.98	-601.63	*	1267.82	822.11	-1.54	-1.48	-445.71	
227812_at	TNFRSF19: tumor necrosis factor receptor superfamily, member 19	BF432648	1399.78	636.21	-2.2	-2.04	-763.58	*	1552.27	1392.45	-1.11	-1.05	-159.83	
230417_at	GALNTL1: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	AI097463	266.35	121.05	-2.2	-1.65	-145.31	*	1116.17	837.58	-1.33	-1.25	-278.59	
244623_at	KCNQ5: potassium voltage-gated channel, KQT-like subfamily, member 5	BF513800	789.06	358.13	-2.2	-2.05	-430.93	*	415.54	306.59	-1.36	-1.19	-108.94	
202575_at	CRABP2: cellular retinoic acid binding protein 2	NM_001878	3478.06	1584.63	-2.19	-1.94	-1893.43	*	9552.27	8557.78	-1.12	-1.07	-994.5	
204803_s_at	RRAD: Ras-related associated with diabetes	NM_004165	1245.47	568.55	-2.19	-2.03	-676.92	*	512.85	437.42	-1.17	-1.13	-75.43	
214708_at	SNTB1: syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	BG484314	361.04	165.52	-2.18	-2.04	-195.51	*	229.81	143.25	-1.6	-1.46	-86.55	
227609_at	EPSTI1: epithelial stromal interaction 1 (breast)	AA633203	1700.85	778.81	-2.18	-2	-922.04	*	1206.72	819.08	-1.47	-1.37	-387.65	
230836_at	ST8SIA4: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	AI422986	194	89.27	-2.17	-1.64	-104.72	*	113.4	125.56	1.11	0.85	12.16	
1569512_at	Hs2.382226.1	BC022883	389.84	179.64	-2.17	-2	-210.2	*	43.15	21.88	-1.97	-1.02	-21.27	
202388_at	RGS2: regulator of G-protein signaling 2, 24kDa	NM_002923	1021.89	476.65	-2.14	-1.85	-545.24	*	839.22	567.55	-1.48	-1.4	-271.67	
202440_s_at	ST5: suppression of tumorigenicity 5	NM_005418	1394.38	652.62	-2.14	-1.96	-741.76	*	1031.58	871.16	-1.18	-1.1	-160.41	
210848_at	g6653225	AF187554	262.41	123.36	-2.13	-1.63	-139.04	*	236.51	330.29	1.4	1.25	93.78	
204254_s_at	VDR: vitamin D (1,25- dihydroxyvitamin D3) receptor	NM_000376	3034.82	1437	-2.11	-1.99	-1597.82	*	2357.03	2119.16	-1.11	-1.07	-237.88	
225601_at	HMGB3: high-mobility group box 3	AI806853	361.81	172.35	-2.1	-1.88	-189.46	*	279.87	307.38	1.1	1.01	27.51	
1569320_at	GPBP1L1: GC-rich promoter binding protein 1-like 1	CA391618	503.73	240.3	-2.1	-1.68	-263.42	*	40.79	69	1.69	1.24	28.21	
242786_at	Hs.133984.1	AI521166	365.55	175.07	-2.09	-1.75	-190.47	*	272.18	197.91	-1.38	-1.24	-74.27	
213006_at	CEBPD: CCAAT/enhancer binding protein (C/EBP), delta	AV655640	274.64	132.27	-2.08	-1.8	-142.37	*	176.9	128.82	-1.37	-1.22	-48.08	
1558378_a_at	AHNAK2: AHNAK nucleoprotein 2	BC004283	361.33	174.97	-2.07	-1.62	-186.36	*	372.03	340.82	-1.09	-1.04	-31.21	
201998_at	ST6GAL1: ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	AI743792	483	234.66	-2.06	-1.81	-248.34	*	507.34	524.47	1.03	0.98	17.14	
202450_s_at	CTSK: cathepsin K	NM_000396	1550.83	755.29	-2.05	-1.65	-795.54	*	6883.99	5897.46	-1.17	-1.1	-986.53	
204908_s_at	BCL3: B-cell CLL/lymphoma 3	NM_005178	1543.98	761.36	-2.03	-1.87	-782.62	*	1112.33	756.02	-1.47	-1.4	-356.31	
207652_s_at	CMKLR1: chemokine-like receptor 1	NM_004072	327.19	162.22	-2.02	-1.7	-164.97	*	377.8	249.89	-1.51	-1.37	-127.91	
202286_s_at	TACSTD2: tumor-associated calcium signal transducer 2	J04152	752.47	375.75	-2	-1.84	-376.72	*	798.84	538.95	-1.48	-1.39	-259.89	
209596_at	MXRA5: matrix-remodelling associated 5	AF245505	914.31	459.98	-1.99	-1.67	-454.33	*	3236.03	2783.14	-1.16	-1.07	-452.89	
218856_at	TNFRSF21: tumor necrosis factor receptor superfamily, member 21	NM_016629	268.69	134.84	-1.99	-1.74	-133.85	*	247.98	198.88	-1.25	-1.13	-49.1	
206417_at	CNGA1: cyclic nucleotide gated channel alpha 1	NM_000087	283.01	142.59	-1.98	-1.75	-140.42	*	215.65	174.34	-1.24	-1.11	-41.31	
244530_at	Hs.16135.0	T86276	205.35	103.6	-1.98	-1.61	-101.75	*	76.09	75.54	-1.01	-0.57	-0.56	
202183_s_at	KIF22: kinesin family member 22	NM_007317	204.54	104.08	-1.97	-1.56	-100.46	*	337.5	306.63	-1.1	-1.03	-30.87	
206363_at	MAF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	NM_005360	262.85	133.34	-1.97	-1.75	-129.51	*	426.62	269.32	-1.58	-1.46	-157.3	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
225842_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	AK026181	2741.44	1394.44	-1.97	-1.85	-1347.01	*	1253.72	809.37	-1.55	-1.37	-444.35	
238725_at	IRF1: interferon regulatory factor 1	AW392551	546.13	279.13	-1.96	-1.77	-267	*	168.59	152.05	-1.11	-0.77	-16.54	
213075_at	OLFML2A: olfactomedin-like 2A	AL050002	466.78	239.69	-1.95	-1.66	-227.09	*	1729.61	1677.53	-1.03	-0.98	-52.08	
52255_s_at	COL5A3: collagen, type V, alpha 3	AI984221	1362.3	698.49	-1.95	-1.67	-663.81	*	3701.58	2401.68	-1.54	-1.48	-1299.91	
201427_s_at	SEPP1: selenoprotein P, plasma, 1	NM_005410	232.24	119.77	-1.94	-1.62	-112.47	*	717.69	734.01	1.02	0.94	16.32	
204359_at	FLRT2: fibronectin leucine rich transmembrane protein 2	NM_013231	2846.81	1470.82	-1.94	-1.74	-1375.99	*	3538.84	2852.36	-1.24	-1.17	-686.48	
1556427_s_at	LRRN4CL: LRRN4 C-terminal like	AL834319	646.3	333.22	-1.94	-1.66	-313.09	*	1444.87	1097.74	-1.32	-1.25	-347.13	
206402_s_at	NPFF: neuropeptide FF-amide peptide precursor	NM_003717	276.04	142.9	-1.93	-1.66	-133.14	*	52.5	127.75	2.43	1.87	75.25	
227922_x_at	Hs.326048.1	AA156779	229.84	119.04	-1.93	-1.55	-110.8	*	109.15	105.76	-1.03	-0.84	-3.39	
228910_at	Hs.164261.0	AI870617	543.96	281.21	-1.93	-1.59	-262.75	*	1003.1	672.41	-1.49	-1.37	-330.69	
229784_at	MGC16121: hypothetical protein MGC16121	AA234096	988.89	513.6	-1.93	-1.76	-475.28	*	462.99	356.41	-1.3	-1.2	-106.58	
235174_s_at	LOC100128822: hypothetical LOC100128822	AW952781	222.59	115.31	-1.93	-1.58	-107.29	*	244.2	226.02	-1.08	-0.97	-18.18	
235046_at	Hs.176376.0	AA456099	326.96	170.42	-1.92	-1.73	-156.54	*	483.75	299.45	-1.62	-1.5	-184.29	
217997_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	AI795908	1240.4	651.45	-1.9	-1.8	-588.95	*	656.54	418.37	-1.57	-1.47	-238.17	
221840_at	PTPRE: protein tyrosine phosphatase, receptor type, E	AA775177	793.62	418.36	-1.9	-1.79	-375.26	*	591.2	395.48	-1.49	-1.39	-195.72	
227300_at	TMEM119: transmembrane protein 119	AL521682	1722.92	905.81	-1.9	-1.69	-817.11	*	2963.52	2956.94	-1	-0.91	-6.59	
230682_x_at	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3	BF515888	245.38	129.48	-1.9	-1.67	-115.9	*	68.17	94.77	1.39	1.07	26.6	
211368_s_at	CASP1: caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13700	631.75	334	-1.89	-1.71	-297.75	*	348.97	282.62	-1.23	-1.14	-66.35	
204255_s_at	VDR: vitamin D (1,25- dihydroxyvitamin D3) receptor	AA772285	2040.75	1087.67	-1.88	-1.78	-953.08	*	1610.52	1426.33	-1.13	-1.09	-184.19	
209417_s_at	IFI35: interferon-induced protein 35	BC001356	789.04	419.83	-1.88	-1.66	-369.21	*	662.11	707.73	1.07	0.99	45.62	
215506_s_at	DIRAS3: DIRAS family, GTP-binding RAS-like 3	AK021882	488.66	261.83	-1.87	-1.59	-226.83	*	558.93	497.97	-1.12	-1.05	-60.96	
221756_at	PIK3IP1: phosphoinositide-3-kinase interacting protein 1	AL540260	660.33	353.87	-1.87	-1.57	-306.46	*	1008.67	1163.3	1.15	1.1	154.64	
228396_at	PRKG1: protein kinase, cGMP-dependent, type I	AW274503	1327.07	711.35	-1.87	-1.75	-615.72	*	1417.54	1086.28	-1.3	-1.23	-331.26	
205818_at	DBC1: deleted in bladder cancer 1	NM_014618	813.99	436.52	-1.86	-1.74	-377.47	*	474.38	362.7	-1.31	-1.21	-111.67	
210659_at	CMKLR1: chemokine-like receptor 1	U79526	240.79	129.47	-1.86	-1.51	-111.33	*	301.9	240.72	-1.25	-1.16	-61.18	
214453_s_at	IFI44: interferon-induced protein 44	NM_006417	626.73	336.97	-1.86	-1.65	-289.76	*	959.94	782.47	-1.23	-1.15	-177.47	
216336_x_at	MT1E /// MT1H /// MT1M: metallothionein 1E /// metallothionein 1H /// metallothionein 1M	AL031602	826.81	445.19	-1.86	-1.66	-381.62	*	734.62	675.94	-1.09	-1.01	-58.68	
225722_at	Hs.95734.0	BF246937	756.06	407.42	-1.86	-1.57	-348.64	*	780.99	562.15	-1.39	-1.3	-218.85	
226438_at	SNTB1: syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	AK025100	491.98	264.97	-1.86	-1.66	-227.01	*	249.18	177.98	-1.4	-1.25	-71.19	
209546_s_at	APOL1: apolipoprotein L, 1	AF323540	1098.35	595.23	-1.85	-1.69	-503.13	*	1014.75	850.6	-1.19	-1.14	-164.15	
226301_at	C6orf192: chromosome 6 open reading frame 192	AV729072	393.29	213.12	-1.85	-1.63	-180.17	*	552.09	360.31	-1.53	-1.4	-191.78	
203153_at	IFIT1: interferon-induced protein with tetratricopeptide repeats 1	NM_001548	1122.01	610.53	-1.84	-1.57	-511.48	*	1817.28	2082.32	1.15	1.06	265.04	
212543_at	AIM1: absent in melanoma 1	U83115	799.35	434	-1.84	-1.69	-365.36	*	1063.09	905	-1.17	-1.12	-158.1	
207119_at	PRKG1: protein kinase, cGMP-dependent, type I	NM_006258	323.72	177.01	-1.83	-1.59	-146.71	*	320.74	250.37	-1.28	-1.16	-70.37	
202350_s_at	MATN2: matrilin 2	NM_002380	501.43	275.92	-1.82	-1.56	-225.51	*	1481.28	1304.05	-1.14	-1.05	-177.23	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
219477_s_at	THSD1 /// THSD1P: thrombospondin, type I, domain containing 1 /// thrombospondin, type I, domain containing 1 pseudogene	NM_018676	2189.13	1208.59	-1.81	-1.7	-980.55	*	1827.61	1565.84	-1.17	-1.07	-261.77	
223827_at	TNFRSF19: tumor necrosis factor receptor superfamily, member 19	AF246998	410.48	226.96	-1.81	-1.65	-183.51	*	427.22	382.53	-1.12	-1.02	-44.69	
228950_s_at	GPR177: G protein-coupled receptor 177	AL534095	1769.65	976.33	-1.81	-1.65	-793.32	*	2373.28	1926.82	-1.23	-1.18	-446.46	
229302_at	TMEM178: transmembrane protein 178	AA058832	249.89	137.91	-1.81	-1.63	-111.98	*	47.29	45.6	-1.04	-0.66	-1.69	
227014_at	ASPHD2: aspartate beta-hydroxylase domain containing 2	BE550881	1194.34	665.1	-1.8	-1.68	-529.24	*	781.62	598.21	-1.31	-1.23	-183.4	
227084_at	DTNA: dystrobrevin, alpha	AW339310	414.54	230.3	-1.8	-1.53	-184.24	*	338.44	240.43	-1.41	-1.28	-98.01	
242093_at	SYTL5: synaptotagmin-like 5	AW263497	326.76	182.02	-1.8	-1.63	-144.74	*	70.76	60.59	-1.17	-0.97	-10.18	
201596_x_at	KRT18: keratin 18	NM_000224	6204.7	3459.95	-1.79	-1.73	-2744.75	*	1398.45	907.72	-1.54	-1.33	-490.73	
205082_s_at	AOX1: aldehyde oxidase 1	AB046692	1423.04	794.16	-1.79	-1.64	-628.88	*	1503.32	1026.05	-1.47	-1.39	-477.27	
229307_at	ANKRD28: ankyrin repeat domain 28	N32051	1122.89	630.24	-1.78	-1.66	-492.65	*	619.75	469.82	-1.32	-1.25	-149.93	
1560821_at	ARHGAP22: Rho GTPase activating protein 22	BG122789	293.66	165.18	-1.78	-1.59	-128.48	*	282.54	183.54	-1.54	-1.38	-99	
212624_s_at	CHN1: chimerin (chimaerin) 1	BF339445	3033.76	1716.4	-1.77	-1.61	-1317.36	*	4935.5	4065.65	-1.21	-1.16	-869.86	
204072_s_at	FRY: furry homolog (Drosophila)	NM_023037	2253.45	1278.54	-1.76	-1.63	-974.91	*	2169.3	1786.68	-1.21	-1.13	-382.62	
205130_at	RAGE: renal tumor antigen	NM_014226	1614.52	918.1	-1.76	-1.6	-696.42	*	827.36	594.39	-1.39	-1.23	-232.97	
223327_x_at	LOC727751 /// LOC727849 /// LOC80154: hypothetical LOC727751 /// similar to cis-Golgi matrix protein GM130 /// hypothetical LOC80154	AF316855	705.34	401.44	-1.76	-1.51	-303.9	*	232.18	360.04	1.55	1.28	127.86	
226769_at	FIBIN: fin bud initiation factor homolog (zebrafish)	AI802391	2640.9	1499.34	-1.76	-1.63	-1141.56	*	2516.22	2036.3	-1.24	-1.18	-479.92	
205968_at	KCNS3: potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	NM_002252	384.73	219.71	-1.75	-1.51	-165.02	*	675.6	587	-1.15	-1.08	-88.6	
208161_s_at	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_020037	1046.81	596.77	-1.75	-1.67	-450.04	*	360.44	418.16	1.16	1.09	57.72	
209640_at	PML: promyelocytic leukemia	M79462	406.54	232.47	-1.75	-1.54	-174.07	*	446.66	350.33	-1.27	-1.21	-96.33	
224701_at	PARP14: poly (ADP-ribose) polymerase family, member 14	AA056548	1332.85	759.54	-1.75	-1.66	-573.32	*	779.86	691.28	-1.13	-1.07	-88.58	
206703_at	CHRNB1: cholinergic receptor, nicotinic, beta 1 (muscle)	NM_000747	298.12	171.15	-1.74	-1.52	-126.97	*	364.4	417.53	1.15	1.06	53.13	
208213_s_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	NM_003471	513.84	296.12	-1.74	-1.54	-217.72	*	443.12	277.02	-1.6	-1.41	-166.1	
209827_s_at	IL16: interleukin 16 (lymphocyte chemoattractant factor)	NM_004513	387.78	222.58	-1.74	-1.59	-165.21	*	221.82	162.33	-1.37	-1.13	-59.49	
221029_s_at	WNT5B: wingless-type MMTV integration site family, member 5B	NM_030775	2437.24	1410.02	-1.73	-1.6	-1027.22	*	2587.77	1717.37	-1.51	-1.42	-870.39	
201015_s_at	JUP: junction plakoglobin	NM_021991	384.72	224.12	-1.72	-1.54	-160.6	*	407.04	246.91	-1.65	-1.48	-160.13	
206298_at	ARHGAP22: Rho GTPase activating protein 22	NM_021226	2097.45	1220	-1.72	-1.54	-877.46	*	2260.85	1504.32	-1.5	-1.42	-756.53	
219550_at	ROBO3: roundabout, axon guidance receptor, homolog 3 (Drosophila)	NM_022370	1459.46	846.65	-1.72	-1.61	-612.81	*	653.52	662.43	1.01	0.96	8.91	
219572_at	CADPS2: Ca++-dependent secretion activator 2	NM_017954	423.64	247.54	-1.71	-1.51	-176.09	*	728	581.67	-1.25	-1.21	-146.34	
233540_s_at	CDK5RAP2: CDK5 regulatory subunit associated protein 2	AK025867	2979.75	1755.32	-1.7	-1.58	-1224.43	*	1454.37	1304.49	-1.11	-1.06	-149.88	
209890_at	TSPAN5: tetraspanin 5	AF065389	2157.23	1277.32	-1.69	-1.53	-879.91	*	1729.25	1378.48	-1.25	-1.19	-350.77	
227488_at	MGC16121: hypothetical protein MGC16121	AV728999	462.01	273	-1.69	-1.55	-189.01	*	205.55	138.72	-1.48	-1.23	-66.83	

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
234986_at	Hs.315562.0	AA630626	1073.89	634.59	-1.69	-1.58	-439.3	*	1004.75	694.93	-1.45	-1.33	-309.82	
223734_at	C4orf49: chromosome 4 open reading frame 49	AF329088	2792.35	1661.26	-1.68	-1.6	-1131.09	*	2298.97	1492.57	-1.54	-1.43	-806.4	
238478_at	BNC2: basonuclin 2	H97386	1530.87	909.4	-1.68	-1.56	-621.47	*	1075.24	819.44	-1.31	-1.25	-255.8	
205529_s_at	RUNX1T1: runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	NM_004349	1431.93	863.6	-1.66	-1.55	-568.33	*	1185.36	981.48	-1.21	-1.14	-203.88	
232568_at	MGC24103: hypothetical MGC24103	AU145658	564.67	340.3	-1.66	-1.56	-224.38	*	26.79	30.77	1.15	0.54	3.98	
204136_at	COL7A1: collagen, type VII, alpha 1	NM_000094	816.81	503.31	-1.62	-1.52	-313.5	*	354.43	557	1.57	1.36	202.57	
213790_at	ADAM12: ADAM metallopeptidase domain 12	W46291	2255.8	1389.72	-1.62	-1.52	-866.08	*	2859.9	2244.36	-1.27	-1.22	-615.54	
41660_at	CELSR1: cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	AL031588	379.06	234.03	-1.62	-1.54	-145.03	*	162.94	152.43	-1.07	-0.94	-10.51	
240165_at	Hs.271498.0	AI678013	653.76	403.97	-1.62	-1.54	-249.79	*	60.57	82.35	1.36	0.98	21.78	
205083_at	AOX1: aldehyde oxidase 1	NM_001159	2164.96	1345.1	-1.61	-1.51	-819.86	*	2045.68	1394.97	-1.47	-1.36	-650.72	
209825_s_at	UCK2: uridine-cytidine kinase 2	BC002906	2452.33	1520.4	-1.61	-1.51	-931.93	*	2356.41	1885.72	-1.25	-1.16	-470.7	
230405_at	C5orf56: chromosome 5 open reading frame 56	AI143416	1219.65	763.68	-1.6	-1.51	-455.97	*	636.86	561.46	-1.13	-1.03	-75.4	

Down-Regulated Genes at Day 10 in Response to 2nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
221829_s_at	TNPO1: transportin 1	AI307759	4785.7	4284.12	-1.12	-0.53	-501.58		19593.51	3323.47	-5.9	-3.78	-16270.04	*
227751_at	PDCD5: programmed cell death 5	AI817145	352.11	262.27	-1.34	-1.24	-89.84		233.26	56.76	-4.11	-2.29	-176.5	*
1558501_at	DNM3: dynamin 3	AI631915	33.91	21.95	-1.55	-0.45	-11.97		202.34	49.83	-4.06	-2.25	-152.51	*
202242_at	TSPAN7: tetraspanin 7	NM_004615	132.08	39.64	-3.33	-2.08	-92.44		308.54	95.02	-3.25	-2.53	-213.52	*
244745_at	RERG: RAS-like, estrogen-regulated, growth inhibitor	BG484193	29.43	14.95	-1.97	-0.94	-14.48		324.53	104.72	-3.1	-2.84	-219.81	*
227758_at	RERG: RAS-like, estrogen-regulated, growth inhibitor	AW294092	88.72	7.22	-12.29	-6.88	-81.5		808.28	261.23	-3.09	-2.83	-547.05	*
200795_at	SPARCL1: SPARC-like 1 (hevin)	NM_004684	19.65	18.64	-1.05	-0.32	-1.01		212.68	69.58	-3.06	-2.39	-143.1	*
203917_at	CXADR: coxsackie virus and adenovirus receptor	NM_001338	102.91	101.75	-1.01	-0.58	-1.16		190.24	63.13	-3.01	-2.06	-127.12	*
219970_at	GIPC2: GIPC PDZ domain containing family, member 2	NM_017655	113.85	52.37	-2.17	-1.79	-61.48		189.99	67.77	-2.8	-2.56	-122.21	*
209395_at	CHI3L1: chitinase 3-like 1 (cartilage glycoprotein-39)	M80927	81.83	16.53	-4.95	-3.62	-65.3		343.85	132.24	-2.6	-2.4	-211.61	*
222722_at	OGN: osteoglycin	AV700059	49.17	31.27	-1.57	-1.14	-17.91		640.79	251.18	-2.55	-2.32	-389.61	*
243438_at	PDE7B: phosphodiesterase 7B	BE968570	197.52	81.87	-2.41	-1.44	-115.66		179.23	72.49	-2.47	-1.54	-106.74	*
219700_at	PLXDC1: plexin domain containing 1	NM_020405	56.18	30.96	-1.81	-1.14	-25.22		392.78	160.4	-2.45	-2.06	-232.38	*
238451_at	MPP7: membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	BF693302	112.51	41.75	-2.69	-1.88	-70.75		172.68	70.97	-2.43	-1.86	-101.71	*
210133_at	CCL11: chemokine (C-C motif) ligand 11	D49372	134.7	85.15	-1.58	-1.25	-49.55		236.01	97.91	-2.41	-1.97	-138.1	*
215783_s_at	ALPL: alkaline phosphatase, liver/bone/kidney	X14174	325.8	238.66	-1.37	-1.17	-87.14		543.02	229.88	-2.36	-2.02	-313.14	*
200803_s_at	TMBIM6: transmembrane BAX inhibitor motif containing 6	AF033095	7670.69	7149.79	-1.07	-0.72	-520.89		19179.82	8188.73	-2.34	-1.67	-10991.08	*
218730_s_at	OGN: osteoglycin	NM_014057	35.87	47.78	1.33	0.93	11.91		359.29	157.31	-2.28	-2.02	-201.98	*
227320_at	FAM101A: family with sequence similarity 101, member A	AW264333	732.28	619.31	-1.18	-1.04	-112.97		841.15	387.13	-2.17	-1.81	-454.02	*
206336_at	CXCL6: chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993	191.7	95.04	-2.02	-1.71	-96.65		1412.53	668.77	-2.11	-2.01	-743.77	*
205266_at	LIF: leukemia inhibitory factor (cholinergic differentiation factor)	NM_002309	1044.1	654.34	-1.6	-1.4	-389.76		643.32	305.73	-2.1	-1.81	-337.6	*
218824_at	PNMAL1: PNMA-like 1	NM_018215	198.49	117.27	-1.69	-1.34	-81.22		411.59	197.19	-2.09	-1.87	-214.39	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
1554685_a_at	KIAA1199: KIAA1199	BC020256	2790.73	1763.52	-1.58	-1.48	-1027.21		2697.29	1301.29	-2.07	-1.96	-1396	*
202995_s_at	FBLN1: fibulin 1	NM_006486	422.29	494.64	1.17	1	72.35		1359.52	666.13	-2.04	-1.86	-693.39	*
202994_s_at	FBLN1: fibulin 1	Z95331	343.48	315.79	-1.09	-0.91	-27.7		1065.49	523.89	-2.03	-1.91	-541.61	*
1553142_at	C13orf31: chromosome 13 open reading frame 31	NM_153218	829.9	526.14	-1.58	-1.46	-303.76		401.64	198.12	-2.03	-1.89	-203.52	*
243010_at	MSI2: musashi homolog 2 (Drosophila)	BE000929	131.72	66.3	-1.99	-1.52	-65.42		202.09	100.25	-2.02	-1.64	-101.85	*
216184_s_at	RIMS1: regulating synaptic membrane exocytosis 1	AF263310	228.47	198.88	-1.15	-1	-29.59		221.54	110.95	-2	-1.58	-110.6	*
235655_at	Hs.53997.0	AI435514	151.41	233.58	1.54	1.33	82.17		338.09	175.44	-1.93	-1.76	-162.66	*
1554474_a_at	MOXD1: monooxygenase, DBH-like 1	BC018756	693.43	547.64	-1.27	-1.16	-145.79		1366.33	709.64	-1.93	-1.84	-656.69	*
205226_at	PDGFRL: platelet-derived growth factor receptor-like	NM_006207	34.55	17.89	-1.93	-0.95	-16.66		292.51	152.52	-1.92	-1.74	-139.99	*
223623_at	C2orf40: chromosome 2 open reading frame 40	AF325503	148.72	58.09	-2.56	-1.82	-90.63		1053.96	560.98	-1.88	-1.78	-492.99	*
201042_at	TGM2: transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	AL031651	3254.33	2317.32	-1.4	-1.35	-937.01		1020.09	550.72	-1.85	-1.6	-469.37	*
217996_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	AA576961	3162.51	2062.91	-1.53	-1.41	-1099.6		2104.46	1137.08	-1.85	-1.68	-967.37	*
205376_at	INPP4B: inositol polyphosphate-4-phosphatase, type II, 105kDa	NM_003866	335.28	227.7	-1.47	-1.33	-107.58		396.68	215.1	-1.84	-1.7	-181.59	*
236140_at	GCLM: glutamate-cysteine ligase, modifier subunit	AI753488	1742.78	1410.78	-1.24	-1.16	-332		1445.91	783.82	-1.84	-1.73	-662.09	*
229127_at	Hs.7107.0	BF195118	150.35	120.46	-1.25	-1.02	-29.89		254.66	139.08	-1.83	-1.6	-115.58	*
204470_at	CXCL1: chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	NM_001511	708.69	459.36	-1.54	-1.34	-249.33		2982.27	1664.15	-1.79	-1.7	-1318.12	*
231986_at	RIMS1: regulating synaptic membrane exocytosis 1	AL035633	706.22	522.98	-1.35	-1.26	-183.24		699.77	389.91	-1.79	-1.65	-309.85	*
1557196_a_at	Hs2.153652.1	AL831886	107.24	140.71	1.31	0.9	33.47		265.92	148.89	-1.79	-1.58	-117.03	*
235736_at	Hs.178144.0	BF000047	81.27	67.14	-1.21	-0.88	-14.13		233.62	131.1	-1.78	-1.52	-102.52	*
209708_at	MOXD1: monooxygenase, DBH-like 1	AY007239	665.83	412.59	-1.61	-1.42	-253.24		1220.32	690.98	-1.77	-1.64	-529.33	*
212613_at	BTN3A2: butyrophilin, subfamily 3, member A2	AI991252	454.58	363.15	-1.25	-1.06	-91.43		784.24	442	-1.77	-1.63	-342.24	*
223537_s_at	WNT5B: wingless-type MMTV integration site family, member 5B	AW007350	522.13	509.27	-1.03	-0.96	-12.86		504.73	287.19	-1.76	-1.58	-217.54	*
1558847_at	Hs2.353773.1	BQ576193	453.93	281.75	-1.61	-1.39	-172.18		521.25	296.89	-1.76	-1.63	-224.36	*
203828_s_at	IL32: interleukin 32	NM_004221	386.01	283.22	-1.36	-1.25	-102.79		1002.01	572.96	-1.75	-1.64	-429.06	*
243065_at	Hs.278177.0	AA809449	282.69	313.78	1.11	0.98	31.09		257.86	148.88	-1.73	-1.54	-108.98	*
206432_at	HAS2: hyaluronan synthase 2	NM_005328	3026.97	2259.55	-1.34	-1.21	-767.41		3262.97	1894.54	-1.72	-1.57	-1368.42	*
1552487_a_at	BNC1: basonuclin 1	NM_001717	347.88	276.62	-1.26	-1.18	-71.26		281.2	164.53	-1.71	-1.51	-116.67	*
202566_s_at	SVIL: supervillin	AF051851	1695.11	1225.88	-1.38	-1.28	-469.23		1763.59	1036.47	-1.7	-1.64	-727.12	*
228635_at	PCDH10: protocadherin 10	AI640307	1313	853.27	-1.54	-1.46	-459.73		947.89	561.78	-1.69	-1.59	-386.11	*
215073_s_at	NR2F2: nuclear receptor subfamily 2, group F, member 2	AL554245	1246.03	1353.54	1.09	1.01	107.51		979.7	582.94	-1.68	-1.51	-396.76	*
218542_at	CEP55: centrosomal protein 55kDa	NM_018131	47.92	46.8	-1.02	-0.57	-1.12		590.01	351.95	-1.68	-1.52	-238.06	*
209506_s_at	NR2F1: nuclear receptor subfamily 2, group F, member 1	BC004154	412.72	610.74	1.48	1.4	198.02		420.91	252.39	-1.67	-1.55	-168.52	*
203382_s_at	APOE: apolipoprotein E	NM_000041	77.13	27.19	-2.84	-1.67	-49.94		1129.56	678.5	-1.66	-1.58	-451.07	*
213060_s_at	CHI3L2: chitinase 3-like 2	U58515	78.78	73.92	-1.07	-0.88	-4.86		377.29	227.21	-1.66	-1.59	-150.08	*
225436_at	FAM108C1: family with sequence similarity 108, member C1	AI339710	669.17	461	-1.45	-1.31	-208.17		811.73	490.89	-1.65	-1.56	-320.84	*
230372_at	HAS2: Hyaluronan synthase 2	AI374739	4185.98	3128.13	-1.34	-1.27	-1057.86		4613.01	2838.08	-1.63	-1.54	-1774.93	*
241986_at	BMPER: BMP binding endothelial regulator	AI423201	480.37	318.93	-1.51	-1.36	-161.44		1205.86	756.75	-1.59	-1.54	-449.12	*

Appendix 1.3 Up-Regulatd Genes in Response to 20nM BMP6

Up-Regulated Genes at Both Days in Response to 20nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
218839_at	HEY1: hairy/enhancer-of-split related with YRPW motif 1	NM_012258	21.03	1084.28	51.55	29.74	1063.24	*	3.12	4081.1	1307.73	322.03	4077.98	*
204379_s_at	FGFR3: fibroblast growth factor receptor 3	NM_000142	29.68	2176.77	73.33	53.56	2147.08	*	15.79	6454.56	408.77	187.34	6438.77	*
1552340_at	SP7: Sp7 transcription factor	NM_152860	35.92	945.41	26.32	15.78	909.5	*	13.26	4440.75	334.92	162.22	4427.49	*
237056_at	INSC: inscuteable homolog (Drosophila)	BF432206	15.75	480.47	30.51	21.42	464.73	*	40.13	4395.89	109.53	72.71	4355.76	*
44783_s_at	HEY1: hairy/enhancer-of-split related with YRPW motif 1	R61374	84.88	1824.44	21.49	14.17	1739.56	*	63.85	6164.56	96.55	59.11	6100.71	*
226814_at	ADAMTS9: ADAM metallopeptidase with thrombospondin type 1 motif, 9	AI431730	36.94	221.88	6.01	4.8	184.94	*	45.09	2808.77	62.29	37.81	2763.68	*
223541_at	HAS3: hyaluronan synthase 3	AF232772	99.32	2549.06	25.66	19.9	2449.74	*	86.88	4461.32	51.35	39.61	4374.44	*
205908_s_at	OMD: osteomodulin	NM_005014	22.89	2015.28	88.05	60	1992.39	*	224.85	10297.54	45.8	27.99	10072.69	*
203700_s_at	DIO2: deiodinase, iodothyronine, type II	NM_013989	113.5	3023.95	26.64	21.46	2910.45	*	126.84	4966.65	39.16	32.35	4839.81	*
208937_s_at	ID1: inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	D13889	121.29	9312.14	76.78	52.25	9190.85	*	267.43	10372.9	38.79	31	10105.47	*
240509_s_at	GREM2: gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	BF064262	15.32	619.28	40.41	24.04	603.96	*	46.36	1689.73	36.45	28.23	1643.37	*
235504_at	GREM2: gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	BE786990	26.95	482.04	17.89	9.91	455.1	*	31.39	1132.86	36.09	22.76	1101.47	*
223723_at	MFI2: antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	BC001875	252.05	697.89	2.77	2.49	445.84	*	216.29	7478.89	34.58	23.84	7262.6	*
228819_at	TSPAN18: tetraspanin 18	AI161133	54.48	198.26	3.64	2.61	143.79	*	45.87	1524.93	33.24	21.08	1479.06	*
235182_at	ISM1: isthmin 1 homolog (zebrafish)	AI816793	27.74	457.32	16.49	11.03	429.58	*	53.68	1772.32	33.02	22.67	1718.64	*
227307_at	TSPAN18: Tetraspanin 18	AL565381	71.08	526.76	7.41	6.38	455.68	*	109.23	3441.89	31.51	26.87	3332.67	*
231240_at	DIO2: deiodinase, iodothyronine, type II	AI038059	109.23	2079.05	19.03	14.24	1969.82	*	114.87	3552.97	30.93	21.48	3438.1	*
220794_at	GREM2: gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	NM_022469	112.67	1636.6	14.53	12.27	1523.92	*	114.83	3343.1	29.11	25.81	3228.27	*
224997_x_at	H19: H19, imprinted maternally expressed transcript (non-protein coding)	AL575306	62.42	1869.39	29.95	23.88	1806.97	*	162.99	4433.49	27.2	23.46	4270.5	*
235775_at	TMTC2: transmembrane and tetratricopeptide repeat containing 2	AI765006	62.77	371.55	5.92	4.44	308.78	*	75.51	2003.32	26.53	21.68	1927.81	*
235911_at	Hs.184727.0	AI885815	839.27	1776.72	2.12	2.02	937.45	*	348.19	8811.25	25.31	18.79	8463.06	*
224022_x_at	WNT16: wingless-type MMTV integration site family, member 16	AF169963	6.23	106.63	17.13	6.37	100.41	*	10.09	247.67	24.55	12.45	237.58	*
219743_at	HEY2: hairy/enhancer-of-split related with YRPW motif 2	NM_012259	47.61	845.24	17.75	13.77	797.63	*	117.58	2718.27	23.12	19.51	2600.69	*
228574_at	TMTC2: Transmembrane and tetratricopeptide repeat containing 2	AI862551	41.95	257.66	6.14	4.09	215.71	*	103.1	2376.69	23.05	19.23	2273.59	*
224646_x_at	H19: H19, imprinted maternally expressed transcript (non-protein coding)	BF569051	92.72	2647.59	28.55	21.74	2554.86	*	275.86	6116.05	22.17	19.7	5840.19	*
1558706_a_at	ATOH8: Atonal homolog 8 (Drosophila)	AL831857	15.89	615.96	38.75	20.74	600.06	*	17.12	355.62	20.77	11.15	338.5	*
205679_x_at	ACAN: aggrecan	NM_013227	628.14	5226.64	8.32	6.7	4598.5	*	504.84	10352.59	20.51	15.56	9847.75	*
207692_s_at	ACAN: aggrecan	NM_001135	610.85	4657.46	7.62	6.2	4046.61	*	485	9722.66	20.05	15.3	9237.66	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
203699_s_at	DIO2: deiodinase, iodothyronine, type II	U53506	61.58	819.97	13.32	7.26	758.39	*	57.16	1145.34	20.04	10.97	1088.18	*
231798_at	NOG: noggin	AL575177	46.78	1679.82	35.91	16.96	1633.04	*	32.47	614.56	18.93	8.07	582.09	*
207147_at	DLX2: distal-less homeobox 2	NM_004405	87.03	1822.45	20.94	16.09	1735.42	*	61.22	1145.9	18.72	13.69	1084.68	*
222921_s_at	HEY2: hairy/enhancer-of-split related with YRPW motif 2	AF232238	52.96	590.77	11.16	9.14	537.81	*	100.4	1833.4	18.26	15.83	1733	*
228195_at	C2orf88: chromosome 2 open reading frame 88	BE645119	72.53	298.63	4.12	2.95	226.1	*	42.12	725.95	17.24	11.2	683.83	*
216604_s_at	SLC7A8: solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	AL365343	11.91	155.42	13.05	6.63	143.51	*	8.9	151.67	17.04	4.76	142.77	*
209652_s_at	PGF: placental growth factor	BC001422	337.4	4525.58	13.41	11.77	4188.18	*	112.27	1882.6	16.77	11.68	1770.32	*
209886_s_at	SMAD6: SMAD family member 6	AI628464	23.92	240.8	10.06	6.37	216.87	*	29.34	478.34	16.31	10.34	449	*
221541_at	CRISPLD2: cysteine-rich secretory protein LCCL domain containing 2	AL136861	375.66	2072.68	5.52	4.9	1697.02	*	189.52	3046.66	16.08	13.01	2857.13	*
205907_s_at	OMD: osteomodulin	AI765819	60.11	3909.4	65.04	52.78	3849.29	*	697.79	11059.03	15.85	9.88	10361.24	*
220190_s_at	GTF2A1L /// STON1 /// STON1-GTF2A1L: general transcription factor IIA, 1-like /// stonin 1 /// STON1-GTF2A1L readthrough transcript	NM_006873	41.41	220.53	5.33	4.43	179.12	*	21.18	332.44	15.7	11.81	311.26	*
204249_s_at	LMO2: LIM domain only 2 (rhombotin-like 1)	NM_005574	23.62	1093.8	46.31	32.68	1070.18	*	28.32	438.14	15.47	10.27	409.81	*
220180_at	CCDC68: coiled-coil domain containing 68	NM_025214	68.39	1591.82	23.28	17.81	1523.43	*	172.86	2668.07	15.43	13.09	2495.21	*
209167_at	GPM6B: glycoprotein M6B	AI419030	135.11	838.02	6.2	5.67	702.91	*	420.45	6397.05	15.21	13.57	5976.6	*
204363_at	F3: coagulation factor III (thromboplastin, tissue factor)	NM_001993	40.83	228.58	5.6	3.94	187.75	*	30.06	453.26	15.08	11.33	423.2	*
215059_at	Hs.51515.0	AA053967	204.74	1155.83	5.65	5.05	951.09	*	281.81	3827.54	13.58	11.78	3545.73	*
209170_s_at	GPM6B: glycoprotein M6B	AF016004	114.37	960.39	8.4	7.07	846.02	*	476.15	6422.46	13.49	10.96	5946.31	*
228890_at	ATOH8: atonal homolog 8 (Drosophila)	BF434995	89.76	2619.58	29.18	18.19	2529.83	*	104.19	1393.78	13.38	8.99	1289.58	*
210279_at	GPR18: G protein-coupled receptor 18	AF261135	55.09	165.47	3	2.46	110.38	*	14.02	178.9	12.76	7.3	164.87	*
216235_s_at	EDNRA: endothelin receptor type A	S81545	114.71	710.34	6.19	4.72	595.63	*	156.93	1988.58	12.67	10.74	1831.65	*
213931_at	ID2 /// ID2B: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)	AI819238	188.07	1289.14	6.85	6.13	1101.07	*	70.14	871.72	12.43	9.94	801.57	*
203698_s_at	FRZB: frizzled-related protein	NM_001463	9.62	132.41	13.76	8.4	122.79	*	61	710.02	11.64	8.23	649.03	*
204463_s_at	EDNRA: endothelin receptor type A	AU118882	281.21	1291.68	4.59	3.89	1010.47	*	289.67	3361.89	11.61	10.6	3072.22	*
204642_at	S1PR1: sphingosine-1-phosphate receptor 1	NM_001400	86.86	209.14	2.41	2.13	122.28	*	80.95	915.16	11.3	9.68	834.21	*
227610_at	TSPAN11: tetraspanin 11	BE858239	38.64	265.22	6.86	4.58	226.59	*	41.06	463.21	11.28	7.13	422.15	*
241560_at	Hs.164225.0	AI927941	306.15	1646.33	5.38	5	1340.17	*	489.19	5496.33	11.24	9.8	5007.14	*
231795_at	STON1: stonin 1	BG289281	80.37	393.4	4.89	3.78	313.03	*	90.22	997.86	11.06	8.55	907.63	*
223754_at	C2orf88: chromosome 2 open reading frame 88	BC005083	42.39	183.25	4.32	2.2	140.87	*	48.45	523.97	10.82	6.4	475.53	*
226492_at	SEMA6D: sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	AL036088	234.59	1188.25	5.07	4.49	953.66	*	258.23	2794.09	10.82	9.87	2535.85	*
233882_s_at	SEMA6D: sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	AK022831	33.39	158.93	4.76	3.55	125.54	*	38.87	397.35	10.22	7.72	358.48	*
224964_s_at	GNG2: guanine nucleotide binding protein (G protein), gamma 2	AK026424	457.28	1974.63	4.32	4.07	1517.35	*	747.71	7581.41	10.14	9.17	6833.69	*
210881_s_at	IGF2 /// INS-IGF2: insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	M17863	93.74	1172.7	12.51	9.71	1078.96	*	132.89	1340.38	10.09	8.52	1207.48	*
204844_at	ENPEP: glutamyl aminopeptidase (aminopeptidase A)	L12468	160.21	385.63	2.41	2.11	225.43	*	132.8	1338.43	10.08	8.54	1205.62	*
1557359_at	LOC285758: hypothetical protein LOC285758	BC037331	136.69	415.28	3.04	2.4	278.59	*	55.87	560.21	10.03	7.27	504.34	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
224925_at	PREX1: phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	AL445192	94.63	327.52	3.46	2.9	232.88	*	34.95	340.9	9.76	7.78	305.96	*
207388_s_at	PTGES: prostaglandin E synthase	NM_004878	65.04	990.74	15.23	10.65	925.69	*	92.24	867.8	9.41	7.78	775.56	*
212850_s_at	LRP4: low density lipoprotein receptor-related protein 4	AA584297	226.99	1425.35	6.28	5.38	1198.36	*	180.71	1691.18	9.36	7.9	1510.47	*
243607_at	Hs.47189.0	AI694327	40.47	375.92	9.29	6.77	335.45	*	25.68	236.08	9.19	5.32	210.41	*
204464_s_at	EDNRA: endothelin receptor type A	NM_001957	338.05	1861.82	5.51	4.66	1523.78	*	555.79	5095.83	9.17	8.17	4540.04	*
1559280_a_at	Hs2.105196.1	AA483467	22.72	131.94	5.81	3.95	109.22	*	22.19	191.45	8.63	6.01	169.26	*
231778_at	DLX3: distal-less homeobox 3	AI769274	40.83	577.61	14.15	7.46	536.78	*	48.09	412.76	8.58	4.87	364.67	*
230319_at	Hs.90250.0	AI222435	555.4	2501.69	4.5	3.83	1946.29	*	638.36	5418.68	8.49	7.51	4780.33	*
213707_s_at	DLX5: distal-less homeobox 5	NM_005221	311.68	2245.67	7.2	6.24	1933.98	*	357.93	3037.97	8.49	7.76	2680.03	*
215306_at	Hs.161283.0	AL049443	284.85	1434.87	5.04	4.52	1150.02	*	315.51	2674.62	8.48	7.51	2359.11	*
229459_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	AV723914	69.51	194.5	2.8	2.24	124.99	*	58.15	492.54	8.47	6.93	434.38	*
236035_at	Hs.65788.0	AW190406	87.68	554.99	6.33	5.19	467.3	*	147.82	1235.53	8.36	7.55	1087.71	*
227719_at	SMAD9: SMAD family member 9	AA934610	328.57	4566.77	13.9	12.77	4238.2	*	404.8	3379.26	8.35	7.67	2974.46	*
1560477_a_at	SAMD11: sterile alpha motif domain containing 11	AK054643	97.33	1075.75	11.05	6.89	978.42	*	90.13	745.78	8.27	5.72	655.66	*
226346_at	MEX3A: mex-3 homolog A (C. elegans)	AA527151	135.38	315.04	2.33	1.92	179.65	*	81.71	666.1	8.15	6.12	584.39	*
210819_x_at	DIO2: deiodinase, iodothyronine, type II	AB041844	32.67	189.95	5.81	3.97	157.28	*	30.72	243.87	7.94	6.12	213.15	*
207069_s_at	SMAD6: SMAD family member 6	NM_005585	298.92	2713.87	9.08	7.59	2414.95	*	355.81	2824.4	7.94	7.07	2468.59	*
228708_at	RAB27B: RAB27B, member RAS oncogene family	BF438386	275.4	1526.08	5.54	4.72	1250.68	*	812.06	6431.58	7.92	7.05	5619.52	*
205290_s_at	BMP2: bone morphogenetic protein 2	NM_001200	55.63	198.61	3.57	2.3	142.98	*	101.28	770.5	7.61	5.19	669.22	*
202410_x_at	IGF2 /// INS-IGF2: insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	NM_000612	188.67	1984.15	10.52	8.82	1795.48	*	272.18	2044.87	7.51	6.47	1772.69	*
201427_s_at	SEPP1: selenoprotein P, plasma, 1	NM_005410	232.24	840.46	3.62	3.21	608.21	*	717.69	5336.73	7.44	6.06	4619.03	*
220975_s_at	C1QTNF1: C1q and tumor necrosis factor related protein 1	NM_030968	314.41	867.99	2.76	2.45	553.58	*	399.82	2968.91	7.43	7.03	2569.1	*
213413_at	STON1: stonin 1	BG434174	964.46	3779.15	3.92	3.5	2814.7	*	799.14	5928.61	7.42	6.64	5129.47	*
218693_at	TSPAN15: tetraspanin 15	NM_012339	26.48	259.88	9.81	4.43	233.39	*	21.54	159.49	7.4	4.74	137.95	*
210948_s_at	LEF1: lymphoid enhancer-binding factor 1	AF294627	122.46	278.9	2.28	2.13	156.43	*	64.99	476.25	7.33	6.54	411.26	*
204014_at	DUSP4: dual specificity phosphatase 4	NM_001394	214.77	657.47	3.06	2.84	442.69	*	57.98	424.43	7.32	5.94	366.45	*
1553840_a_at	CCDC149: coiled-coil domain containing 149	NM_173463	37.37	168.72	4.51	1.88	131.35	*	48.96	357.85	7.31	4.08	308.89	*
219747_at	C4orf31: chromosome 4 open reading frame 31	NM_024574	784.19	3211.03	4.09	3.72	2426.84	*	1023.82	7478.08	7.3	6.71	6454.26	*
206746_at	BFSP1: beaded filament structural protein 1, filensin	NM_001195	98.05	824.01	8.4	6.97	725.96	*	97.7	711.53	7.28	5.55	613.83	*
209291_at	ID4: inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AW157094	611.75	5041.81	8.24	7.65	4430.05	*	455.18	3307.17	7.27	6.76	2851.99	*
209466_x_at	PTN: pleiotrophin	M57399	316.74	669.69	2.11	1.78	352.94	*	460.16	3338.8	7.26	6.42	2878.64	*
209292_at	ID4: Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AL022726	105.74	1188.82	11.24	9.58	1083.08	*	86.67	621.51	7.17	6.05	534.83	*
205016_at	TGFA: transforming growth factor, alpha	NM_003236	57.35	263.06	4.59	3.44	205.71	*	44.36	301.96	6.81	4.6	257.61	*
207826_s_at	ID3: inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	NM_002167	1429.73	10646.87	7.45	6.31	9217.14	*	1717.39	11524.28	6.71	5.48	9806.89	*
235194_at	TPCN2: two pore segment channel 2	BF663662	54.29	166.94	3.07	1.72	112.65	*	37.93	254.16	6.7	3.75	216.23	*
229778_at	C12orf39: chromosome 12 open reading frame 39	BE326710	506.09	884.69	1.75	1.65	378.61	*	37.34	244.55	6.55	4.94	207.21	*
221658_s_at	IL21R: interleukin 21 receptor	AF269133	47.9	391.51	8.17	6.23	343.61	*	40.57	263.09	6.48	4.92	222.51	*
211737_x_at	PTN: pleiotrophin	BC005916	369.16	935.2	2.53	2.2	566.04	*	659.21	4163.77	6.32	5.65	3504.56	*
242940_x_at	DLX6: distal-less homeobox 6	AA040332	168.25	1109.23	6.59	5.73	940.97	*	218.91	1378.42	6.3	5.72	1159.51	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
237753_at	Hs.126232.0	AW504569	34.32	243.46	7.09	4.5	209.14	*	27.56	172.5	6.26	3.75	144.94	*
208530_s_at	RARB: retinoic acid receptor, beta	NM_016152	141.64	631.98	4.46	3.84	490.34	*	145.17	902.52	6.22	5.3	757.35	*
215783_s_at	ALPL: alkaline phosphatase, liver/bone/kidney	X14174	325.8	606.48	1.86	1.72	280.68	*	543.02	3370.06	6.21	4.41	2827.04	*
210367_s_at	PTGES: prostaglandin E synthase	AF010316	310.92	3970.09	12.77	11.34	3659.17	*	514.64	3152.4	6.13	5.53	2637.76	*
221558_s_at	LEF1: lymphoid enhancer-binding factor 1	AF288571	439.35	1122.16	2.55	2.29	682.82	*	344.96	2083.59	6.04	5.35	1738.63	*
209465_x_at	PTN: pleiotrophin	AL565812	299.71	731.76	2.44	2.15	432.05	*	768.03	4634	6.03	5.43	3865.96	*
209540_at	IGF1: insulin-like growth factor 1 (somatomedin C)	AU144912	116.22	366	3.15	2.7	249.78	*	515.9	3062.49	5.94	5.15	2546.59	*
239309_at	DLX6: distal-less homeobox 6	T65128	159.55	745.66	4.67	4.27	586.12	*	137.54	807.23	5.87	5.27	669.7	*
226933_s_at	LOC100287917: hypothetical protein LOC100287917	AV646610	52.41	557.35	10.63	8.41	504.94	*	54.3	318.25	5.86	4.86	263.95	*
221245_s_at	FZD5: frizzled homolog 5 (Drosophila)	NM_030804	137.86	428.33	3.11	2.59	290.46	*	218.4	1278.27	5.85	5.12	1059.87	*
228988_at	ZNF711: zinc finger protein 711	AU157017	304.05	536.74	1.77	1.63	232.69	*	188.33	1087.87	5.78	5.34	899.54	*
211577_s_at	IGF1: insulin-like growth factor 1 (somatomedin C)	M37484	175.96	337.75	1.92	1.77	161.79	*	334.45	1920.5	5.74	4.81	1586.05	*
228176_at	S1PR3: sphingosine-1-phosphate receptor 3	AA534817	395.42	1223.59	3.09	2.77	828.17	*	782.3	4465.13	5.71	5.41	3682.83	*
204452_s_at	FZD1: frizzled homolog 1 (Drosophila)	AF072872	178.79	1028.06	5.75	5.1	849.27	*	274.99	1561.83	5.68	5.28	1286.84	*
229661_at	SALL4: sal-like 4 (Drosophila)	NM_020436	102.31	253.08	2.47	1.99	150.77	*	58.54	332	5.67	4.27	273.46	*
203886_s_at	FBLN2: fibulin 2	NM_001998	319.35	2246.48	7.03	6.32	1927.13	*	580.28	3282.43	5.66	5.22	2702.15	*
219682_s_at	TBX3: T-box 3	NM_016569	255.65	967.75	3.79	3.5	712.1	*	196.06	1106.39	5.64	5.06	910.33	*
1568598_at	KAZALD1: Kazal-type serine peptidase inhibitor domain 1	BF434771	59.27	292.62	4.94	3.17	233.35	*	76.74	432.75	5.64	4.12	356.01	*
241355_at	HR: hairless homolog (mouse)	BF528433	205.7	464.53	2.26	1.95	258.83	*	200.2	1125.42	5.62	4.95	925.22	*
217511_at	KAZALD1: Kazal-type serine peptidase inhibitor domain 1	W28828	112.71	569.44	5.05	4.1	456.74	*	201.2	1129.33	5.61	4.94	928.13	*
226034_at	Hs.166975.4	BE222344	364.69	1199.4	3.29	3.11	834.71	*	160.76	878.73	5.47	4.73	717.97	*
224197_s_at	C1QTNF1: C1q and tumor necrosis factor related protein 1	AF232905	148.55	292.16	1.97	1.6	143.61	*	156.89	850.61	5.42	4.82	693.73	*
1552365_at	SCIN: scinderin	NM_033128	97.06	249.97	2.58	2.15	152.92	*	123.8	663.25	5.36	4.36	539.45	*
224325_at	FZD8: frizzled homolog 8 (Drosophila)	AB043703	293.21	1102.27	3.76	3.26	809.07	*	471.55	2524.25	5.35	4.97	2052.7	*
225544_at	TBX3: T-box 3	AI806338	551.34	1711.16	3.1	2.87	1159.82	*	433.83	2286.82	5.27	4.92	1852.99	*
205080_at	RARB: retinoic acid receptor, beta	NM_000965	316.37	1099.73	3.48	3.16	783.36	*	314.5	1592.52	5.06	4.68	1278.02	*
235147_at	FLJ32063: Hypothetical LOC150538	R56118	902.48	1769.79	1.96	1.75	867.31	*	664.7	3354.15	5.05	4.54	2689.45	*
228623_at	Hs.181195.2	AI224133	906.98	516.51	-1.76	-1.65	-390.47	*	26.71	133.86	5.01	3.29	107.15	*
242979_at	IRS1: insulin receptor substrate 1	AI474666	314.67	697.92	2.22	2.04	383.25	*	163.28	802.61	4.92	4.35	639.33	*
205289_at	BMP2: bone morphogenetic protein 2	AA583044	47.66	195.41	4.1	2.93	147.75	*	159.95	778.19	4.87	4.26	618.23	*
223809_at	RGS18: regulator of G-protein signaling 18	AF076642	45.15	517.5	11.46	8.97	472.35	*	41.45	201.42	4.86	3.61	159.97	*
209293_x_at	ID4: inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	U16153	656.69	4275.07	6.51	5.97	3618.38	*	592.66	2842.7	4.8	4.36	2250.03	*
224909_s_at	PREX1: phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	BF308645	85.45	222.06	2.6	2	136.61	*	66.09	313.46	4.74	3.73	247.37	*
209035_at	MDK: midkine (neurite growth-promoting factor 2)	M69148	1009.47	2338.77	2.32	2.19	1329.3	*	442.89	2093.89	4.73	4.22	1650.99	*
235874_at	PRSS35: protease, serine, 35	AL574912	163.5	416.98	2.55	2.32	253.49	*	624	2939.76	4.71	4.3	2315.76	*
221000_s_at	KAZALD1: Kazal-type serine peptidase inhibitor domain 1	NM_030929	213.37	988.85	4.63	3.55	775.48	*	277.13	1275.17	4.6	3.79	998.04	*
205959_at	MMP13: matrix metallopeptidase 13 (collagenase 3)	NM_002427	29.31	425.76	14.53	9.72	396.45	*	95.04	430.62	4.53	3.84	335.58	*
231911_at	ERMN: ermin, ERM-like protein	AA736604	191.99	390.76	2.04	1.7	198.77	*	285.63	1290.64	4.52	4.11	1005.01	*
1555980_a_at	FLJ39609: Similar to hCG1995469	CA447406	44.34	207.17	4.67	3.88	162.83	*	38.61	172.56	4.47	2.77	133.96	*
203372_s_at	SOCS2: suppressor of cytokine signaling 2	AB004903	754.57	1341.41	1.78	1.58	586.85	*	626.01	2791.19	4.46	4.19	2165.18	*
242138_at	DLX1: distal-less homeobox 1	BF060783	188.03	949.67	5.05	4.51	761.64	*	252	1117.12	4.43	4.04	865.12	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
212325_at	LIMCH1: LIM and calponin homology domains 1	AK027231	339.07	844.9	2.49	2.08	505.83	*	463.48	2050.62	4.42	4.05	1587.14	*
209541_at	IGF1: insulin-like growth factor 1 (somatomedin C)	AI972496	248.8	888.42	3.57	3.23	639.62	*	1233.07	5419.01	4.39	4.02	4185.94	*
234951_s_at	COL12A1: collagen, type XII, alpha 1	AL080250	408.38	714.27	1.75	1.55	305.89	*	508.2	2210.93	4.35	4.08	1702.73	*
214954_at	SUSD5: sushi domain containing 5	BF977837	480.71	1040.91	2.17	1.98	560.19	*	691.97	3011.2	4.35	4.15	2319.22	*
203373_at	SOCS2: suppressor of cytokine signaling 2	NM_003877	1168.81	2231.34	1.91	1.7	1062.53	*	937.91	4002.75	4.27	3.95	3064.84	*
209875_s_at	SPP1: secreted phosphoprotein 1	M83248	2125.2	4112.18	1.93	1.59	1986.98	*	3218.01	13672.51	4.25	3.74	10454.5	*
213668_s_at	SOX4: SRY (sex determining region Y)-box 4	AI989477	423.34	834.96	1.97	1.78	411.62	*	196.05	828.16	4.22	3.36	632.11	*
204015_s_at	DUSP4: dual specificity phosphatase 4	BC002671	293.24	781.91	2.67	2.39	488.67	*	170.99	716.09	4.19	3.69	545.1	*
205498_at	GHR: growth hormone receptor	NM_000163	330.57	1038.46	3.14	2.8	707.89	*	689.15	2840.97	4.12	3.81	2151.83	*
212328_at	LIMCH1: LIM and calponin homology domains 1	AB029025	620.18	1837.07	2.96	2.64	1216.88	*	862.37	3547.71	4.11	3.74	2685.34	*
206730_at	GRIA3: glutamate receptor, ionotrophic, AMPA 3	NM_007325	99.47	240.87	2.42	2	141.4	*	60.59	246.75	4.07	3.32	186.16	*
224397_s_at	TMTC1: transmembrane and tetratricopeptide repeat containing 1	AF319520	50.91	163.5	3.21	2.26	112.58	*	137.82	559.68	4.06	3.44	421.87	*
217161_x_at	ACAN: aggrecan	X17406	3296.49	7373.85	2.24	1.61	4077.37	*	3120.98	12574.12	4.03	2.78	9453.14	*
241473_at	Hs.174870.0	AI624440	504.78	1314.38	2.6	2.48	809.6	*	56.72	227.5	4.01	2.83	170.78	*
209343_at	EFHD1: EF-hand domain family, member D1	BC002449	248.44	490.33	1.97	1.85	241.89	*	169.21	676.88	4	3.29	507.67	*
210869_s_at	MCAM: melanoma cell adhesion molecule	M29277	1400.82	3774.06	2.69	2.47	2373.24	*	1270.43	5078.48	4	3.83	3808.05	*
212909_at	LYPD1: LY6/PLAUR domain containing 1	AL567376	266.46	503.93	1.89	1.69	237.47	*	93.69	373.86	3.99	3.29	280.17	*
203435_s_at	MME: membrane metallo-endopeptidase	NM_007287	246.04	121.27	-2.03	-1.79	-124.77	*	476.47	1886.58	3.96	3.32	1410.1	*
202409_at	IGF2 /// INS-IGF2: insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	X07868	1166.86	6203.59	5.32	4.45	5036.73	*	1796.4	7089.54	3.95	3.39	5293.14	*
203222_s_at	TLE1: transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	NM_005077	129.74	279.61	2.16	1.85	149.88	*	141.87	554.82	3.91	3.36	412.95	*
209086_x_at	MCAM: melanoma cell adhesion molecule	BE964361	659.4	1716.75	2.6	2.39	1057.35	*	719.74	2798.68	3.89	3.59	2078.94	*
201212_at	LGMN: legumain	D55696	1042.26	3405.26	3.27	2.92	2363	*	1425.2	5480.98	3.85	3.48	4055.78	*
200644_at	MARCKSL1: MARCKS-like 1	NM_023009	972.12	1776.06	1.83	1.56	803.94	*	1107.21	4254.88	3.84	3.51	3147.67	*
209087_x_at	MCAM: melanoma cell adhesion molecule	AF089868	1057.15	3101.57	2.93	2.67	2044.42	*	1371.31	5255.86	3.83	3.64	3884.55	*
226632_at	CYGB: cytoglobin	AL513673	200.68	653.46	3.26	3.08	452.78	*	136.08	514.34	3.78	3.21	378.25	*
210702_s_at	PTGIS: prostaglandin I2 (prostacyclin) synthase	D38145	137.43	545.86	3.97	3.17	408.43	*	57	215.17	3.78	2.58	158.17	*
201566_x_at	ID2: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	D13891	1403.48	6348.44	4.52	4.1	4944.96	*	1218.67	4604.59	3.78	3.43	3385.92	*
219729_at	PRRX2: paired related homeobox 2	NM_016307	427.89	2712.13	6.34	4.75	2284.24	*	816.16	3078.2	3.77	3.24	2262.04	*
228481_at	Hs.163443.0	BG541187	1832.62	3414.08	1.86	1.74	1581.45	*	620.08	2331.15	3.76	3.26	1711.07	*
211340_s_at	MCAM: melanoma cell adhesion molecule	M28882	1168.9	3322.97	2.84	2.64	2154.07	*	1521.72	5726.68	3.76	3.61	4204.96	*
219310_at	TMEM90B: transmembrane protein 90B	NM_024893	371.54	1085.48	2.92	2.62	713.95	*	288.23	1083.91	3.76	3.34	795.68	*
213001_at	ANGPTL2: angiopoietin-like 2	AF007150	328.42	1022.38	3.11	2.72	693.97	*	632.54	2371.13	3.75	3.51	1738.59	*
241701_at	ARHGAP21: Rho GTPase activating protein 21	BF369489	494.75	1095.79	2.21	2.03	601.04	*	238.86	885.59	3.71	3	646.73	*
213395_at	MLC1: megalencephalic leukoencephalopathy with subcortical cysts 1	AL022327	85.46	254.26	2.98	2.4	168.8	*	74.57	275.32	3.69	3.21	200.75	*
214036_at	EFNA5: ephrin-A5	BE464799	302.35	609.66	2.02	1.8	307.31	*	279.91	1013.14	3.62	3.3	733.23	*
205608_s_at	ANGPT1: angiopoietin 1	U83508	1146.89	2145.57	1.87	1.73	998.69	*	1229.67	4425.37	3.6	3.38	3195.7	*
232406_at	Hs.224012.0	AU151465	497.28	1034.68	2.08	1.93	537.4	*	141.24	508.21	3.6	3	366.97	*
212327_at	LIMCH1: LIM and calponin homology domains 1	AK026815	775.68	2505.5	3.23	2.92	1729.81	*	1279.48	4576.28	3.58	3.36	3296.8	*
226931_at	TMTC1: transmembrane and tetratricopeptide repeat containing 1	AU151239	66.1	180.83	2.74	2.24	114.74	*	96.51	344.57	3.57	3.23	248.06	*
228284_at	TLE1: transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	BE302305	203.49	451.54	2.22	1.92	248.05	*	218.93	779.03	3.56	3	560.1	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
230147_at	F2RL2: coagulation factor II (thrombin) receptor-like 2	AI378647	537.87	1662.29	3.09	2.81	1124.42	*	571.84	2034.2	3.56	3.39	1462.37	*
214433_s_at	SELENBP1: selenium binding protein 1	NM_003944	402.85	791.76	1.97	1.72	388.91	*	928.52	3297.44	3.55	3.45	2368.92	*
235683_at	SESN3: sestrin 3	BF685808	126.91	386.21	3.04	2.43	259.3	*	219.21	774.67	3.53	3.17	555.46	*
227405_s_at	FZD8: frizzled homolog 8 (Drosophila)	AW340311	1033.94	3094.47	2.99	2.73	2060.52	*	1535.08	5365.58	3.5	3.28	3830.51	*
218559_s_at	MAFB: v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	NM_005461	534.78	1255.56	2.35	2.09	720.78	*	1114.46	3870.92	3.47	3.29	2756.46	*
1557543_at	Hs2.376974.1	AL832672	428.39	239.1	-1.79	-1.67	-189.29	*	40.79	141.16	3.46	2.47	100.37	*
225540_at	MAP2: microtubule-associated protein 2	BF342661	132.54	238.82	1.8	1.5	106.28	*	98.13	334.41	3.41	3.13	236.28	*
1555471_a_at	FMN2: formin 2	BC014364	497.15	1467.73	2.95	2.67	970.57	*	388.47	1325.63	3.41	3.1	937.16	*
201565_s_at	ID2: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_002166	2551.34	9616.26	3.77	2.97	7064.92	*	2099.33	7107.95	3.39	2.72	5008.62	*
227361_at	HS3ST3B1: heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	AA780067	836.51	1430.14	1.71	1.61	593.63	*	731.58	2462.26	3.37	3.21	1730.68	*
226322_at	TMTC1: transmembrane and tetratricopeptide repeat containing 1	BF109231	176.44	500.74	2.84	2.48	324.3	*	320.73	1080.2	3.37	3.13	759.47	*
233814_at	EFNA5: ephrin-A5	AK025909	175.86	434.73	2.47	2.02	258.87	*	208.21	693.11	3.33	2.86	484.9	*
1561908_a_at	HS3ST3B1: Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	AL832823	213.48	410.13	1.92	1.62	196.66	*	304.12	1003.29	3.3	2.97	699.17	*
235684_s_at	SESN3: sestrin 3	BF685808	74.24	320.58	4.32	3.95	246.34	*	145.02	477.25	3.29	3.06	332.23	*
230144_at	GRIA3: glutamate receptor, ionotrophic, AMPA 3	AW294729	102.45	314.85	3.07	2.74	212.4	*	124.13	407.03	3.28	2.96	282.9	*
242899_at	Hs.271953.0	N78412	90.79	340.11	3.75	3.02	249.32	*	161.75	529.64	3.27	2.9	367.9	*
202980_s_at	SIAH1: seven in absentia homolog 1 (Drosophila)	AI953523	1096.86	2155.44	1.97	1.84	1058.57	*	736.4	2401.66	3.26	3.11	1665.27	*
203304_at	BAMBI: BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	NM_012342	1619.91	4540.77	2.8	2.55	2920.86	*	2514.07	8179.04	3.25	2.96	5664.97	*
223316_at	CCDC3: coiled-coil domain containing 3	AL136562	68.34	209.35	3.06	2.28	141	*	146.89	476.12	3.24	2.55	329.23	*
230664_at	H2BFM /// H2BFXP: H2B histone family, member M /// H2B histone family, member X, pseudogene	H09657	192.05	363.35	1.89	1.71	171.3	*	115.26	371.75	3.23	2.93	256.5	*
204602_at	DKK1: dickkopf homolog 1 (Xenopus laevis)	NM_012242	2543.3	5093.18	2	1.85	2549.88	*	1878.85	6050.36	3.22	2.92	4171.51	*
201860_s_at	PLAT: plasminogen activator, tissue	NM_000930	2124.78	6173.64	2.91	2.73	4048.86	*	1869.77	6027.83	3.22	2.97	4158.06	*
242906_at	Hs.196734.0	BE787063	71.49	235.47	3.29	2.83	163.98	*	74.98	241.34	3.22	2.65	166.35	*
223321_s_at	FGFRL1: fibroblast growth factor receptor-like 1	AF312678	417.52	1720.81	4.12	3.43	1303.29	*	529.68	1706.93	3.22	2.81	1177.25	*
204686_at	IRS1: insulin receptor substrate 1	NM_005544	1916.91	3177.43	1.66	1.57	1260.53	*	1370.8	4395.67	3.21	3.03	3024.87	*
227955_s_at	EFNA5: ephrin-A5	BE670307	641.61	1111.68	1.73	1.63	470.07	*	521.9	1660.85	3.18	3.02	1138.95	*
228771_at	ADRBK2: adrenergic, beta, receptor kinase 2	AI651212	218.24	391.74	1.79	1.64	173.5	*	196.04	618.58	3.16	2.88	422.54	*
47560_at	LPHN1: latrophilin 1	AI525402	297.97	653.11	2.19	2.06	355.14	*	201.37	631.04	3.13	2.91	429.67	*
222670_s_at	MAFB: v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	AW135013	302.26	720.94	2.39	2.16	418.68	*	565.26	1755.12	3.11	2.93	1189.87	*
207012_at	MMP16: matrix metallopeptidase 16 (membrane-inserted)	U79292	444.81	1218.7	2.74	2.6	773.89	*	298.03	917.75	3.08	2.77	619.72	*
208396_s_at	PDE1A: phosphodiesterase 1A, calmodulin-dependent	NM_005019	43.11	158.19	3.67	2.72	115.08	*	245.85	756.97	3.08	2.78	511.13	*
1554547_at	FAM13C: family with sequence similarity 13, member C	BC036453	271.75	786.84	2.9	2.7	515.09	*	255.28	782.52	3.07	2.89	527.24	*
227347_x_at	HES4: hairy and enhancer of split 4 (Drosophila)	NM_021170	256.36	960.08	3.75	3.27	703.72	*	349	1068.04	3.06	2.78	719.04	*
228503_at	Hs.234478.0	AW025023	66.91	174.93	2.61	1.97	108.02	*	70.54	214.63	3.04	2.56	144.09	*
203708_at	PDE4B: phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_002600	192.5	493.04	2.56	2.16	300.53	*	253.82	760.76	3	2.6	506.94	*
213479_at	NPTX2: neuronal pentraxin II	U26662	48.06	153.85	3.2	2.28	105.79	*	106.85	318.67	2.98	2.41	211.82	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
219514_at	ANGPTL2: angiopoietin-like 2	NM_012098	141.31	282.44	2	1.62	141.13	*	242.13	719.84	2.97	2.75	477.71	*
211302_s_at	PDE4B: phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	L20966	126.23	332.78	2.64	2.19	206.55	*	195.12	577.62	2.96	2.8	382.5	*
209462_at	APLP1: amyloid beta (A4) precursor-like protein 1	U48437	363.82	865.56	2.38	2.12	501.74	*	513.39	1516.22	2.95	2.72	1002.82	*
204184_s_at	ADRBK2: adrenergic, beta, receptor kinase 2	NM_005160	86.84	223.52	2.57	1.98	136.67	*	55.24	162.84	2.95	1.83	107.6	*
219480_at	SNAI1: snail homolog 1 (Drosophila)	NM_005985	274.24	1034.25	3.77	3.37	760.01	*	417.04	1230.01	2.95	2.69	812.97	*
226325_at	ADSSL1: adenylosuccinate synthase like 1	BF593252	308.58	554.56	1.8	1.69	245.98	*	87.19	256.68	2.94	2.42	169.49	*
223618_at	FMN2: formin 2	AF225426	618.17	1709.33	2.77	2.64	1091.16	*	470.97	1380.85	2.93	2.74	909.87	*
202981_x_at	SIAH1: seven in absentia homolog 1 (Drosophila)	NM_003031	2799.13	5363.18	1.92	1.8	2564.05	*	1868.84	5427.44	2.9	2.69	3558.61	*
232392_at	SFRS3: Splicing factor, arginine/serine-rich 3	BE927772	503.76	828.76	1.65	1.56	325	*	258.89	740.02	2.86	2.57	481.14	*
205991_s_at	PRRX1: paired related homeobox 1	NM_006902	1457.28	2525.7	1.73	1.58	1068.42	*	2018.36	5718.46	2.83	2.64	3700.1	*
212188_at	KCTD12: potassium channel tetramerisation domain containing 12	AA551075	2821.63	6301.32	2.23	1.98	3479.69	*	3135.18	8828.45	2.82	2.48	5693.27	*
207029_at	KITLG: KIT ligand	NM_000899	99.67	295.62	2.97	2.44	195.95	*	125.67	354.04	2.82	2.39	228.37	*
201416_at	SOX4: SRY (sex determining region Y)-box 4	BG528420	2604.24	4242.64	1.63	1.54	1638.4	*	1769.95	4945.53	2.79	2.58	3175.58	*
227188_at	C21orf63: chromosome 21 open reading frame 63	AI744591	307.33	527.19	1.72	1.61	219.86	*	184.16	512.54	2.78	2.64	328.39	*
204321_at	NEO1: neogenin homolog 1 (chicken)	NM_002499	1487.96	2771.23	1.86	1.77	1283.27	*	1302.7	3609.31	2.77	2.65	2306.61	*
227198_at	AFF3: AF4/FMR2 family, member 3	AW085505	415.83	832.9	2	1.87	417.07	*	171.57	475.13	2.77	2.48	303.56	*
206070_s_at	EPHA3: EPH receptor A3	AF213459	745.31	1808.82	2.43	2.21	1063.51	*	1525.08	4222.59	2.77	2.51	2697.51	*
210001_s_at	SOCS1: suppressor of cytokine signaling 1	AB005043	198.09	348.33	1.76	1.58	150.24	*	269.89	746.17	2.76	2.57	476.27	*
203823_at	RGS3: regulator of G-protein signaling 3	NM_021106	2665.66	5238.5	1.97	1.74	2572.84	*	4132.74	11350.31	2.75	2.46	7217.57	*
242100_at	CHSY3: chondroitin sulfate synthase 3	AI076484	871.44	1733.63	1.99	1.79	862.19	*	1315.48	3583	2.72	2.56	2267.52	*
219145_at	LPHN1: latrophilin 1	NM_024679	280.23	646.27	2.31	2.19	366.04	*	226.29	614.66	2.72	2.56	388.37	*
208131_s_at	PTGIS: prostaglandin I2 (prostacyclin) synthase	NM_000961	2344.71	5706.02	2.43	2.17	3361.31	*	1052.96	2859.63	2.72	2.25	1806.67	*
203498_at	RCAN2: regulator of calcineurin 2	NM_005822	763.76	2041.28	2.67	2.46	1277.52	*	837.65	2273.93	2.71	2.55	1436.28	*
201362_at	IVNS1ABP: influenza virus NS1A binding protein	AF205218	1012.18	2927.63	2.89	2.72	1915.45	*	1138.48	3080.3	2.71	2.58	1941.82	*
243661_at	ZNF273: zinc finger protein 273	AW172914	107.09	211.87	1.98	1.64	104.77	*	101.04	272.88	2.7	2.3	171.84	*
211124_s_at	KITLG: KIT ligand	AF119835	109.16	273.4	2.5	2.09	164.25	*	151.92	409.91	2.7	2.34	257.99	*
214051_at	TMSB15B: thymosin beta 15B	BF677486	357.86	619.66	1.73	1.54	261.8	*	547.98	1476.4	2.69	2.58	928.42	*
226695_at	PRRX1: paired related homeobox 1	AA775472	3092.2	5383.79	1.74	1.59	2291.59	*	3629.42	9766.09	2.69	2.48	6136.68	*
235150_at	Hs.34636.0	AW376955	105.71	274.53	2.6	2.09	168.82	*	175.73	472.48	2.69	2.27	296.75	*
204451_at	FZD1: frizzled homolog 1 (Drosophila)	NM_003505	2119.15	6444.86	3.04	2.62	4325.71	*	2765.58	7348.44	2.66	2.33	4582.86	*
212192_at	KCTD12: potassium channel tetramerisation domain containing 12	AI718937	3170.54	7324.08	2.31	2.1	4153.54	*	3891.07	10303.78	2.65	2.46	6412.71	*
204720_s_at	DNAJC6: DnaJ (Hsp40) homolog, subfamily C, member 6	AV729634	323.53	956.63	2.96	2.76	633.1	*	305.56	808.83	2.65	2.43	503.27	*
235355_at	Hs.122593.0	AL037998	179.31	308.52	1.72	1.51	129.22	*	311.71	819.31	2.63	2.49	507.6	*
242405_at	Hs.266701.0	BF358386	602.64	348.83	-1.73	-1.63	-253.82	*	75.31	196.46	2.61	1.9	121.15	*
205609_at	ANGPT1: angiopoietin 1	NM_001146	1191.92	2062.65	1.73	1.58	870.73	*	1309.46	3416.56	2.61	2.34	2107.11	*
235228_at	CCDC85A: coiled-coil domain containing 85A	AI376433	83.17	318.11	3.82	2.9	234.94	*	160.75	418.93	2.61	2.28	258.19	*
224559_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AF001540	8643.56	4209.27	-2.05	-1.84	-4434.29	*	2107.31	5488.95	2.6	2.23	3381.64	*
214761_at	ZNF423: zinc finger protein 423	AW149417	715.35	2039.1	2.85	2.67	1323.74	*	687.99	1761.29	2.56	2.34	1073.3	*
238852_at	Hs.283549.0	AA424567	423.75	770.01	1.82	1.7	346.26	*	482.83	1229.36	2.55	2.41	746.54	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
210674_s_at	PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2: protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	AF152308	108.03	250.4	2.32	1.91	142.37	*	150.07	382.92	2.55	2.31	232.85	*
228999_at	CHD2: chromodomain helicase DNA binding protein 2	AW514564	146.4	301.56	2.06	1.78	155.16	*	83.9	213.36	2.54	2.2	129.47	*
214862_x_at	Hs.139006.0	AL080082	81.19	198.6	2.45	1.97	117.41	*	113.82	289.26	2.54	2.25	175.45	*
225123_at	Hs.159441.0	BE883841	744.96	1953.21	2.62	2.34	1208.24	*	992.09	2516.72	2.54	2.37	1524.64	*
219093_at	PID1: phosphotyrosine interaction domain containing 1	NM_017933	2894.8	5085.68	1.76	1.66	2190.88	*	2153.89	5451.31	2.53	2.38	3297.42	*
223627_at	MEX3B: mex-3 homolog B (C. elegans)	AL136778	427.41	1135.69	2.66	2.3	708.28	*	255.91	646.14	2.52	2.12	390.23	*
219681_s_at	RAB11FIP1: RAB11 family interacting protein 1 (class I)	NM_025151	276.23	148.9	-1.86	-1.58	-127.33	*	278.78	698.19	2.5	2.31	419.42	*
235238_at	SHC4: SHC (Src homology 2 domain containing) family, member 4	BF676462	166.5	399.17	2.4	2.11	232.67	*	120.28	299.04	2.49	2.18	178.76	*
213004_at	ANGPTL2: angiopoietin-like 2	AI074333	681.69	1316.6	1.93	1.79	634.91	*	1078.28	2676.22	2.48	2.39	1597.94	*
226534_at	KITLG: KIT ligand	AI446414	1504.5	2986.69	1.99	1.86	1482.19	*	1529.73	3788.42	2.48	2.38	2258.69	*
213125_at	OLFML2B: olfactomedin-like 2B	AW007573	922.02	3848.53	4.17	3.78	2926.51	*	3540.38	8769.75	2.48	2.34	5229.37	*
336_at	TBXA2R: thromboxane A2 receptor	D38081	220.84	465.34	2.11	1.86	244.5	*	537.77	1322.8	2.46	2.23	785.03	*
211892_s_at	PTGIS: prostaglandin I2 (prostacyclin) synthase	AF297052	245.33	627.25	2.56	2.36	381.92	*	126.13	310.12	2.46	2.17	183.99	*
220940_at	ANKRD36B: ankyrin repeat domain 36B	NM_025190	1105.75	701.31	-1.58	-1.5	-404.44	*	170.26	416.33	2.45	2.08	246.07	*
225270_at	NEO1: neogenin homolog 1 (chicken)	AL355708	1831.91	3135.39	1.71	1.58	1303.48	*	1397.34	3420.05	2.45	2.28	2022.71	*
223854_at	PCDHB10: protocadherin beta 10	AF131761	264.02	452.92	1.72	1.55	188.9	*	416.11	1016.09	2.44	2.31	599.99	*
232231_at	RUNX2: runt-related transcription factor 2	AL353944	1849.14	3243.42	1.75	1.59	1394.28	*	1483.24	3620.05	2.44	2.24	2136.81	*
208167_s_at	MMP16: matrix metallopeptidase 16 (membrane-inserted)	NM_022564	131.83	275.28	2.09	1.7	143.46	*	103.37	252.06	2.44	2.05	148.69	*
235944_at	HMCN1: hemicentin 1	BF446673	1949.78	4999.23	2.56	2.43	3049.45	*	1524.33	3705.24	2.43	2.24	2180.91	*
214023_x_at	TUBB2B: tubulin, beta 2B	AL533838	180.85	518.94	2.87	2.68	338.09	*	213.2	518.14	2.43	2.25	304.94	*
226618_at	FLJ25076: probable ubiquitin-conjugating enzyme E2 FLJ25076	AW572911	144.08	329.74	2.29	1.87	185.66	*	202.38	488.83	2.42	2.17	286.44	*
237435_at	Hs.61596.0	AI093492	110.55	308.79	2.79	2.43	198.24	*	81.34	197.16	2.42	2.07	115.82	*
235028_at	Hs.173830.0	BG288330	2063.41	909.92	-2.27	-2.13	-1153.49	*	109.62	263.86	2.41	2.04	154.23	*
232889_at	Hs.283742.0	AU147591	1068.9	598.24	-1.79	-1.69	-470.66	*	96.6	232.18	2.4	1.9	135.58	*
200884_at	CKB: creatine kinase, brain	NM_001823	390.34	1408.94	3.61	3.24	1018.6	*	1684.63	4022.61	2.39	2.25	2337.99	*
225177_at	RAB11FIP1: RAB11 family interacting protein 1 (class I)	AA143793	677.72	366.93	-1.85	-1.65	-310.8	*	745.64	1771.59	2.38	2.25	1025.95	*
227929_at	Hs.22545.0	AU151342	121.03	253.6	2.1	1.83	132.57	*	190.36	450.64	2.37	2.07	260.28	*
228793_at	JMJD1C: jumonji domain containing 1C	BF002296	570.21	354.39	-1.61	-1.52	-215.82	*	128.48	303.34	2.36	1.94	174.85	*
204111_at	HNMT: histamine N-methyltransferase	N40285	272.38	543.22	1.99	1.71	270.84	*	299.7	708.22	2.36	2.01	408.52	*
235417_at	SPOCD1: SPOC domain containing 1	BF689253	915.97	1654.96	1.81	1.71	738.99	*	502.49	1180.86	2.35	2.01	678.37	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
203386_at	TBC1D4: TBC1 domain family, member 4	AI650848	725.55	1258.25	1.73	1.61	532.69	*	884.93	2054.88	2.32	2.23	1169.95	*
204529_s_at	TOX: thymocyte selection-associated high mobility group box	AI961231	118.16	236.46	2	1.67	118.3	*	343.43	798.17	2.32	2.11	454.74	*
230882_at	DLX6AS: DLX6 antisense RNA (non-protein coding)	AA129217	201.29	402.95	2	1.61	201.66	*	180.16	415.44	2.31	1.8	235.27	*
229554_at	Hs.79914.1	AI141861	476.29	986.39	2.07	1.77	510.1	*	1659	3836.32	2.31	2.22	2177.32	*
227401_at	IL17D: interleukin 17D	BE856748	151.84	469.97	3.1	2.63	318.12	*	234.97	539.41	2.3	1.97	304.44	*
224764_at	ARHGAP21: Rho GTPase activating protein 21	AB037845	2844.16	5579.54	1.96	1.82	2735.38	*	2714.73	6219.77	2.29	2.17	3505.04	*
218032_at	SNN: stannin	AF070673	526.5	943.43	1.79	1.69	416.93	*	524.69	1194.03	2.28	2.13	669.35	*
219760_at	LIN7B: lin-7 homolog B (C. elegans)	NM_022165	394.19	823.92	2.09	1.94	429.73	*	377.16	860.56	2.28	2.09	483.39	*
201363_s_at	IVNS1ABP: influenza virus NS1A binding protein	AB020657	1066.44	2444.89	2.29	2.08	1378.45	*	1065.17	2428.33	2.28	2.11	1363.16	*
239624_at	Hs.120456.0	AA725362	195.38	514.27	2.63	2.24	318.88	*	288	655.57	2.28	2.03	367.56	*
227900_at	CBLB: Cas-Br-M (murine) ecotropic retroviral transforming sequence b	AV701750	794.48	1350.85	1.7	1.61	556.37	*	368.98	835.19	2.26	2.07	466.21	*
205425_at	HIP1: huntingtin interacting protein 1	NM_005338	605.64	1110.27	1.83	1.73	504.64	*	330.6	744.32	2.25	2.08	413.72	*
241345_at	ZRANB2: zinc finger, RAN-binding domain containing 2	AV653878	182.45	316.9	1.74	1.61	134.45	*	111.99	251.14	2.24	1.92	139.16	*
204790_at	SMAD7: SMAD family member 7	NM_005904	2713.04	5786.07	2.13	1.97	3073.03	*	2241.18	5015.83	2.24	2.1	2774.65	*
238044_at	Hs.236524.0	AW002073	175.93	341.29	1.94	1.7	165.36	*	115.71	256.65	2.22	1.81	140.93	*
226584_s_at	FAM110A: family with sequence similarity 110, member A	AL118502	114.1	318.05	2.79	2.39	203.95	*	124.04	275.72	2.22	1.84	151.68	*
207013_s_at	MMP16: matrix metallopeptidase 16 (membrane-inserted)	AB009303	75.91	246.29	3.24	2.87	170.38	*	90.98	202.19	2.22	1.82	111.21	*
226364_at	HIP1: Huntingtin interacting protein 1	AU145049	909.72	1870.16	2.06	1.96	960.44	*	669.29	1482.37	2.21	2.06	813.09	*
203387_s_at	TBC1D4: TBC1 domain family, member 4	NM_014832	492.8	896.74	1.82	1.53	403.94	*	724.98	1596.01	2.2	2.08	871.03	*
1569290_s_at	GRIA3: glutamate receptor, ionotrophic, AMPA 3	BC032004	345.59	673.27	1.95	1.76	327.68	*	317.98	698.44	2.2	2.02	380.47	*
218665_at	FZD4: frizzled homolog 4 (Drosophila)	NM_012193	341.85	1314.51	3.85	3.55	972.66	*	361.07	795.52	2.2	2	434.45	*
215506_s_at	DIRAS3: DIRAS family, GTP-binding RAS-like 3	AK021882	488.66	235.1	-2.08	-1.74	-253.56	*	558.93	1224.96	2.19	2.09	666.03	*
223614_at	MMP16: matrix metallopeptidase 16 (membrane-inserted)	AL136588	1405.7	3783.03	2.69	2.5	2377.33	*	1250.7	2740.14	2.19	1.99	1489.44	*
227576_at	Hs.14947.0	AW003140	1101.67	621.21	-1.77	-1.69	-480.46	*	101.78	221.72	2.18	1.55	119.94	*
239251_at	Hs.269339.0	AW963634	1752.74	1021.02	-1.72	-1.6	-731.72	*	194.68	424.9	2.18	1.79	230.23	*
225339_at	SPAG9: sperm associated antigen 9	BG290577	1648.16	2985.96	1.81	1.69	1337.79	*	1524.4	3329.87	2.18	2.03	1805.46	*
39966_at	CSPG5: chondroitin sulfate proteoglycan 5 (neuroglycan C)	AF059274	197.15	361.86	1.84	1.7	164.71	*	129.7	280.13	2.16	1.54	150.43	*
230333_at	Hs.28491.4	BE326919	796.5	1348.56	1.69	1.55	552.06	*	514.99	1105.37	2.15	1.87	590.38	*
202709_at	FMOD: fibromodulin	NM_002023	483.12	949.34	1.97	1.65	466.22	*	900.23	1932.64	2.15	2.03	1032.41	*
229144_at	RP1-21O18.1: kazrin	AA989362	915.14	3429	3.75	3.56	2513.86	*	1054.08	2264.56	2.15	2.04	1210.48	*
226974_at	NEDD4L: neural precursor cell expressed, developmentally down-regulated 4-like	AL536553	222.61	408.6	1.84	1.64	185.99	*	262.44	561.16	2.14	1.98	298.71	*
227827_at	Hs.71721.0	AW138143	243.28	508.13	2.09	1.82	264.86	*	699.84	1495.24	2.14	2.04	795.4	*
225263_at	HS6ST1: heparan sulfate 6-O-sulfotransferase 1	BC001196	365.03	622.17	1.7	1.53	257.14	*	415.24	883.71	2.13	1.94	468.47	*
230933_at	DSTN: Destrin (actin depolymerizing factor)	AA458636	228.11	1318.04	5.78	4.87	1089.93	*	284.17	605.68	2.13	1.84	321.51	*
241957_x_at	LIN7B: lin-7 homolog B (C. elegans)	AI686521	274.96	662.37	2.41	2.18	387.42	*	302.4	641.83	2.12	1.9	339.43	*
222931_s_at	THNSL1: threonine synthase-like 1 (S. cerevisiae)	AI809864	280.15	579.89	2.07	1.9	299.74	*	296.36	625.56	2.11	1.93	329.2	*
205092_x_at	ZBTB1: zinc finger and BTB domain containing 1	NM_014950	267.77	473.37	1.77	1.62	205.6	*	256.45	537.39	2.1	1.93	280.94	*
227826_s_at	Hs.71721.0	AW138143	252.73	485.72	1.92	1.74	232.99	*	687.35	1443.82	2.1	1.98	756.48	*
228882_at	TUB: tubby homolog (mouse)	AL042088	940.92	1578.1	1.68	1.55	637.18	*	1329.19	2768.41	2.08	1.99	1439.23	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
225864_at	FAM84B: family with sequence similarity 84, member B	AL039862	163.74	281.53	1.72	1.55	117.8	*	93.44	194.07	2.08	1.69	100.63	*
203488_at	LPHN1: latrophilin 1	NM_014921	143.28	275.05	1.92	1.7	131.76	*	115.79	240.59	2.08	1.68	124.8	*
37022_at	PRELP: proline/arginine-rich end leucine-rich repeat protein	U41344	246.95	589.28	2.39	2	342.33	*	2006.02	4163.05	2.08	1.99	2157.02	*
1564573_at	LOC402778: similar to RIKEN cDNA 6330512M04 gene (mouse)	BC036199	523.29	1175.63	2.25	2.07	652.34	*	502.91	1041.33	2.07	1.91	538.42	*
228850_s_at	Hs.110373.0	AI963304	1433.29	2437.88	1.7	1.6	1004.59	*	1532.4	3150.6	2.06	1.93	1618.2	*
204400_at	EFS: embryonal Fyn-associated substrate	NM_005864	878.94	1739.32	1.98	1.82	860.39	*	1244.68	2568.5	2.06	1.91	1323.82	*
202434_s_at	CYP1B1: cytochrome P450, family 1, subfamily B, polypeptide 1	N21019	379.48	784.32	2.07	1.78	404.84	*	959.7	1972.37	2.06	1.91	1012.66	*
206315_at	CRLF1: cytokine receptor-like factor 1	NM_004750	1405.19	4020.67	2.86	2.59	2615.48	*	1220.9	2521.05	2.06	1.88	1300.16	*
239108_at	FAR2: Fatty acyl CoA reductase 2	H16791	271.19	459.56	1.69	1.55	188.37	*	195.3	401.31	2.05	1.84	206.01	*
217979_at	TSPAN13: tetraspanin 13	NM_014399	863.4	1685.7	1.95	1.71	822.31	*	2100.89	4303.24	2.05	1.88	2202.35	*
221176_x_at	WBSCR23: Williams-Beuren syndrome chromosome region 23	NM_025042	765.08	420.01	-1.82	-1.68	-345.08	*	100.84	205.43	2.04	1.76	104.59	*
228224_at	PRELP: proline/arginine-rich end leucine-rich repeat protein	AA573140	210.89	505.92	2.4	2.1	295.02	*	1631.1	3329.43	2.04	1.96	1698.32	*
222820_at	TNRC6C: trinucleotide repeat containing 6C	AW005818	650.93	1112.79	1.71	1.56	461.86	*	752.16	1530.27	2.03	1.92	778.11	*
204223_at	PRELP: proline/arginine-rich end leucine-rich repeat protein	NM_002725	368.5	958.22	2.6	2.23	589.72	*	3263.61	6629.64	2.03	1.92	3366.03	*
219647_at	POPDC2: popeye domain containing 2	NM_022135	135.31	274.69	2.03	1.76	139.38	*	122.21	246.88	2.02	1.66	124.67	*
220092_s_at	ANTXR1: anthrax toxin receptor 1	NM_018153	913.94	2155.46	2.36	2.2	1241.52	*	1206.57	2443.31	2.02	1.91	1236.73	*
228889_at	C14orf128: chromosome 14 open reading frame 128	BF223658	123.73	391.36	3.16	2.45	267.63	*	140.99	282.83	2.01	1.67	141.85	*
212701_at	TLN2: talin 2	AB002318	232.93	421.88	1.81	1.69	188.95	*	157.47	313.89	1.99	1.75	156.42	*
210089_s_at	LAMA4: laminin, alpha 4	BC004241	238.36	604.59	2.54	2.3	366.23	*	398.67	788.31	1.98	1.78	389.64	*
1553185_at	RASEF: RAS and EF-hand domain containing	NM_152573	1146.36	708.91	-1.62	-1.51	-437.45	*	158.88	309.93	1.95	1.69	151.06	*
213321_at	BCKDHB: branched chain keto acid dehydrogenase E1, beta polypeptide	AL531533	136.31	247.55	1.82	1.55	111.23	*	196.85	384.8	1.95	1.78	187.96	*
206078_at	KALRN: kalirin, RhoGEF kinase	NM_007064	91.59	214.2	2.34	1.72	122.6	*	240.88	470.03	1.95	1.81	229.15	*
231735_s_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	NM_014086	1201.48	1932.68	1.61	1.51	731.21	*	639.9	1243.54	1.94	1.56	603.64	*
227032_at	PLXNA2: plexin A2	AI694545	205.22	522.38	2.55	2.21	317.16	*	276.43	535.01	1.94	1.74	258.58	*
210990_s_at	LAMA4: laminin, alpha 4	U77706	439.78	1098.74	2.5	2.24	658.96	*	652.7	1260.34	1.93	1.74	607.64	*
209098_s_at	JAG1: jagged 1 (Alagille syndrome)	U61276	933.45	2347.37	2.51	2.33	1413.93	*	1182.79	2270.46	1.92	1.79	1087.67	*
203499_at	EPHA2: EPH receptor A2	NM_004431	1956.77	3323.34	1.7	1.59	1366.58	*	1335.89	2554.42	1.91	1.8	1218.53	*
227660_at	ANTXR1: anthrax toxin receptor 1	AL569575	1479.85	3159.76	2.14	1.98	1679.91	*	2001.9	3830.34	1.91	1.8	1828.44	*
227410_at	FAM43A: family with sequence similarity 43, member A	AW264102	805.54	2131.25	2.65	2.45	1325.71	*	297.48	566.8	1.91	1.66	269.33	*
1553186_x_at	RASEF: RAS and EF-hand domain containing	NM_152573	1120.82	646.29	-1.73	-1.68	-474.52	*	155.98	295.02	1.89	1.66	139.04	*
231851_at	RAVER2: ribonucleoprotein, PTB-binding 2	AL359613	236.64	571.63	2.42	2.19	334.99	*	175.9	332.85	1.89	1.61	156.95	*
224375_at	LOC100293563: DC48	AF271776	438.26	1002.59	2.29	2.16	564.32	*	282.2	531.85	1.88	1.65	249.65	*
203394_s_at	HES1: hairy and enhancer of split 1, (Drosophila)	BE973687	469.74	1864.48	3.97	3.66	1394.74	*	367.4	690.36	1.88	1.61	322.96	*
206245_s_at	IVNS1ABP: influenza virus NS1A binding protein	NM_006469	1644.25	4130.49	2.51	2.32	2486.23	*	2037.15	3818.95	1.87	1.75	1781.8	*
217984_at	RNASET2: ribonuclease T2	NM_003730	1295.84	3848.63	2.97	2.79	2552.79	*	1410.31	2627.92	1.86	1.77	1217.61	*
212542_s_at	PHIP: pleckstrin homology domain interacting protein	BF224151	750.79	1211.58	1.61	1.54	460.79	*	452.62	837.08	1.85	1.66	384.46	*
229744_at	SSFA2: Sperm specific antigen 2	AL556611	246.19	433.64	1.76	1.61	187.45	*	252.68	467.15	1.85	1.69	214.47	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
213478_at	RP1-21O18.1: kazrin	AB028949	1357.67	4043.42	2.98	2.79	2685.75	*	1467.76	2708.97	1.85	1.71	1241.21	*
232098_at	DST: dystonin	AK025142	937.87	437.5	-2.14	-2.03	-500.37	*	144.25	262.24	1.82	1.58	118	*
32029_at	PDPK1: 3-phosphoinositide dependent protein kinase-1	AC005591	268.14	431.71	1.61	1.53	163.58	*	130.77	238.17	1.82	1.63	107.4	*
228210_at	NXPH3: neurexophilin 3	T10030	119.52	282.47	2.36	1.67	162.96	*	240.51	437.2	1.82	1.56	196.7	*
206910_x_at	CFHR2: complement factor H-related 2	NM_005666	854.11	2212.98	2.59	2.47	1358.87	*	1003.32	1824.98	1.82	1.71	821.67	*
229970_at	Hs.48578.0	BE672291	233.45	457.7	1.96	1.72	224.24	*	339.22	615.49	1.81	1.67	276.27	*
241981_at	FAM20A: family with sequence similarity 20, member A	AW291369	393.68	142.13	-2.77	-2.57	-251.55	*	317.36	570.53	1.8	1.69	253.18	*
218974_at	SOBP: sine oculis binding protein homolog (Drosophila)	NM_018013	274.13	142.5	-1.92	-1.63	-131.63	*	444.05	800.3	1.8	1.73	356.25	*
206377_at	FOXF2: forkhead box F2	NM_001452	482.86	926.3	1.92	1.83	443.44	*	402.42	724.52	1.8	1.67	322.1	*
1568779_a_at	ECM2: extracellular matrix protein 2, female organ and adipocyte specific	AI473096	850.22	1629.23	1.92	1.74	779.01	*	1608.4	2896.46	1.8	1.64	1288.06	*
228580_at	HTRA3: HtrA serine peptidase 3	AI828007	99.95	263.82	2.64	2.08	163.87	*	409.34	738.68	1.8	1.71	329.35	*
236901_at	Hs.17733.0	AA035730	298.52	961.16	3.22	2.97	662.63	*	517.22	932.88	1.8	1.68	415.65	*
204794_at	DUSP2: dual specificity phosphatase 2	NM_004418	82.96	440.21	5.31	4.68	357.25	*	214.71	387.3	1.8	1.73	172.59	*
203989_x_at	F2R: coagulation factor II (thrombin) receptor	NM_001992	1051.45	3203.42	3.05	2.76	2151.97	*	1742.06	3100.2	1.78	1.65	1358.14	*
227911_at	ARHGAP28: Rho GTPase activating protein 28	AI935647	405.25	157.2	-2.58	-2	-248.05	*	841.24	1492.09	1.77	1.7	650.85	*
206385_s_at	ANK3: ankyrin 3, node of Ranvier (ankyrin G)	NM_020987	404.43	651.98	1.61	1.51	247.55	*	753.56	1331.76	1.77	1.67	578.2	*
205525_at	CALD1: caldesmon 1	NM_018495	3260.05	1852.48	-1.76	-1.66	-1407.57	*	394.55	694.7	1.76	1.57	300.15	*
243221_at	FAM20A: family with sequence similarity 20, member A	AA579773	235.54	86.15	-2.73	-2.34	-149.4	*	270.47	468.25	1.73	1.63	197.78	*
1560445_x_at	ARHGEF1: Rho guanine nucleotide exchange factor (GEF) 1	AK026781	749.54	478.45	-1.57	-1.52	-271.1	*	142.79	245.41	1.72	1.54	102.61	*
213040_s_at	NPTXR: neuronal pentraxin receptor	AL008583	243.07	470.65	1.94	1.64	227.58	*	478.2	817.58	1.71	1.56	339.38	*
203523_at	LSP1: lymphocyte-specific protein 1	NM_002339	422.38	1159.08	2.74	2.47	736.7	*	1300.72	2218.59	1.71	1.63	917.87	*
214454_at	ADAMTS2: ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_014244	790.8	2453.09	3.1	2.84	1662.29	*	1066.32	1819.72	1.71	1.61	753.4	*
228486_at	SLC44A1: solute carrier family 44, member 1	AW165999	212.85	381.46	1.79	1.67	168.6	*	260.63	444.15	1.7	1.59	183.52	*
231721_at	JAM3: junctional adhesion molecule 3	AF356518	499.09	898.12	1.8	1.7	399.04	*	812.16	1383.71	1.7	1.63	571.55	*
228683_s_at	KCTD15: potassium channel tetramerisation domain containing 15	AI925361	144.44	282.43	1.96	1.61	137.99	*	143.2	244.08	1.7	1.55	100.88	*
202202_s_at	LAMA4: laminin, alpha 4	NM_002290	2133.67	4308.73	2.02	1.88	2175.06	*	3089.08	5264.85	1.7	1.62	2175.77	*
217983_s_at	RNASET2: ribonuclease T2	NM_003730	2234.34	5608.54	2.51	2.41	3374.2	*	2471.45	4197.2	1.7	1.61	1725.74	*
206204_at	GRB14: growth factor receptor-bound protein 14	NM_004490	134.46	531.34	3.95	3.33	396.88	*	342.84	583.69	1.7	1.55	240.85	*
230266_at	RAB7B: RAB7B, member RAS oncogene family	AI127991	557.37	1222.52	2.19	2.01	665.15	*	1264.55	2113.12	1.67	1.57	848.57	*
231183_s_at	JAG1: Jagged 1 (Alagille syndrome)	AI457817	491.19	1348.19	2.74	2.58	857	*	602.15	1007.48	1.67	1.55	405.34	*
203395_s_at	HES1: hairy and enhancer of split 1, (Drosophila)	NM_005524	595.99	2414.31	4.05	3.66	1818.32	*	596.93	985.35	1.65	1.54	388.42	*
229116_at	CNKSR2: connector enhancer of kinase suppressor of Ras 2	AI670947	901.94	262.87	-3.43	-3.09	-639.07	*	498.02	811.78	1.63	1.54	313.76	*
210997_at	HGF: hepatocyte growth factor (hepapoietin A; scatter factor)	M77227	118.42	338.02	2.85	2.52	219.6	*	351.97	562.15	1.6	1.53	210.18	*
202994_s_at	FBLN1: fibulin 1	Z95331	343.48	755.79	2.2	2.04	412.31	*	1065.49	645.82	-1.65	-1.59	-419.67	*
203835_at	LRRC32: leucine rich repeat containing 32	NM_005512	506.95	1448.94	2.86	2.64	941.99	*	776.69	458.41	-1.69	-1.51	-318.28	*
210664_s_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AF021834	2474.27	5025.97	2.03	1.9	2551.7	*	3218.17	1833.43	-1.76	-1.68	-1384.74	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
213258_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	BF511231	3371.7	5679.97	1.68	1.61	2308.28	*	3740.26	1978.3	-1.89	-1.76	-1761.96	*
226907_at	PPP1R14C: protein phosphatase 1, regulatory (inhibitor) subunit 14C	N32557	546.01	930.08	1.7	1.6	384.08	*	583.24	299.5	-1.95	-1.69	-283.74	*
202995_s_at	FBLN1: fibulin 1	NM_006486	422.29	716.89	1.7	1.56	294.6	*	1359.52	690.58	-1.97	-1.84	-668.94	*
209676_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	J03225	2218.34	4012.4	1.81	1.7	1794.06	*	2713.14	1369.52	-1.98	-1.89	-1343.62	*
211506_s_at	IL8: interleukin 8	AF043337	244.15	516.98	2.12	1.87	272.83	*	379.26	172.03	-2.2	-1.91	-207.24	*
219230_at	TMEM100: transmembrane protein 100	NM_018286	145.35	441.57	3.04	2.62	296.23	*	521.07	203.67	-2.56	-2.24	-317.4	*

Up-Regulated Genes at Day 4 in Response to 20nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
213565_s_at	SMAD6: SMAD family member 6	AI193899	7.43	121.26	16.32	7.2	113.83	*	20.28	98.31	4.85	3.87	78.03	
206320_s_at	SMAD9: SMAD family member 9	NM_005905	28.33	224.28	7.92	6.18	195.95	*	10.23	107.75	10.53	5.25	97.52	
204351_at	S100P: S100 calcium binding protein P	NM_005980	30.31	177.69	5.86	3.09	147.38	*	28.59	41.39	1.45	0.93	12.8	
239262_at	Hs.25930.0	AI498395	57.98	337.79	5.83	4.46	279.81	*	32.84	58.58	1.78	1.18	25.74	
219014_at	PLAC8: placenta-specific 8	NM_016619	29.96	151.05	5.04	3.57	121.09	*	17.6	110.22	6.26	3.8	92.62	
1555564_a_at	CFI: complement factor I	BC020718	38.04	184.8	4.86	3.89	146.76	*	7.51	35.6	4.74	1.99	28.09	
203680_at	PRKAR2B: protein kinase, cAMP-dependent, regulatory, type II, beta	NM_002736	66.23	317.96	4.8	3.86	251.74	*	90.91	159.15	1.75	1.29	68.24	
219058_x_at	TINAGL1: tubulointerstitial nephritis antigen-like 1	NM_022164	35.94	169.74	4.72	3.59	133.8	*	59.55	142.61	2.4	1.53	83.07	
203854_at	CFI: complement factor I	NM_000204	54.07	238.66	4.41	3.34	184.59	*	41.74	75.27	1.8	1.28	33.53	
205934_at	PLCL1: phospholipase C-like 1	NM_006226	69	298.61	4.33	3.76	229.61	*	158.53	216.58	1.37	1.21	58.05	
221172_at	C7orf69: chromosome 7 open reading frame 69	NM_025031	222.2	961.33	4.33	3.82	739.13	*	28.84	16.81	-1.72	-0.02	-12.03	
226944_at	HTRA3: HtrA serine peptidase 3	AW518728	133.29	571.48	4.29	3.64	438.19	*	925.16	1213.95	1.31	1.26	288.79	
212670_at	ELN: elastin	AA479278	1195.75	4715.18	3.94	3.06	3519.43	*	4663.03	5459.81	1.17	1.07	796.78	
221991_at	NXPH3: neurexophilin 3	AI937333	114.21	448.55	3.93	3.06	334.34	*	287.41	479.26	1.67	1.47	191.85	
235666_at	Hs.153717.0	AA903473	496.85	1923.83	3.87	3.56	1426.98	*	125.05	207.65	1.66	1.36	82.59	
216269_s_at	ELN: elastin	M24782	69.99	264.94	3.79	3.3	194.95	*	475.65	703.28	1.48	1.4	227.62	
230308_at	FAM120AOS: family with sequence similarity 120A opposite strand	AI091434	42.6	147.53	3.46	1.77	104.93	*	31.77	55.05	1.73	0.23	23.27	
226731_at	PELO: Pelota homolog (Drosophila)	AA156873	297.62	943.96	3.17	3.01	646.34	*	537.91	449.7	-1.2	-1.1	-88.22	
213942_at	MEGF6: multiple EGF-like-domains 6	AL134303	339.87	1037.63	3.05	2.79	697.76	*	243.14	322.09	1.32	1.12	78.95	
205384_at	FXYD1: FXYD domain containing ion transport regulator 1	NM_005031	73.74	224.1	3.04	1.96	150.36	*	227.6	344.08	1.51	1.32	116.47	
222802_at	EDN1: endothelin 1	J05008	574.15	1746.68	3.04	2.84	1172.53	*	223.68	390.93	1.75	1.39	167.25	
217580_x_at	Hs.150551.0	AW301806	78.24	236.63	3.02	2.58	158.4	*	255.46	221.53	-1.15	-1.05	-33.93	
204396_s_at	GRK5: G protein-coupled receptor kinase 5	NM_005308	464.44	1389.84	2.99	2.83	925.4	*	636.98	514.71	-1.24	-1.13	-122.27	
214265_at	ITGA8: integrin, alpha 8	AI193623	198.11	591.42	2.99	2.57	393.3	*	38.71	53.26	1.38	0.81	14.56	
218995_s_at	EDN1: endothelin 1	NM_001955	223.8	664.1	2.97	2.65	440.3	*	70.82	120.26	1.7	1.19	49.44	
226021_at	RDH10: retinol dehydrogenase 10 (all-trans)	AW150720	999.51	2930.55	2.93	2.78	1931.04	*	1544.52	1348.53	-1.15	-1.08	-196	
204011_at	SPRY2: sprouty homolog 2 (Drosophila)	NM_005842	608.03	1748.34	2.88	2.73	1140.32	*	540.41	852.48	1.58	1.43	312.07	
211355_x_at	LEPR: leptin receptor	U52914	413.6	1191.3	2.88	2.6	777.7	*	833.61	666.35	-1.25	-1.15	-167.25	
238178_at	Hs.264433.0	BF110268	119.69	344.17	2.88	2.56	224.48	*	151.7	96.61	-1.57	-1.36	-55.09	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
236782_at	SAMD3: sterile alpha motif domain containing 3	AI129628	232.13	665.28	2.87	2.7	433.15	*	65.12	95.66	1.47	1.09	30.54	
214660_at	PELO: Pelota homolog (Drosophila)	X68742	390.66	1115.93	2.86	2.72	725.27	*	616.04	676.83	1.1	1.05	60.79	
211356_x_at	LEPR: leptin receptor	U66495	435.05	1238.26	2.85	2.58	803.21	*	877.37	722.44	-1.21	-1.13	-154.93	
226869_at	MEGF6: multiple EGF-like-domains 6	AI655611	1158.55	3282.77	2.83	2.67	2124.21	*	607.59	743.86	1.22	1.11	136.27	
204472_at	GEM: GTP binding protein overexpressed in skeletal muscle	NM_005261	504.46	1423.69	2.82	2.63	919.23	*	904.34	1101.66	1.22	1.13	197.33	
215652_at	SDHD: succinate dehydrogenase complex, subunit D, integral membrane protein	AK024382	122.3	344.72	2.82	2.38	222.42	*	91.56	95.26	1.04	0.82	3.7	
239907_at	Hs.226376.0	BF508839	74.22	208.56	2.81	2.26	134.34	*	62.36	112.07	1.8	1.29	49.71	
211354_s_at	LEPR: leptin receptor	U52913	434.87	1214.84	2.79	2.59	779.97	*	823.63	655.54	-1.26	-1.17	-168.1	
223710_at	CCL26: chemokine (C-C motif) ligand 26	AF096296	70.27	193.35	2.75	2.36	123.08	*	43.6	30.14	-1.45	-1.08	-13.46	
227697_at	SOCS3: suppressor of cytokine signaling 3	AI244908	729.93	1995.56	2.73	2.58	1265.63	*	1081.09	1604.46	1.48	1.4	523.37	
215138_s_at	RP1-21O18.1: kazrin	AB015329	225.85	608.9	2.7	2.46	383.05	*	272.11	418.59	1.54	1.33	146.48	
227467_at	RDH10: retinol dehydrogenase 10 (all-trans)	AV697515	496.91	1304.63	2.63	2.37	807.72	*	722.99	634.36	-1.14	-1.05	-88.63	
200840_at	KARS: lysyl-tRNA synthetase	NM_005548	7121.4	18540.31	2.6	1.91	11418.91	*	5920.34	6688.56	1.13	0.74	768.23	
210755_at	HGF: hepatocyte growth factor (hepapoietin A; scatter factor)	U46010	77.77	199.7	2.57	2.05	121.93	*	154.6	243.91	1.58	1.43	89.3	
236719_at	Hs.48784.0	AI042187	87.73	225.63	2.57	2.16	137.89	*	63.97	143.34	2.24	1.74	79.36	
218330_s_at	NAV2: neuron navigator 2	NM_018162	133.3	340.6	2.56	2.3	207.3	*	179.04	207.21	1.16	1.03	28.17	
209355_s_at	PPAP2B: phosphatidic acid phosphatase type 2B	AB000889	1962.59	5003.54	2.55	2.35	3040.96	*	2925.78	2881.48	-1.02	-0.95	-44.3	
230137_at	TMEM155: transmembrane protein 155	BF673779	97.39	247.12	2.54	2.01	149.72	*	186.8	297.9	1.59	1.37	111.1	
218353_at	RGS5: regulator of G-protein signaling 5	NM_025226	270.87	686.52	2.53	2.25	415.65	*	251	264.87	1.06	0.93	13.87	
203571_s_at	C10orf116: chromosome 10 open reading frame 116	NM_006829	1235.84	3078.31	2.49	2.25	1842.47	*	3363.15	4227.94	1.26	1.22	864.79	
233289_at	Hs.300827.0	AU155234	125.36	309.6	2.47	2.14	184.24	*	59.94	121.46	2.03	1.35	61.52	
228750_at	Hs.28625.0	AI693516	201.17	494.66	2.46	2.14	293.49	*	660.43	901.44	1.36	1.28	241.01	
222968_at	Hs.109798.0	NM_016947	216.03	528.59	2.45	2.02	312.56	*	106.79	185.64	1.74	1.25	78.86	
1554195_a_at	C5orf46: chromosome 5 open reading frame 46	BC021680	887.1	2171.72	2.45	2.26	1284.62	*	334.61	259.51	-1.29	-1.05	-75.1	
210665_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AF021834	487.12	1180.28	2.42	2.23	693.16	*	725.94	501.8	-1.45	-1.33	-224.14	
239672_at	Hs.40840.0	AW960100	144.97	347.74	2.4	2.16	202.77	*	48.31	129.27	2.68	2.1	80.95	
238479_at	Hs.56004.0	BG398977	120.78	283.38	2.35	2.05	162.59	*	115.28	155.03	1.34	1.16	39.75	
209071_s_at	RGS5: regulator of G-protein signaling 5	AF159570	582.11	1356.53	2.33	2.16	774.41	*	474.59	421.63	-1.13	-0.92	-52.96	
243409_at	FOXL1: forkhead box L1	AI005407	272.27	635.04	2.33	2.13	362.77	*	201.01	338.52	1.68	1.45	137.51	
1553207_at	ARL10: ADP-ribosylation factor-like 10	NM_173664	120.84	280.25	2.32	2	159.41	*	100.84	109.59	1.09	0.85	8.75	
1556103_at	Hs2.323409.1	AI453268	231.6	535.72	2.31	2.09	304.12	*	238.45	242.89	1.02	0.91	4.44	
201044_x_at	DUSP1: dual specificity phosphatase 1	AA530892	373.33	858.57	2.3	1.99	485.24	*	382.57	372.93	-1.03	-0.87	-9.64	
210998_s_at	HGF: hepatocyte growth factor (hepapoietin A; scatter factor)	M77227	112.58	259.03	2.3	1.68	146.45	*	237.77	395.34	1.66	1.46	157.57	
225424_at	GPAM: glycerol-3-phosphate acyltransferase, mitochondrial	AB046780	554.18	1269.68	2.29	2.11	715.5	*	434.59	645.36	1.48	1.29	210.77	
201467_s_at	NQO1: NAD(P)H dehydrogenase, quinone 1	AI039874	997.95	2271.73	2.28	2.14	1273.78	*	979.57	1258.88	1.29	1.19	279.3	
204748_at	PTGS2: prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_000963	172.8	390.73	2.26	2.01	217.93	*	118.53	158.95	1.34	1.12	40.42	
230050_at	NACC2: NACC family member 2, BEN and BTB (POZ) domain containing	AI825645	137.2	307.15	2.24	1.83	169.96	*	140.78	236.43	1.68	1.35	95.65	
212865_s_at	COL14A1: collagen, type XIV, alpha 1	BF449063	485.23	1081.25	2.23	2.02	596.02	*	1733	2187.99	1.26	1.2	454.99	
209070_s_at	RGS5: regulator of G-protein signaling 5	AI183997	462.99	1023.4	2.21	1.99	560.41	*	422.68	405.08	-1.04	-0.91	-17.6	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
244231_at	BPI /// LOC149684: bactericidal/permeability-increasing protein /// hypothetical protein LOC149684	AW451313	137.66	299.23	2.17	1.91	161.57	*	87.37	109.25	1.25	1	21.87	
219599_at	EIF4B: eukaryotic translation initiation factor 4B	NM_018507	271.13	576.04	2.12	1.97	304.91	*	237.03	338.91	1.43	1.3	101.88	
242552_x_at	ZBED5: zinc finger, BED-type containing 5	AW274047	262.94	557.24	2.12	1.85	294.3	*	236.6	119.38	-1.98	-1.21	-117.22	
212367_at	FEM1B: fem-1 homolog b (C. elegans)	AI799061	324.92	685.96	2.11	1.83	361.04	*	658.39	1036.26	1.57	1.48	377.87	
228360_at	LYPD6B: LY6/PLAUR domain containing 6B	BF060747	560.86	1184.75	2.11	1.94	623.89	*	331.51	189.21	-1.75	-1.25	-142.3	
225420_at	GPAM: glycerol-3-phosphate acyltransferase, mitochondrial	AV699379	643.79	1347.06	2.09	1.91	703.28	*	373.7	608.45	1.63	1.41	234.75	
235099_at	CMTM8: CKLF-like MARVEL transmembrane domain containing 8	AW080832	120.44	251.3	2.09	1.8	130.86	*	129.35	188.72	1.46	1.25	59.37	
1552698_at	MGC16703: tubulin, alpha pseudogene	NM_145042	186.34	385.34	2.07	1.75	199.01	*	154.66	285.77	1.85	1.48	131.1	
208534_s_at	LOC100132214 /// RASA4 /// RASA4P: similar to calcium-promoted Ras inactivator /// RAS p21 protein activator 4 /// RAS p21 protein activator 4 pseudogene	NM_006989	104.08	214.52	2.06	1.73	110.45	*	105.45	156.69	1.49	1.21	51.23	
219778_at	ZFPM2: zinc finger protein, multitype 2	NM_012082	112.54	229.32	2.04	1.75	116.78	*	78.94	88.99	1.13	0.88	10.05	
241401_at	C4orf12: chromosome 4 open reading frame 12	BG496631	97.18	198.3	2.04	1.65	101.12	*	72.58	116.43	1.6	1.29	43.85	
213800_at	CFH: complement factor H	X04697	1277.8	2590.8	2.03	1.85	1313	*	2156.04	3138.88	1.46	1.36	982.83	
232330_at	C7orf44: Chromosome 7 open reading frame 44	AK024861	143.49	290.99	2.03	1.77	147.5	*	30.18	98.53	3.26	2.07	68.34	
230015_at	PRCD: progressive rod-cone degeneration	AV729651	99.78	201.33	2.02	1.57	101.55	*	82.67	141.46	1.71	1.3	58.79	
230546_at	VASH1: vasohibin 1	AA142893	107.54	217.21	2.02	1.71	109.67	*	150.29	208.17	1.39	1.29	57.88	
237860_at	Hs.137101.0	AI821998	119.86	242.25	2.02	1.73	122.39	*	126.17	109.88	-1.15	-0.89	-16.29	
204864_s_at	IL6ST: interleukin 6 signal transducer (gp130, oncostatin M receptor)	NM_002184	600.05	1203.9	2.01	1.89	603.86	*	506.82	613.4	1.21	1.1	106.58	
209322_s_at	SH2B1: SH2B adaptor protein 1	AF227968	178.58	358.73	2.01	1.75	180.15	*	137.03	223.84	1.63	1.42	86.81	
227006_at	PPP1R14A: protein phosphatase 1, regulatory (inhibitor) subunit 14A	AA156998	944.76	1879.3	1.99	1.79	934.54	*	715.07	1107.92	1.55	1.43	392.85	
1554880_at	DKFZP434K028: hypothetical LOC26070	BC021187	200.04	397.25	1.99	1.85	197.21	*	81.95	163.86	2	1.29	81.91	
212706_at	LOC100286937 /// LOC100287164 /// RASA4: similar to HSPC047 protein /// similar to HSPC047 protein /// RAS p21 protein activator 4	AB011110	733.52	1449.94	1.98	1.89	716.41	*	545.72	824.87	1.51	1.44	279.15	
219177_at	BXDC2: brix domain containing 2	NM_018321	969.92	1921.91	1.98	1.89	951.99	*	701.09	1059.7	1.51	1.43	358.62	
236281_x_at	HTR7: 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	R44298	135.78	269	1.98	1.61	133.22	*	105.48	112.07	1.06	0.78	6.59	
1553982_a_at	RAB7B: RAB7B, member RAS oncogene family	AY094596	209.06	413.15	1.98	1.76	204.1	*	581.45	918.71	1.58	1.49	337.25	
214520_at	FOXC2: forkhead box C2 (MFH-1, mesenchyme forkhead 1)	NM_005251	239.12	465.47	1.95	1.75	226.35	*	163.36	225.95	1.38	1.13	62.59	
236207_at	SSFA2: sperm specific antigen 2	BE083088	265.55	518.44	1.95	1.84	252.89	*	219.91	239.38	1.09	0.98	19.47	
213764_s_at	MFAP5: microfibrillar associated protein 5	AW665892	898.37	1746.3	1.94	1.76	847.93	*	3558.3	2781.99	-1.28	-1.2	-776.31	
205260_s_at	ACYP1: acylphosphatase 1, erythrocyte (common) type	NM_001107	428.25	825.42	1.93	1.81	397.17	*	383.72	439.44	1.15	1.07	55.72	
203837_at	MAP3K5: mitogen-activated protein kinase kinase kinase 5	NM_005923	1009.09	1936.99	1.92	1.81	927.91	*	630.95	744.66	1.18	1.04	113.7	
205713_s_at	COMP: cartilage oligomeric matrix protein	NM_000095	1183.05	2273.18	1.92	1.82	1090.13	*	2561.63	3609.8	1.41	1.36	1048.17	
212993_at	NACC2: NACC family member 2, BEN and BTB (POZ) domain containing	AA114166	2587.26	4936.32	1.91	1.81	2349.06	*	1979.91	2593.02	1.31	1.21	613.1	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
213630_at	NACAD: NAC alpha domain containing	AB002361	147.68	282.69	1.91	1.63	135.01	*	237.92	347.79	1.46	1.25	109.87	
207302_at	SGCG: sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	NM_000231	185.65	350.8	1.89	1.74	165.15	*	40.02	57.41	1.43	1.07	17.39	
239207_at	KDM5C: lysine (K)-specific demethylase 5C	BE503653	200.08	377.73	1.89	1.68	177.65	*	131.22	164.48	1.25	0.98	33.27	
224770_s_at	NAV1: neuron navigator 1	AI937060	522.88	981.31	1.88	1.77	458.43	*	380.77	340.4	-1.12	-0.98	-40.37	
1559942_at	MDFIC: MyoD family inhibitor domain containing	BC040713	117.24	220.06	1.88	1.52	102.81	*	174.66	284.06	1.63	1.46	109.4	
1557786_s_at	CHIC1: cysteine-rich hydrophobic domain 1	AA062610	266.3	497.95	1.87	1.74	231.65	*	160.58	262.04	1.63	1.24	101.46	
222312_s_at	Hs.105791.1	AW969803	356.17	660.76	1.86	1.75	304.59	*	252.03	319.03	1.27	1.15	67	
211538_s_at	HSPA2: heat shock 70kDa protein 2	U56725	520.07	962.12	1.85	1.72	442.06	*	495.31	763.13	1.54	1.42	267.83	
239847_at	Hs.105791.0	AA631103	341.11	632.73	1.85	1.74	291.62	*	221.21	290.65	1.31	1.11	69.44	
203836_s_at	MAP3K5: mitogen-activated protein kinase kinase kinase 5	D84476	749.59	1376.99	1.84	1.71	627.4	*	390.51	452.19	1.16	1.05	61.68	
214535_s_at	ADAMTS2: ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_021599	432.08	796.4	1.84	1.59	364.32	*	469.57	463.95	-1.01	-0.92	-5.62	
212952_at	Hs.16488.2	AA910371	448.89	820.55	1.83	1.62	371.66	*	348.99	440.27	1.26	1.08	91.27	
243041_s_at	Hs.126083.1	AI217028	712.41	1296.09	1.82	1.75	583.68	*	594.4	633.17	1.07	1	38.77	
243641_at	Hs.279643.0	BE219067	195.77	355.7	1.82	1.63	159.93	*	152.33	232.66	1.53	1.33	80.33	
213765_at	MFAP5: microfibrillar associated protein 5	AW665892	1298.93	2340.05	1.8	1.58	1041.12	*	5326.06	3822.97	-1.39	-1.33	-1503.09	
214041_x_at	RPL37A: Ribosomal protein L37a	BE857772	544.62	982.93	1.8	1.71	438.31	*	494.21	638.11	1.29	1.21	143.91	
227337_at	ANKRD37: ankyrin repeat domain 37	AA886870	1629.58	2938.15	1.8	1.73	1308.56	*	681.81	575.54	-1.18	-1.04	-106.27	
231720_s_at	JAM3: junctional adhesion molecule 3	AF356518	407.47	734.97	1.8	1.62	327.49	*	689.96	1086.68	1.57	1.46	396.71	
226715_at	FOXK1: forkhead box K1	AW007319	748.24	1336.48	1.79	1.63	588.24	*	674.99	770.22	1.14	1.04	95.23	
230076_at	PITPNM3: PITPNM family member 3	BF063164	138.46	247.29	1.79	1.58	108.84	*	376.71	392.97	1.04	0.98	16.26	
240382_at	LOC100131914: Hypothetical protein LOC100131914	AW444944	503.54	901.9	1.79	1.68	398.37	*	477.02	325.76	-1.46	-1.34	-151.26	
230290_at	SCUBE3: signal peptide, CUB domain, EGF-like 3	BE674338	2075.47	3692.36	1.78	1.69	1616.89	*	1493.85	1888.34	1.26	1.16	394.49	
224771_at	NAV1: neuron navigator 1	AI937060	995.09	1762.07	1.77	1.65	766.98	*	805.51	869.4	1.08	0.99	63.89	
204926_at	INHBA: inhibin, beta A	NM_002192	1065.24	1876.97	1.76	1.66	811.73	*	524.89	398.64	-1.32	-1.2	-126.25	
215555_at	Hs.273099.0	AU158442	159.17	279.7	1.76	1.54	120.53	*	19.24	45.43	2.36	1.26	26.2	
208557_at	HOXA6: homeobox A6	NM_024014	205.62	360.45	1.75	1.6	154.83	*	119.96	176.88	1.47	1.2	56.91	
212427_at	KIAA0368: KIAA0368	AB002366	440.57	771.61	1.75	1.62	331.04	*	278.93	418.35	1.5	1.31	139.43	
229397_s_at	GRLF1: Glucocorticoid receptor DNA binding factor 1	AI275597	200.19	349.7	1.75	1.62	149.51	*	132.74	192.69	1.45	1.29	59.95	
242245_at	Hs.94445.0	N90719	263.66	460.31	1.75	1.56	196.65	*	181.57	265.24	1.46	1.23	83.66	
201309_x_at	C5orf13: chromosome 5 open reading frame 13	U36189	3212.98	5583.56	1.74	1.53	2370.58	*	7707.64	8598.63	1.12	1.08	891	
210145_at	PLA2G4A: phospholipase A2, group IVA (cytosolic, calcium-dependent)	M68874	462.08	804.1	1.74	1.63	342.02	*	1074.4	1652.82	1.54	1.47	578.43	
227299_at	CCNI: Cyclin I	AA020986	156.5	271.92	1.74	1.51	115.42	*	134.51	145.52	1.08	0.85	11.01	
227705_at	TCEAL7: transcription elongation factor A (SII)-like 7	BF591534	878.55	1524.86	1.74	1.6	646.31	*	1438.55	2183.53	1.52	1.45	744.98	
235492_at	RNF217: ring finger protein 217	AI888256	378.75	659.19	1.74	1.59	280.44	*	271.16	320.68	1.18	1.05	49.52	
202481_at	DHRS3: dehydrogenase/reductase (SDR family) member 3	NM_004753	652.99	1131.96	1.73	1.6	478.97	*	86.71	69.03	-1.26	-0.92	-17.68	
225474_at	MAGI1: membrane associated guanylate kinase, WW and PDZ domain containing 1	AI141556	908.72	1572.97	1.73	1.66	664.25	*	542.91	731.45	1.35	1.19	188.54	
235331_x_at	PCGF5: polycomb group ring finger 5	AI341142	1490.24	2559.77	1.72	1.66	1069.54	*	1142.66	1696.31	1.48	1.43	553.65	
238015_at	C4orf46: chromosome 4 open reading frame 46	BE620598	243.93	418.21	1.71	1.58	174.28	*	555.99	634.44	1.14	1.07	78.45	
229488_at	OTUD7B: OTU domain containing 7B	AW450442	477.59	810.52	1.7	1.57	332.93	*	366.22	399.1	1.09	0.85	32.88	
223925_s_at	MTPN: myotrophin	AF130088	255.33	431.89	1.69	1.62	176.56	*	279.71	386.91	1.38	1.33	107.2	
224199_at	DKK2: dickkopf homolog 2 (Xenopus laevis)	AB033941	389.53	656.01	1.68	1.63	266.48	*	340	216.96	-1.57	-1.43	-123.05	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
226641_at	Hs.11571.0	AU157224	703.39	1180.89	1.68	1.57	477.5	*	491.12	776.21	1.58	1.41	285.09	
202674_s_at	LMO7: LIM domain 7	NM_005358	448.55	747.58	1.67	1.52	299.04	*	267.35	345.81	1.29	1.13	78.47	
211000_s_at	IL6ST: interleukin 6 signal transducer (gp130, oncostatin M receptor)	AB015706	2401.12	3994.9	1.66	1.59	1593.78	*	1223.55	1313.41	1.07	0.99	89.86	
210020_x_at	CALML3: calmodulin-like 3	M58026	230.44	377.54	1.64	1.54	147.09	*	210.3	151.68	-1.39	-1.23	-58.62	
234994_at	TMEM200A: transmembrane protein 200A	AA088177	5184.57	8491.81	1.64	1.53	3307.24	*	3433.43	4635.71	1.35	1.22	1202.29	
52975_at	FAM125B: family with sequence similarity 125, member B	AA534894	378.22	614.63	1.63	1.51	236.41	*	272.12	341.01	1.25	1.14	68.89	
235004_at	RBM24: RNA binding motif protein 24	AI677701	569.4	928.74	1.63	1.55	359.34	*	359.55	373.12	1.04	0.94	13.56	
231130_at	FKBP7: FK506 binding protein 7	AA683602	585.43	948.73	1.62	1.52	363.29	*	1231.04	1956.03	1.59	1.48	724.99	
242137_at	Hs.151145.0	H10545	527.22	852.41	1.62	1.5	325.19	*	426.58	373.03	-1.14	-1.07	-53.54	
213260_at	FOXC1: forkhead box C1	AU145890	2165.17	3445.01	1.59	1.52	1279.84	*	1276.97	1833.6	1.44	1.35	556.63	

Up-Regulated Genes at Day 10 in Response to 20nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
205572_at	ANGPT2: angiopoietin 2	NM_001147	16.65	36.28	2.18	1.41	19.63		2.19	159.68	72.87	21.14	157.48	*
228665_at	CYYR1: cysteine/tyrosine-rich 1	AI458003	15.06	52.49	3.48	2.6	37.43		3.12	197.28	63.23	27.54	194.16	*
226145_s_at	FRAS1: Fraser syndrome 1	AL157471	63.48	146.46	2.31	1.92	82.99		56.1	2128.65	37.95	31.11	2072.55	*
1560490_at	FAT3: FAT tumor suppressor homolog 3 (Drosophila)	BC016722	24.58	31.89	1.3	0.78	7.31		25.73	802.96	31.21	20.11	777.23	*
208650_s_at	CD24: CD24 molecule	BG327863	156.75	189.4	1.21	1.06	32.64		149.2	3659.37	24.53	22.43	3510.17	*
1561141_at	Hs2.384608.1	AF086258	33.92	41.4	1.22	0.69	7.47		70.12	1501.62	21.42	16.81	1431.5	*
236029_at	FAT3: FAT tumor suppressor homolog 3 (Drosophila)	AI283093	163.93	221.09	1.35	1.19	57.16		179.57	3672.01	20.45	17.9	3492.44	*
1563899_at	LCTL: lactase-like	AK090598	44.57	73.96	1.66	1.29	29.39		30.33	582.45	19.2	15.47	552.11	*
1557924_s_at	ALPL: alkaline phosphatase, liver/bone/kidney	S76738	45.29	60.39	1.33	1.03	15.1		58.44	1119.84	19.16	11.45	1061.4	*
219478_at	WFDC1: WAP four-disulfide core domain 1	NM_021197	90.82	166.14	1.83	1.26	75.32		121.38	2289.47	18.86	13.98	2168.08	*
209169_at	GPM6B: glycoprotein M6B	N63576	44.84	133.44	2.98	2.38	88.6		82.63	1535.55	18.58	14.51	1452.92	*
209771_x_at	CD24: CD24 molecule	AA761181	488.35	553.35	1.13	0.96	65.01		397.45	7125.79	17.93	15.51	6728.34	*
217143_s_at	TRA@ /// TRD@: T cell receptor alpha locus /// T cell receptor delta locus	X06557	21.01	66.98	3.19	2.03	45.97		45.88	769.33	16.77	11.68	723.45	*
232195_at	GPR158: G protein-coupled receptor 158	R41459	51.46	93.59	1.82	1.44	42.13		38.83	633.35	16.31	12.71	594.52	*
208651_x_at	CD24: CD24 molecule	M58664	265.31	270.38	1.02	0.9	5.06		240.88	3900.22	16.19	14.62	3659.34	*
216379_x_at	CD24: CD24 molecule	AK000168	472.85	509.98	1.08	0.93	37.13		431.88	6931.01	16.05	14.05	6499.13	*
236517_at	MEGF10: multiple EGF-like-domains 10	AI968440	52.79	54.05	1.02	0.63	1.26		16.17	256.71	15.87	11.15	240.54	*
244270_at	Hs.153351.0	AI125785	37.47	54.89	1.46	0.49	17.42		11.25	169.59	15.08	6.51	158.34	*
1555766_a_at	GNG2: guanine nucleotide binding protein (G protein), gamma 2	AF493870	14.85	62.17	4.19	2.56	47.32		25.39	367.98	14.5	8.41	342.6	*
204845_s_at	ENPEP: glutamyl aminopeptidase (aminopeptidase A)	NM_001977	93.36	186.48	2	1.74	93.11		57.87	811.53	14.02	9.97	753.66	*
242672_at	Hs.291741.0	AA743129	112.34	59.49	-1.89	-1.49	-52.85		8.98	124.71	13.89	4.61	115.73	*
1558964_at	FAT3: FAT tumor suppressor homolog 3 (Drosophila)	AA334950	128.4	152.4	1.19	1	24		118.17	1580.77	13.38	7.96	1462.6	*
266_s_at	CD24: CD24 molecule	L33930	359.73	337.19	-1.07	-0.96	-22.54		273.3	3604.28	13.19	11.46	3330.98	*
233801_s_at	SEMA6D: sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	AK022747	30.71	129.2	4.21	2.67	98.49		34.28	432.2	12.61	7.66	397.92	*
219511_s_at	SNCAIP: synuclein, alpha interacting protein	NM_005460	147.49	140.36	-1.05	-0.81	-7.13		153.2	1859.64	12.14	7.28	1706.43	*
235343_at	VASH2: vasohibin 2	AI961235	24	103.44	4.31	3.15	79.43		35.66	425.92	11.95	8.67	390.26	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
206439_at	EPYC: epiphycan	NM_004950	46.65	132.02	2.83	2.21	85.37		33.54	395.97	11.8	10.28	362.43	*
1570469_at	Hs2.382186.1	BC017988	67.13	106.34	1.58	1.21	39.21		71.46	837.1	11.71	8.73	765.64	*
233109_at	COL12A1: Collagen, type XII, alpha 1	AU146651	490.07	708.66	1.45	1.34	218.59		74.67	801.41	10.73	9.02	726.74	*
230746_s_at	LOC100288985: hypothetical protein LOC100288985	AW003173	174.19	284.03	1.63	1.44	109.84		31.12	322.08	10.35	7.49	290.96	*
204380_s_at	FGFR3: fibroblast growth factor receptor 3	M58051	36.98	84.66	2.29	1.65	47.68		43.74	448.64	10.26	7.06	404.91	*
209772_s_at	CD24: CD24 molecule	X69397	268.29	230.31	-1.16	-0.96	-37.98		247.06	2499.03	10.11	7.45	2251.97	*
227189_at	CPNE5: copine V	AB046819	33.8	57.54	1.7	1.13	23.74		18.81	183.08	9.73	5.46	164.27	*
228948_at	EPHA4: EPH receptor A4	T15545	77.42	141.82	1.83	1.22	64.4		54.28	527.73	9.72	7.04	473.45	*
232523_at	MEGF10: multiple EGF-like-domains 10	AU144892	139.34	234.25	1.68	1.39	94.91		68.58	663.62	9.68	8.33	595.04	*
207017_at	RAB27B: RAB27B, member RAS oncogene family	NM_004163	47.87	40.24	-1.19	-0.81	-7.63		24.24	232.04	9.57	4.54	207.81	*
214043_at	PTPRD: protein tyrosine phosphatase, receptor type, D	BF062299	177.1	192.66	1.09	0.98	15.56		174.38	1652.88	9.48	8.42	1478.49	*
237833_s_at	SNCAIP: synuclein, alpha interacting protein	BF062366	104.34	99.42	-1.05	-0.83	-4.92		105.13	951.83	9.05	6.3	846.7	*
203474_at	IQGAP2: IQ motif containing GTPase activating protein 2	NM_006633	5.46	39.91	7.3	4.07	34.44		23.35	208.74	8.94	5.87	185.39	*
203887_s_at	THBD: thrombomodulin	NM_000361	31.95	55.54	1.74	1.12	23.59		20.52	176.86	8.62	4.97	156.34	*
209168_at	GPM6B: glycoprotein M6B	AW148844	190.05	337.29	1.77	1.44	147.24		253.9	2160.45	8.51	4.26	1906.55	*
236088_at	NTNG1: netrin G1	AV723308	46.69	64.81	1.39	1.11	18.12		43.97	368.39	8.38	6.09	324.42	*
227297_at	ITGA9: integrin, alpha 9	AI479176	7.86	38.31	4.88	2.66	30.46		24.03	200.45	8.34	5.2	176.42	*
211215_x_at	DIO2: deiodinase, iodothyronine, type II	AB041843	42.75	99.88	2.34	1.76	57.13		27.03	220.93	8.17	6.29	193.9	*
237094_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	AI953086	22.5	102.21	4.54	2.98	79.72		37.8	308.43	8.16	6.42	270.63	*
212094_at	PEG10: paternally expressed 10	AL582836	163.98	177.89	1.08	0.96	13.91		244.06	1986.75	8.14	7.3	1742.69	*
204597_x_at	STC1: stanniocalcin 1	NM_003155	277.59	355.42	1.28	1.16	77.84		60.64	473.4	7.81	6.08	412.75	*
238784_at	DPY19L2: dpy-19-like 2 (C. elegans)	AI039361	138.28	140.47	1.02	0.85	2.19		41.87	322.37	7.7	5.92	280.5	*
229070_at	C6orf105: chromosome 6 open reading frame 105	AA470369	53.24	48.04	-1.11	-0.76	-5.2		19.46	148.42	7.63	4.45	128.96	*
203180_at	ALDH1A3: aldehyde dehydrogenase 1 family, member A3	NM_000693	1089.98	1155.09	1.06	0.84	65.1		919.77	6901.96	7.5	6.58	5982.19	*
227480_at	SUSD2: sushi domain containing 2	Z92546	61.17	127.79	2.09	1.43	66.62		135.98	1019.21	7.5	5.99	883.23	*
226828_s_at	HEYL: hairy/enhancer-of-split related with YRPW motif-like	AL040198	61.02	121.08	1.98	1.47	60.06		39.88	298.7	7.49	5.2	258.82	*
204437_s_at	FOLR1: folate receptor 1 (adult)	NM_016725	54.18	91.14	1.68	1.36	36.95		50.77	379.87	7.48	5.16	329.1	*
221796_at	NTRK2: neurotrophic tyrosine kinase, receptor, type 2	AA707199	19.47	117.16	6.02	4.42	97.69		19.09	142.78	7.48	4.58	123.69	*
206136_at	FZD5: frizzled homolog 5 (Drosophila)	NM_003468	16.77	59.97	3.58	2.39	43.19		31.4	233.38	7.43	6.04	201.98	*
235763_at	SLC44A5: solute carrier family 44, member 5	AA001450	12.7	31.96	2.52	1.66	19.27		33.58	247.84	7.38	5.34	214.26	*
209883_at	GLT25D2: glycosyltransferase 25 domain containing 2	AF288389	277.93	314.75	1.13	0.99	36.81		193.78	1409.71	7.27	6.54	1215.93	*
205051_s_at	KIT: v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	NM_000222	58.74	143.32	2.44	2.15	84.57		39.09	282.93	7.24	5.13	243.84	*
214248_s_at	TRIM2: tripartite motif-containing 2	AW071795	42.53	74.09	1.74	1.22	31.57		21.6	153.45	7.1	4.14	131.85	*
237483_at	Hs.188614.0	AI990790	517.07	455.6	-1.13	-1.09	-61.48		61.64	433.24	7.03	5.24	371.6	*
220301_at	CCDC102B: coiled-coil domain containing 102B	NM_024781	20.31	54.68	2.69	1.75	34.37		69.12	484.72	7.01	5.9	415.6	*
213909_at	LRRC15: leucine rich repeat containing 15	AU147799	236.76	317.44	1.34	0.98	80.69		783.85	5453.4	6.96	6.21	4669.55	*
229655_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	N66656	28.26	105.79	3.74	2.24	77.52		74.49	516.67	6.94	5.91	442.18	*
207781_s_at	ZNF711: zinc finger protein 711	NM_021998	78.6	154.81	1.97	1.57	76.21		42.41	293.17	6.91	5.75	250.76	*
213362_at	PTPRD: protein tyrosine phosphatase, receptor type, D	N73931	120.2	131.65	1.1	0.97	11.45		113.23	781.19	6.9	5.64	667.96	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
227933_at	LINGO1: leucine rich repeat and Ig domain containing 1	AI193252	23.28	85.69	3.68	1.95	62.41		42.83	295.52	6.9	5.56	252.69	*
215695_s_at	GYG2: glycogenin 2	U94357	133.13	125.42	-1.06	-0.85	-7.71		62.1	424.4	6.83	5.94	362.3	*
216005_at	TNC: Tenascin C	BF434846	648.99	625.54	-1.04	-0.97	-23.45		85.06	574.93	6.76	5.5	489.86	*
230261_at	ST8SIA4: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	AA552969	85.7	72.42	-1.18	-0.93	-13.28		59.2	396.69	6.7	5.58	337.49	*
210657_s_at	SEPT4: septin 4	U88870	81.36	140.06	1.72	1.28	58.7		124.32	808.79	6.51	4.29	684.47	*
240581_at	LOC644135: Hypothetical LOC644135	AW007727	62.19	144.88	2.33	1.79	82.69		41.32	264.84	6.41	4.85	223.53	*
230577_at	Hs.170953.0	AW014022	19.67	24.37	1.24	0.53	4.7		31.04	193.92	6.25	4.03	162.88	*
229623_at	FLJ12993: Hypothetical LOC441027	BF508344	26.5	34.9	1.32	0.86	8.41		39.09	243.66	6.23	4.73	204.57	*
210964_s_at	GYG2: glycogenin 2	U94364	90.39	84.67	-1.07	-0.74	-5.72		59.47	369.15	6.21	5.07	309.68	*
1552367_a_at	SCIN: scinderin	AF276507	30.11	69.78	2.32	1.58	39.67		29.29	181.89	6.21	5.01	152.59	*
244832_at	Hs.135238.0	AI088707	25.33	69.81	2.76	1.45	44.48		37.98	235.35	6.2	4.22	197.37	*
204595_s_at	STC1: stanniocalcin 1	AI300520	265.7	412.32	1.55	1.42	146.62		83.44	509.14	6.1	4.73	425.71	*
243555_at	Hs.150941.0	AA573452	37.93	119.92	3.16	2.19	82		47.69	289.12	6.06	4.81	241.43	*
218678_at	NES: nestin	NM_024609	328.68	404.52	1.23	0.97	75.83		501	2982.03	5.95	5.34	2481.03	*
212092_at	PEG10: paternally expressed 10	BE858180	53.58	53.11	-1.01	-0.72	-0.47		100.04	593.02	5.93	4.38	492.98	*
230158_at	DPY19L2: dpy-19-like 2 (C. elegans)	AA758751	62.17	64.45	1.04	0.78	2.28		34.07	201.79	5.92	4.8	167.72	*
206243_at	TIMP4: TIMP metallopeptidase inhibitor 4	NM_003256	93.14	129.12	1.39	1.08	35.98		70.28	412.79	5.87	4.76	342.51	*
213622_at	COL9A2: collagen, type IX, alpha 2	AI733465	47.31	71.49	1.51	0.89	24.18		52.39	306.86	5.86	4.16	254.47	*
227002_at	FAM78A: family with sequence similarity 78, member A	BF515132	48.03	48.57	1.01	0.44	0.54		38.92	226.75	5.83	3.93	187.83	*
242943_at	ST8SIA4: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	AA352113	150.86	121.79	-1.24	-0.98	-29.07		98.85	572.97	5.8	5.1	474.13	*
227899_at	VIT: vitrin	AI817458	36.97	58.98	1.6	1.1	22.02		62.89	363.57	5.78	3.71	300.67	*
235044_at	CYYR1: cysteine/tyrosine-rich 1	H06649	34.39	10.64	-3.23	-1.61	-23.75		24.79	143.33	5.78	4.11	118.55	*
211148_s_at	ANGPT2: angiopoietin 2	AF187858	32.98	38.22	1.16	0.73	5.24		25.67	145.16	5.66	2.1	119.49	*
213167_s_at	SLC5A3: solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	BF982927	67.87	66.15	-1.03	-0.77	-1.72		101.21	564.46	5.58	4.77	463.25	*
230836_at	ST8SIA4: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	AI422986	194	155.49	-1.25	-1.08	-38.51		113.4	631.66	5.57	4.6	518.26	*
1557263_s_at	LOC100131731: Hypothetical protein LOC100131731	AK092855	192.34	176.57	-1.09	-0.98	-15.77		22.79	125.26	5.5	4.28	102.48	*
227819_at	LGR6: leucine-rich repeat-containing G protein-coupled receptor 6	AA524536	24.1	38.86	1.61	0.94	14.76		71.02	386.52	5.44	3.94	315.5	*
227449_at	EPHA4: EPH receptor A4	AI799018	439.01	600.92	1.37	1.27	161.91		365.91	1980.25	5.41	4.84	1614.33	*
237314_at	ENKUR: enkurin, TRPC channel interacting protein	AW119023	30.81	127.59	4.14	2.82	96.78		32.16	173.54	5.4	3.71	141.38	*
216757_at	Hs.306739.0	AK024995	49.15	91.72	1.87	1.09	42.57		45.51	242.43	5.33	3.67	196.91	*
220144_s_at	ANKRD5: ankyrin repeat domain 5	NM_022096	36.57	129.2	3.53	2.38	92.62		55.46	293.54	5.29	4.48	238.08	*
223823_at	KCNMB2: potassium large conductance calcium-activated channel, subfamily M, beta member 2	AF209747	13.84	31.19	2.25	1.5	17.35		35.53	185.5	5.22	3.12	149.97	*
211401_s_at	FGFR2: fibroblast growth factor receptor 2	AB030078	30.97	25.06	-1.24	-0.68	-5.91		47.12	243.14	5.16	4.02	196.02	*
213164_at	SLC5A3: solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	AI867198	1090.32	1161.71	1.07	0.94	71.38		961.61	4951.16	5.15	4.83	3989.55	*
242517_at	KISS1R: KISS1 receptor	AI819198	17.61	7.44	-2.37	-0.02	-10.17		25.13	129.39	5.15	2.77	104.26	*
228766_at	CD36: CD36 molecule (thrombospondin receptor)	AW299226	25.32	40.14	1.59	1.06	14.82		44.18	226.14	5.12	3.12	181.96	*
227250_at	KREMEN1: kringle containing transmembrane protein 1	BF221745	270.79	402.09	1.48	1.3	131.31		379.04	1936.32	5.11	4.87	1557.28	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
244378_at	C12orf51: Chromosome 12 open reading frame 51	AI340730	105.41	81.39	-1.3	-1.08	-24.02		31.29	159.96	5.11	3.2	128.67	*
206488_s_at	CD36: CD36 molecule (thrombospondin receptor)	NM_000072	42.76	68.83	1.61	1.12	26.07		158.66	808.15	5.09	3.6	649.49	*
1553313_s_at	SLC5A3: solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	NM_006933	42.13	34.41	-1.22	-0.74	-7.72		41.51	211.32	5.09	4.07	169.81	*
203697_at	FRZB: frizzled-related protein	U91903	96.42	171.7	1.78	1.38	75.29		126.45	639.92	5.06	2.5	513.47	*
1554897_s_at	RHBDL2: rhomboid, veinlet-like 2 (Drosophila)	BC013103	138.33	133.96	-1.03	-0.76	-4.37		216.76	1095.27	5.05	4.45	878.51	*
220988_s_at	AMACR /// C1QTNF3: alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	NM_030945	136.84	165.84	1.21	0.54	29		1076.75	5405.99	5.02	4.73	4329.24	*
233959_at	LOC221442: adenylate cyclase 10 pseudogene	W26606	106.39	111.61	1.05	0.89	5.22		39.85	200.03	5.02	3.92	160.18	*
207996_s_at	C18orf1: chromosome 18 open reading frame 1	NM_004338	62.4	18	-3.47	-2.2	-44.39		88.83	444.77	5.01	3.6	355.94	*
203638_s_at	FGFR2: fibroblast growth factor receptor 2	NM_022969	392.41	357.11	-1.1	-0.98	-35.31		572.36	2818.17	4.92	4.64	2245.81	*
227204_at	PARD6G: par-6 partitioning defective 6 homolog gamma (C. elegans)	AI817448	222.13	277.34	1.25	0.96	55.21		294.64	1449.6	4.92	4.2	1154.96	*
207370_at	IBSP: integrin-binding sialoprotein	NM_004967	990.26	751.47	-1.32	-1.16	-238.79		398.45	1946.54	4.89	4.24	1548.08	*
205698_s_at	MAP2K6: mitogen-activated protein kinase kinase 6	NM_002758	65.89	85.77	1.3	0.97	19.88		136.25	664.5	4.88	3.92	528.25	*
228326_at	WDR27: WD repeat domain 27	AI016894	192.92	172.06	-1.12	-1	-20.86		57.02	277.9	4.87	3.91	220.88	*
219106_s_at	KBTBD10: kelch repeat and BTB (POZ) domain containing 10	NM_006063	47.5	51.09	1.08	0.68	3.59		31.02	150.86	4.86	3.49	119.84	*
237169_at	Hs.135261.0	AI266750	107.3	189.79	1.77	1.52	82.49		86.54	419.46	4.85	4.19	332.92	*
203639_s_at	FGFR2: fibroblast growth factor receptor 2	M80634	87.38	72.9	-1.2	-0.88	-14.49		161.71	779.56	4.82	4.33	617.86	*
204466_s_at	SNCA: synuclein, alpha (non A4 component of amyloid precursor)	BG260394	44.67	49.34	1.1	0.79	4.67		40.85	196.8	4.82	3.38	155.95	*
233224_at	Hs.270062.0	AL137645	165.49	264.9	1.6	1.46	99.41		26.71	128.84	4.82	3.31	102.13	*
224396_s_at	ASPN: asporin	AF316824	165.65	205.28	1.24	1	39.63		2507.84	11963.25	4.77	3.9	9455.41	*
229374_at	EPHA4: EPH receptor A4	AI758962	145.34	244.85	1.68	1.4	99.52		137.75	656.41	4.77	3.86	518.66	*
242868_at	Hs.307559.0	T70087	392.14	436.45	1.11	1.03	44.3		27.56	130.91	4.75	3.43	103.35	*
223523_at	TMEM108: transmembrane protein 108	BC000568	113.98	190.34	1.67	1.37	76.36		79.32	373.33	4.71	3.93	294.01	*
236034_at	ANGPT2: angiopoietin 2	AA083514	40.88	54.65	1.34	0.77	13.77		30.28	142.69	4.71	3.27	112.4	*
205403_at	IL1R2: interleukin 1 receptor, type II	NM_004633	18.55	32.77	1.77	0.38	14.23		42.37	199.2	4.7	3.31	156.82	*
209582_s_at	CD200: CD200 molecule	H23979	330.32	325.41	-1.02	-0.9	-4.91		179.03	839.49	4.69	4.34	660.46	*
212944_at	SLC5A3: solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	AK024896	936.67	1130.02	1.21	1.08	193.36		943.63	4426.08	4.69	4.26	3482.45	*
225606_at	BCL2L11: BCL2-like 11 (apoptosis facilitator)	AI949179	228.57	237.57	1.04	0.89	9		126.59	593.87	4.69	3.8	467.28	*
205375_at	MDFI: MyoD family inhibitor	NM_005586	150.34	148.95	-1.01	-0.33	-1.39		193.41	904.47	4.68	3.04	711.06	*
205316_at	SLC15A2: solute carrier family 15 (H+/peptide transporter), member 2	BF223679	43.38	21.62	-2.01	-1.24	-21.77		32.96	153.85	4.67	3.64	120.89	*
228221_at	SLC44A3: solute carrier family 44, member 3	AA809640	55.62	87.18	1.57	1.17	31.55		62.52	289.81	4.64	3.85	227.29	*
230280_at	TRIM9: tripartite motif-containing 9	BF057241	22.24	30.75	1.38	0.57	8.51		37.72	175.11	4.64	3.41	137.39	*
230419_at	FLJ37644 /// LOC727973: hypothetical gene supported by AK094963 /// hypothetical protein LOC727973	AA778530	100.67	163.22	1.62	1.29	62.55		89.98	415.29	4.62	4.12	325.32	*
205303_at	KCNJ8: potassium inwardly-rectifying channel, subfamily J, member 8	BF514158	91.91	159.89	1.74	1.35	67.99		97.13	446.57	4.6	3.49	349.44	*
227626_at	PAQR8: progestin and adipoQ receptor family member VIII	AI655524	260.44	285.64	1.1	0.93	25.2		197.64	910.04	4.6	4.16	712.4	*
203434_s_at	MME: membrane metallo-endopeptidase	AI433463	253.37	170.85	-1.48	-1.24	-82.52		601.06	2742.26	4.56	4.24	2141.2	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
208228_s_at	FGFR2: fibroblast growth factor receptor 2	M87771	284.21	272.28	-1.04	-0.95	-11.94		373.19	1688.16	4.52	4.31	1314.96	*
1558695_at	Hs2.38348.1	AF085937	446.94	323.7	-1.38	-1.25	-123.24		48.48	218.19	4.5	3.14	169.71	*
233607_at	Hs.301626.0	AU145679	581.59	385.3	-1.51	-1.4	-196.29		43.56	193.07	4.43	2.8	149.52	*
218730_s_at	OGN: osteoglycin	NM_014057	35.87	40.26	1.12	0.76	4.39		359.29	1587.04	4.42	3.92	1227.75	*
209583_s_at	CD200: CD200 molecule	AF063591	821.19	889.99	1.08	1.01	68.8		433.96	1908.38	4.4	4.05	1474.43	*
204044_at	QPRT: quinolinate phosphoribosyltransferase	NM_014298	29.78	90.59	3.04	1.75	60.81		211.57	924.32	4.37	3.86	712.75	*
237248_at	PDE11A: phosphodiesterase 11A	AI919276	65.71	37.22	-1.77	-1.18	-28.49		61.48	268.25	4.36	3.84	206.77	*
216587_s_at	FZD8: frizzled homolog 8 (Drosophila)	AL121749	84.53	109.92	1.3	0.98	25.39		70.25	305.58	4.35	3.33	235.33	*
226423_at	PAQR8: progestin and adipoQ receptor family member VIII	AW006774	271.78	361.9	1.33	1.18	90.12		223.11	969.66	4.35	3.95	746.55	*
239433_at	LRRC8E: leucine rich repeat containing 8 family, member E	AA532807	123.32	141.28	1.15	0.86	17.97		133.72	579.57	4.33	3.94	445.85	*
242592_at	GPR137C: G protein-coupled receptor 137C	AV727446	25.58	123.34	4.82	3.4	97.76		53.43	231.26	4.33	3.65	177.84	*
217164_at	Hs.142677.0	AK024108	341.46	263.16	-1.3	-1.18	-78.3		30.52	131.31	4.3	3.18	100.78	*
206925_at	ST8SIA4: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	NM_005668	64.87	33.81	-1.92	-1.35	-31.06		40.42	173.19	4.28	3.35	132.77	*
220738_s_at	RPS6KA6: ribosomal protein S6 kinase, 90kDa, polypeptide 6	NM_014496	48.37	88.6	1.83	1.31	40.24		41.46	176.62	4.26	3.5	135.16	*
1569108_a_at	ZNF589: zinc finger protein 589	BC028160	61.26	47.44	-1.29	-0.74	-13.82		45.68	193.49	4.24	2.74	147.81	*
209459_s_at	ABAT: 4-aminobutyrate aminotransferase	AF237813	334.33	460.82	1.38	1.25	126.49		472.23	1997.36	4.23	4.06	1525.14	*
209840_s_at	LRRN3: leucine rich repeat neuronal 3	AI221950	61.35	88.26	1.44	1.01	26.9		164.12	693.75	4.23	3.71	529.64	*
220613_s_at	SYTL2: synaptotagmin-like 2	NM_017695	62.24	99.1	1.59	1.27	36.86		121.85	513.99	4.22	3.64	392.14	*
226844_at	MOBKL2B: MOB1, Mps One Binder kinase activator-like 2B (yeast)	AI375115	74.04	65.18	-1.14	-0.64	-8.86		67.39	284.28	4.22	2.99	216.89	*
209460_at	ABAT: 4-aminobutyrate aminotransferase	AF237813	260.45	341.28	1.31	1.12	80.83		340.48	1430.89	4.2	3.96	1090.42	*
209200_at	MEF2C: myocyte enhancer factor 2C	AL536517	496.3	792.23	1.6	1.43	295.94		560.7	2339.69	4.17	3.6	1779	*
1552960_at	LRRC15: leucine rich repeat containing 15	NM_130830	32.78	19.16	-1.71	-1.11	-13.62		46.87	195.22	4.17	2.54	148.36	*
230560_at	STXBP6: syntaxin binding protein 6 (amisyn)	N21096	117.35	29.25	-4.01	-2.79	-88.09		168.41	700.15	4.16	3.85	531.73	*
207018_s_at	RAB27B: RAB27B, member RAS oncogene family	NM_004163	107.39	155.82	1.45	1.17	48.44		130.16	538.79	4.14	1.77	408.63	*
204197_s_at	RUNX3: runt-related transcription factor 3	NM_004350	219.86	286.25	1.3	1.12	66.39		155.84	644.05	4.13	3.87	488.21	*
205098_at	CCR1: chemokine (C-C motif) receptor 1	AI421071	21.79	15.61	-1.4	-0.62	-6.18		35.64	147.03	4.13	2.07	111.39	*
1562275_at	Hs2.201008.1	AL832835	36.18	36.87	1.02	0.52	0.69		32.43	134.1	4.13	2.98	101.66	*
203547_at	CD4: CD4 molecule	U47924	1.77	20.36	11.47	3.85	18.58		47.12	192.99	4.1	3.3	145.87	*
228740_at	Hs.26766.0	BF059276	84.07	145.19	1.73	1.43	61.12		156.49	636.32	4.07	3.69	479.83	*
1554636_at	Hs2.368843.1	BC032569	132.43	161.18	1.22	1.1	28.75		34.22	139.27	4.07	3.1	105.06	*
241769_at	Hs.208558.0	AW962458	560.27	600.77	1.07	1.02	40.5		52.3	212.3	4.06	2.76	160	*
242671_at	Hs.122516.0	BF055144	188.7	214.04	1.13	1.04	25.34		59.14	239.55	4.05	3.17	180.41	*
209199_s_at	MEF2C: myocyte enhancer factor 2C	N22468	577.34	883.97	1.53	1.39	306.63		558.67	2253.65	4.03	3.78	1694.99	*
223524_s_at	TMEM108: transmembrane protein 108	BC000568	438.63	641.8	1.46	1.36	203.17		348.92	1405.49	4.03	3.81	1056.57	*
212183_at	NUDT4: nudix (nucleoside diphosphate linked moiety X)-type motif 4	AW511135	594.75	676.05	1.14	1.01	81.3		449.99	1811.14	4.02	3.71	1361.15	*
222780_s_at	BAALC: brain and acute leukemia, cytoplasmic	AI870583	356.65	490.33	1.37	1.24	133.68		227.64	915.84	4.02	3.46	688.2	*
223843_at	SCARA3: scavenger receptor class A, member 3	AB007830	100.32	199.4	1.99	1.64	99.08		124.8	501.32	4.02	3.41	376.52	*
201340_s_at	ENC1: ectodermal-neural cortex (with BTB-like domain)	AF010314	662.54	695.05	1.05	1	32.51		273.23	1094.27	4.01	3.59	821.05	*
206402_s_at	NPFF: neuropeptide FF-amide peptide precursor	NM_003717	276.04	253.88	-1.09	-1.03	-22.16		52.5	208.57	3.97	3.11	156.07	*
242365_at	Hs.222110.0	AA921687	83.77	118.75	1.42	1.11	34.98		59.75	237.51	3.97	2.75	177.75	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
229653_at	VPS53: vacuolar protein sorting 53 homolog (S. cerevisiae)	AA514634	651.72	407.9	-1.6	-1.39	-243.82		165.08	646.41	3.92	2.49	481.33	*
237351_at	Hs.116524.0	AI732190	100.98	47.78	-2.11	-1.64	-53.2		47.68	187.05	3.92	3.18	139.37	*
232528_at	Hs.270124.0	AI338705	370.32	343.54	-1.08	-1	-26.78		39.16	152.14	3.89	2.9	112.98	*
210783_x_at	CLEC11A: C-type lectin domain family 11, member A	D86586	601.36	913.46	1.52	1.3	312.1		963.12	3737.81	3.88	3.56	2774.68	*
242558_at	Hs.162459.0	AW362945	636.46	509.77	-1.25	-1.17	-126.69		52.4	203.49	3.88	2.84	151.09	*
205712_at	PTPRD: protein tyrosine phosphatase, receptor type, D	NM_002839	179.21	185.47	1.03	0.95	6.26		158.77	612.86	3.86	2.49	454.09	*
235405_at	GSTA4: glutathione S-transferase alpha 4	N79662	399.53	442.86	1.11	1.04	43.33		98.66	379.97	3.85	3.06	281.31	*
204198_s_at	RUNX3: runt-related transcription factor 3	AA541630	318.17	465.68	1.46	1.29	147.51		254.88	979.07	3.84	3.46	724.19	*
209815_at	PTCH1: patched homolog 1 (Drosophila)	BG054916	141.25	211.39	1.5	1.31	70.14		89.81	344.84	3.84	3.12	255.04	*
215029_at	Hs.293563.0	AL117451	300.4	237.95	-1.26	-1.17	-62.46		56.25	214.36	3.81	3.03	158.11	*
201497_x_at	MYH11: myosin, heavy chain 11, smooth muscle	NM_022844	129.88	49.95	-2.6	-1.33	-79.93		223.7	837.23	3.74	2.71	613.53	*
212181_s_at	NUDT4 /// NUDT4P1: nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	AF191654	2278.72	3423.1	1.5	1.29	1144.38		1605.11	5980.39	3.73	3.27	4375.29	*
236028_at	IBSP: integrin-binding sialoprotein	BE466675	3607.92	2626.29	-1.37	-1.27	-981.63		1681.29	6262.53	3.72	3.43	4581.23	*
222722_at	OGN: osteoglycin	AV700059	49.17	68.42	1.39	0.92	19.24		640.79	2374.59	3.71	3.42	1733.8	*
1552502_s_at	RHBDL2: rhomboid, veinlet-like 2 (Drosophila)	NM_017821	213.85	188.94	-1.13	-0.96	-24.91		366.43	1360.26	3.71	3.43	993.83	*
205206_at	KAL1: Kallmann syndrome 1 sequence	NM_000216	35.13	28.47	-1.23	-0.54	-6.67		52.54	193.24	3.68	2.78	140.7	*
223044_at	SLC40A1: solute carrier family 40 (iron-regulated transporter), member 1	AL136944	199.62	170.08	-1.17	-0.99	-29.54		658.48	2412.12	3.66	3.48	1753.64	*
226884_at	LRRN1: leucine rich repeat neuronal 1	N71874	67.48	9.73	-6.94	-4	-57.76		108.01	393.99	3.65	3.2	285.99	*
213791_at	PENK: proenkephalin	NM_006211	362.96	483.78	1.33	1.17	120.82		885.25	3221.61	3.64	3.28	2336.36	*
239070_at	Hs.164259.0	AI434790	67.46	70.99	1.05	0.66	3.53		45.42	163.09	3.59	2.12	117.67	*
242403_at	Hs.172759.0	AI459177	565.86	408.31	-1.39	-1.3	-157.55		71.62	256.36	3.58	2.64	184.74	*
1558017_s_at	Hs2.116735.1	BG109597	504.97	472.7	-1.07	-1.01	-32.27		79.62	284.78	3.58	2.86	205.17	*
220817_at	TRPC4: transient receptor potential cation channel, subfamily C, member 4	NM_016179	273.93	343	1.25	1.13	69.07		255.85	912.22	3.57	3.38	656.37	*
204596_s_at	STC1: stanniocalcin 1	U46768	87.75	131.92	1.5	1.27	44.18		43.75	155.87	3.56	2.82	112.12	*
223842_s_at	SCARA3: scavenger receptor class A, member 3	AB007830	137.76	190.29	1.38	1.19	52.53		154.2	549.64	3.56	3.19	395.45	*
206805_at	SEMA3A: sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	NM_006080	82.61	54.37	-1.52	-1.09	-28.24		129.1	458.16	3.55	2.92	329.05	*
213593_s_at	TRA2A: transformer 2 alpha homolog (Drosophila)	AW978896	1226.3	938.7	-1.31	-1.26	-287.61		99.25	352.34	3.55	3.14	253.09	*
241938_at	QKI: Quaking homolog, KH domain RNA binding (mouse)	AA935633	318.94	258.19	-1.24	-1.11	-60.75		52.81	187.34	3.55	2.43	134.53	*
242669_at	UFM1: Ubiquitin-fold modifier 1	BF514975	562.9	473.77	-1.19	-1.11	-89.13		102.96	365.27	3.55	2.91	262.31	*
209159_s_at	NDRG4: NDRG family member 4	AV724216	145.37	248.53	1.71	1.5	103.16		172.57	610.54	3.54	3.12	437.96	*
229568_at	MOBKL2B: MOB1, Mps One Binder kinase activator-like 2B (yeast)	AI692878	42.67	37.97	-1.12	-0.79	-4.69		70.36	249.18	3.54	2.79	178.82	*
218899_s_at	BAALC: brain and acute leukemia, cytoplasmic	NM_024812	423.55	646.02	1.53	1.44	222.46		312.36	1100.69	3.52	3.18	788.34	*
215501_s_at	DUSP10: dual specificity phosphatase 10	AK022513	382.48	645.94	1.69	1.44	263.46		294.05	1029.76	3.5	2.96	735.71	*
1557383_a_at	Hs2.212617.1	AI925316	44.82	57.62	1.29	0.95	12.79		47.68	166.33	3.49	2.69	118.65	*
227921_at	Hs.18714.0	AI797678	588.35	449.69	-1.31	-1.19	-138.66		528.77	1832.66	3.47	3.28	1303.89	*
228228_at	DACT3: dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	AI809234	328.43	485.25	1.48	1.24	156.82		545.3	1892.19	3.47	3.24	1346.89	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
222857_s_at	KCNMB4: potassium large conductance calcium-activated channel, subfamily M, beta member 4	AF160967	151.32	125.97	-1.2	-0.99	-25.34		163.27	563.8	3.45	2.49	400.54	*
233181_at	Hs.118327.0	AK021584	71.24	68.55	-1.04	-0.83	-2.68		70.43	242.88	3.45	1.73	172.45	*
219087_at	ASPN: asporin	NM_017680	381.81	367.72	-1.04	-0.64	-14.09		4084.48	14068.95	3.44	3.11	9984.47	*
230312_at	Hs.88045.0	AI146812	111.15	76.5	-1.45	-1.1	-34.65		63.57	217.96	3.43	2.69	154.38	*
1569956_at	MYLK: myosin light chain kinase	BC033713	187.31	152.28	-1.23	-1.12	-35.03		72.55	248.23	3.42	3.01	175.68	*
205131_x_at	CLEC11A: C-type lectin domain family 11, member A	NM_002975	1101.51	1744.64	1.58	1.4	643.12		1833.33	6253.59	3.41	3.22	4420.26	*
212980_at	USP34: ubiquitin specific peptidase 34	AL050376	507.44	631.5	1.24	1.17	124.06		96.02	327.07	3.41	2.9	231.06	*
220174_at	LRRC8E: leucine rich repeat containing 8 family, member E	NM_025061	162.69	144.94	-1.12	-0.87	-17.75		159.17	543.3	3.41	2.88	384.13	*
202341_s_at	TRIM2: tripartite motif-containing 2	AA149745	727.33	814.16	1.12	1.02	86.84		569.04	1935.74	3.4	3.2	1366.69	*
209841_s_at	LRRN3: leucine rich repeat neuronal 3	AL442092	115	162.36	1.41	0.85	47.36		253.59	857.67	3.38	2.85	604.08	*
224219_s_at	TRPC4: transient receptor potential cation channel, subfamily C, member 4	AF063825	194.14	220.37	1.14	1.04	26.23		166.42	562.39	3.38	3.01	395.96	*
213435_at	SATB2: SATB homeobox 2	AB028957	1098.92	1506.64	1.37	1.29	407.72		1052.07	3541.64	3.37	3.19	2489.58	*
224220_x_at	TRPC4: transient receptor potential cation channel, subfamily C, member 4	AF063824	151.42	201.83	1.33	1.1	50.41		157.17	529.15	3.37	3.06	371.98	*
232458_at	COL3A1: Collagen, type III, alpha 1	AU146808	1543.12	1321.74	-1.17	-1.11	-221.38		889.66	2967.98	3.34	3.13	2078.32	*
239265_at	TMEM20: transmembrane protein 20	R56424	111.17	158.12	1.42	1.06	46.95		146.16	488.79	3.34	2.83	342.63	*
235408_x_at	ZNF117: zinc finger protein 117	AW058673	254.05	328.2	1.29	1.14	74.15		84.57	280.51	3.32	2.89	195.94	*
242447_at	C3orf70: chromosome 3 open reading frame 70	AI656180	60.82	86.86	1.43	1	26.04		79.53	263.61	3.31	2.89	184.08	*
243140_at	ACTA2: Actin, alpha 2, smooth muscle, aorta	AI917901	519.9	551.35	1.06	1	31.44		78.29	258.97	3.31	2.67	180.69	*
213845_at	GRIK2: glutamate receptor, ionotropic, kainate 2	AL355532	75.83	107.34	1.42	1.11	31.51		73.98	244.15	3.3	2.81	170.17	*
202743_at	PIK3R3: phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	BE622627	199.76	206.99	1.04	0.9	7.23		592.58	1950.43	3.29	3.11	1357.85	*
226877_at	RPL32P3: ribosomal protein L32 pseudogene 3	AL117606	266.36	255.22	-1.04	-0.94	-11.13		59.16	193.92	3.28	2.68	134.76	*
229574_at	TRA2A: transformer 2 alpha homolog (Drosophila)	AI268231	941.14	798.04	-1.18	-1.11	-143.1		109.15	358.02	3.28	2.66	248.87	*
205798_at	IL7R: interleukin 7 receptor	NM_002185	142.66	208.15	1.46	1.3	65.48		102.55	334.85	3.27	2.7	232.3	*
220283_at	HHIPL2: HHIP-like 2	NM_024746	64.46	93.42	1.45	0.99	28.97		51.89	169.16	3.26	2.35	117.27	*
229848_at	ZNF10: zinc finger protein 10	W72653	162.84	213.62	1.31	1.13	50.78		61.15	199.59	3.26	2.44	138.44	*
238933_at	IRS1: Insulin receptor substrate 1	AA644178	126.11	134.94	1.07	0.85	8.83		69.82	227.71	3.26	2.58	157.89	*
230292_at	LOC100131993: similar to hCG2020760	AA868809	150.42	142.13	-1.06	-0.92	-8.29		46.14	150.17	3.25	1.93	104.03	*
239942_at	Hs.118502.0	AW052186	52.11	61.24	1.18	0.81	9.13		45.31	147.09	3.25	2.57	101.79	*
225288_at	COL27A1: collagen, type XXVII, alpha 1	AI949136	249.03	224.54	-1.11	-0.97	-24.49		200.67	649.99	3.24	2.82	449.32	*
225316_at	MFSD2: major facilitator superfamily domain containing 2	AL572488	91.2	109.95	1.21	0.87	18.74		100.82	326.5	3.24	2.48	225.68	*
232797_at	Hs.169068.0	AU144005	776.37	779.87	1	0.94	3.5		110.15	357.04	3.24	2.95	246.89	*
236859_at	RUNX2: runt-related transcription factor 2	AW469546	175.6	311.61	1.77	1.44	136		239.13	774.17	3.24	2.82	535.04	*
1559965_at	LOC100192378: hypothetical LOC100192378	BC037827	589.42	513.54	-1.15	-1.07	-75.88		439.42	1425.42	3.24	3.07	986	*
223679_at	CTNNB1: catenin (cadherin-associated protein), beta 1, 88kDa	AF130085	520.34	640.33	1.23	1.15	119.99		206.89	666.27	3.22	2.73	459.38	*
239260_at	CORIN: corin, serine peptidase	AI338960	32.52	74.36	2.29	1.71	41.84		85.8	274.14	3.2	2.81	188.35	*
242414_at	QPRT: quinolinate phosphoribosyltransferase	AW960707	68.81	111.51	1.62	1.02	42.7		265.55	850.11	3.2	2.95	584.56	*
230142_s_at	CIRBP: cold inducible RNA binding protein	AW088030	987.07	1048.76	1.06	0.99	61.69		251.12	800.66	3.19	2.77	549.54	*
1557176_a_at	C14orf37: chromosome 14 open reading frame 37	BU074567	57.87	86.48	1.49	1.1	28.61		160.95	512.8	3.19	2.83	351.84	*
220818_s_at	TRPC4: transient receptor potential cation channel, subfamily C, member 4	NM_016179	164.61	209.79	1.27	1.08	45.18		171.04	543.05	3.18	2.8	372.01	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
226663_at	ANKRD10: ankyrin repeat domain 10	BE670056	1092.59	1106.13	1.01	0.97	13.54		172.73	549.36	3.18	2.78	376.63	*
239290_at	FRMPD4: FERM and PDZ domain containing 4	AA984414	72.71	64.68	-1.12	-0.82	-8.03		80.49	255.6	3.18	2.49	175.11	*
205304_s_at	KCNJ8: potassium inwardly-rectifying channel, subfamily J, member 8	NM_004982	94.56	122.22	1.29	1.05	27.66		85.65	271.94	3.17	2.59	186.29	*
211580_s_at	PIK3R3: phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	AF028785	25.53	44.54	1.74	0.97	19.01		55.93	177.02	3.17	2.35	121.09	*
47550_at	LZTS1: leucine zipper, putative tumor suppressor 1	N21184	130.48	198.23	1.52	1.38	67.75		105.3	333.39	3.17	2.88	228.09	*
230387_at	Hs.48948.0	AL038450	436.46	437.51	1	0.92	1.05		80.75	255.32	3.16	2.62	174.57	*
229983_at	TIGD2: tigger transposable element derived 2	AI610112	452.99	621.46	1.37	1.28	168.48		206.66	651.29	3.15	2.92	444.63	*
201496_x_at	MYH11: myosin, heavy chain 11, smooth muscle	S67238	44.4	32.73	-1.36	-0.75	-11.67		99.9	313.95	3.14	2.68	214.05	*
209082_s_at	COL18A1: collagen, type XVIII, alpha 1	AF018081	419.01	499.16	1.19	1.04	80.15		367.12	1152.54	3.14	2.81	785.42	*
209766_at	PRDX3: peroxiredoxin 3	AF118073	195.55	138.49	-1.41	-1.22	-57.06		76.16	239.3	3.14	2.11	163.14	*
235898_at	Hs.192116.0	AW105010	41.02	40.31	-1.02	-0.63	-0.71		50.72	159.42	3.14	2.35	108.7	*
236234_at	PDE1A: phosphodiesterase 1A, calmodulin-dependent	AW614381	12.25	27.65	2.26	0.6	15.4		75.95	238.76	3.14	2.45	162.81	*
226318_at	TBRG1: transforming growth factor beta regulator 1	AI701055	954.76	914.72	-1.04	-0.99	-40.04		217.22	680.64	3.13	2.74	463.42	*
239487_at	FAM98A: Family with sequence similarity 98, member A	AI743261	223.17	262.8	1.18	1.1	39.63		56.24	176.05	3.13	2.54	119.81	*
219416_at	SCARA3: scavenger receptor class A, member 3	NM_016240	369.74	490.81	1.33	1.14	121.07		617.06	1928.13	3.12	2.93	1311.07	*
222803_at	PRTFDC1: phosphoribosyl transferase domain containing 1	AI871620	737.77	1139.61	1.54	1.43	401.84		770.5	2407.47	3.12	2.94	1636.97	*
207968_s_at	MEF2C: myocyte enhancer factor 2C	NM_002397	123.82	170.04	1.37	1.14	46.21		115.66	359.16	3.11	2.55	243.5	*
204537_s_at	GABRE: gamma-aminobutyric acid (GABA) A receptor, epsilon	NM_004961	592.67	871.42	1.47	1.42	278.75		184.98	572.54	3.1	2.88	387.56	*
244033_at	C14orf145: chromosome 14 open reading frame 145	AI937080	59.85	106.52	1.78	1.34	46.67		78.29	242.39	3.1	2.7	164.1	*
225207_at	PDK4: pyruvate dehydrogenase kinase, isozyme 4	AV707102	130.98	188.08	1.44	1.16	57.1		99.51	307.04	3.09	2.84	207.53	*
226857_at	ARHGEF19: Rho guanine nucleotide exchange factor (GEF) 19	AW170520	354.65	546.61	1.54	1.42	191.96		434.68	1343.46	3.09	2.88	908.77	*
211555_s_at	GUCY1B3: guanylate cyclase 1, soluble, beta 3	AF020340	28.53	58.44	2.05	1.28	29.91		115.55	354.18	3.07	2.73	238.63	*
222217_s_at	SLC27A3: solute carrier family 27 (fatty acid transporter), member 3	BC003654	405.02	487.6	1.2	1.03	82.59		468.47	1436.95	3.07	2.75	968.48	*
236219_at	Hs.134069.0	AI452512	44.4	94.58	2.13	1.4	50.18		62.99	193.51	3.07	2.52	130.52	*
236862_at	GOPC: Golgi associated PDZ and coiled-coil motif containing	AA279958	1015.55	1201.45	1.18	1.13	185.89		206.15	632.65	3.07	2.54	426.5	*
1555216_a_at	LOC645722: hypothetical LOC645722	BC009278	121.9	184.44	1.51	1.22	62.54		59.75	183.49	3.07	2.35	123.73	*
222860_s_at	PDGFD: platelet derived growth factor D	AB033832	73.84	57.39	-1.29	-0.86	-16.45		144.48	441.82	3.06	2.57	297.34	*
219304_s_at	PDGFD: platelet derived growth factor D	NM_025208	250.71	182.7	-1.37	-1	-68		619.08	1885.86	3.05	2.76	1266.79	*
221563_at	DUSP10: dual specificity phosphatase 10	N36770	527.54	764.97	1.45	1.31	237.43		362.03	1105.44	3.05	2.81	743.4	*
235392_at	IRS1: Insulin receptor substrate 1	BG403162	322.72	371.65	1.15	1.02	48.93		330.9	1008.93	3.05	2.86	678.03	*
1559966_a_at	LOC100192378: hypothetical LOC100192378	BC037827	272.43	262.71	-1.04	-0.94	-9.72		202.12	615.58	3.05	2.71	413.45	*
201341_at	ENC1: ectodermal-neural cortex (with BTB-like domain)	NM_003633	2217.48	2695.33	1.22	1.15	477.85		1806.86	5487.77	3.04	2.89	3680.92	*
203636_at	MID1: midline 1 (Opitz/BBB syndrome)	BE967532	581.81	730.37	1.26	1.15	148.56		480.04	1459.2	3.04	2.78	979.17	*
204136_at	COL7A1: collagen, type VII, alpha 1	NM_000094	816.81	764.49	-1.07	-1.01	-52.32		354.43	1078	3.04	2.71	723.57	*
231688_at	MMP8: matrix metallopeptidase 8 (neutrophil collagenase)	AW337833	15.23	35.19	2.31	0.97	19.96		141.71	430.71	3.04	2.55	289	*
236044_at	PPAPDC1A: phosphatidic acid phosphatase type 2 domain containing 1A	BF130943	887.36	913.1	1.03	0.96	25.74		419.86	1276.96	3.04	2.85	857.09	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
206114_at	EPHA4: EPH receptor A4	NM_004438	176.31	194.27	1.1	0.96	17.96		128.11	387.22	3.02	2.54	259.1	*
219685_at	TMEM35: transmembrane protein 35	NM_021637	96.02	119.58	1.25	0.93	23.55		179.16	540.39	3.02	2.76	361.23	*
242482_at	PRKAR1A: protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	AI682905	412.36	392.97	-1.05	-0.97	-19.39		141.07	426.14	3.02	2.73	285.07	*
213830_at	TRD@: T cell receptor delta locus	AW007751	78.79	89.9	1.14	0.83	11.11		98.54	296.96	3.01	2.2	198.41	*
215945_s_at	TRIM2: tripartite motif-containing 2	BC005016	1003.97	1072.66	1.07	1	68.69		847.64	2549.2	3.01	2.93	1701.56	*
227557_at	SCARF2: scavenger receptor class F, member 2	AI127800	622.47	928.5	1.49	1.39	306.02		371.06	1117.08	3.01	2.73	746.02	*
204140_at	TPST1: tyrosylprotein sulfotransferase 1	NM_003596	1741.58	2558.6	1.47	1.31	817.02		1796.66	5390.35	3	2.79	3593.69	*
228030_at	Hs.173993.1	AI041522	466.84	604.91	1.3	1.18	138.07		254.22	758.48	2.98	2.69	504.26	*
1552665_at	LOC84989: hypothetical LOC84989	NM_032903	104.92	157.37	1.5	1.15	52.46		115.18	340.45	2.96	2.28	225.26	*
223821_s_at	SUSD4: sushi domain containing 4	BC004888	17.11	23.74	1.39	0.78	6.62		64.6	190.34	2.95	1.76	125.74	*
229073_at	PRTG: protogenin homolog (Gallus gallus)	AA912476	86.59	73.67	-1.18	-0.93	-12.92		65.38	192.84	2.95	2.52	127.46	*
213691_at	Hs.227429.0	AL050131	170.53	229.67	1.35	1.21	59.14		62.01	182.51	2.94	2.46	120.49	*
223629_at	PCDHB5: protocadherin beta 5	BC001186	84.71	149.19	1.76	1.39	64.48		182.29	535.59	2.94	2.68	353.3	*
228214_at	SOX6: SRY (sex determining region Y)-box 6	AW242286	453.38	382.59	-1.19	-1.08	-70.79		170.46	499.57	2.93	2.56	329.11	*
228570_at	BTBD11: BTB (POZ) domain containing 11	BF510581	37.17	65.87	1.77	1.2	28.7		59.83	175.56	2.93	2.48	115.72	*
225107_at	HNRNPA2B1: heterogeneous nuclear ribonucleoprotein A2/B1	AI963008	1299.42	1612.27	1.24	1.2	312.85		337.59	987.08	2.92	2.61	649.49	*
201286_at	SDC1: syndecan 1	Z48199	546.85	601.11	1.1	0.99	54.26		583.62	1698.37	2.91	2.77	1114.75	*
233547_x_at	PDE1A: phosphodiesterase 1A, calmodulin-dependent	N53248	39.21	46.95	1.2	0.55	7.74		171.68	499.59	2.91	2.64	327.91	*
233599_at	hCG_2003663: hCG2003663	AK025151	1103.78	793.74	-1.39	-1.31	-310.04		99.43	289.02	2.91	2.24	189.59	*
202935_s_at	SOX9: SRY (sex determining region Y)-box 9	AI382146	1713.39	1445.57	-1.19	-1.11	-267.82		915.73	2659.18	2.9	2.77	1743.45	*
229899_s_at	C20orf199: chromosome 20 open reading frame 199	AI625235	239.73	236.94	-1.01	-0.89	-2.79		61.77	179.21	2.9	2.24	117.44	*
1562367_at	C15orf54: chromosome 15 open reading frame 54	AK096850	53.98	47.54	-1.14	-0.74	-6.43		58.58	169.03	2.89	2.04	110.45	*
202036_s_at	SFRP1: secreted frizzled-related protein 1	AF017987	67.06	59.49	-1.13	-0.75	-7.57		88.43	254.37	2.88	2.44	165.94	*
227004_at	Hs.158196.2	AI611074	745.74	860.41	1.15	1.07	114.68		467.21	1339.51	2.87	2.71	872.3	*
228098_s_at	MYLIP: myosin regulatory light chain interacting protein	AW292746	148.05	123.5	-1.2	-1.06	-24.55		133.79	383.4	2.87	2.67	249.61	*
1557828_a_at	C5orf28: Chromosome 5 open reading frame 28	BE675061	1436.5	1176.15	-1.22	-1.16	-260.35		190.65	547.16	2.87	2.57	356.51	*
203426_s_at	IGFBP5: insulin-like growth factor binding protein 5	M65062	98.26	89.8	-1.09	-0.89	-8.46		355.83	1019.13	2.86	2.65	663.31	*
204491_at	PDE4D: phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	R40917	340.33	392.55	1.15	1.04	52.22		194.6	556.56	2.86	2.57	361.96	*
223475_at	CRISPLD1: cysteine-rich secretory protein LCCL domain containing 1	AF142573	210	337.03	1.6	1.44	127.03		664.98	1901.01	2.86	2.66	1236.03	*
227909_at	NCRNA00086 /// NCRNA00087: non-protein coding RNA 86 /// non-protein coding RNA 87	AI742434	153.39	214.1	1.4	1.25	60.71		130.17	371.67	2.86	2.58	241.49	*
244511_at	Hs.187369.0	AV700591	1038.59	774.81	-1.34	-1.28	-263.77		76.87	219.9	2.86	2.23	143.03	*
1556190_s_at	PRNP: prion protein	AK056897	146.16	203.29	1.39	1.21	57.13		189.47	541.24	2.86	2.62	351.77	*
206748_s_at	SPAG9: sperm associated antigen 9	NM_003971	583.36	785.85	1.35	1.24	202.49		541.59	1545.07	2.85	2.69	1003.48	*
1557360_at	LRPPRC: leucine-rich PPR-motif containing	CA430402	295.38	256.87	-1.15	-1.06	-38.51		62.65	178.56	2.85	2.19	115.91	*
206795_at	F2RL2: coagulation factor II (thrombin) receptor-like 2	NM_004101	40.07	104.61	2.61	2.07	64.54		62.28	176.78	2.84	2.32	114.5	*
209692_at	EYA2: eyes absent homolog 2 (Drosophila)	U71207	756.51	1172.27	1.55	1.41	415.76		453.91	1290.05	2.84	2.59	836.14	*
230243_at	RG9MTD2: RNA (guanine-9-) methyltransferase domain containing 2	BE671949	294.62	263.25	-1.12	-0.97	-31.37		121.38	344.78	2.84	2.11	223.39	*
230624_at	SLC25A27: solute carrier family 25, member 27	AW779950	220.12	235.9	1.07	0.96	15.79		60.3	171.06	2.84	2.31	110.75	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
242918_at	NASP: Nuclear autoantigenic sperm protein (histone-binding)	AU144734	301.86	354.51	1.17	1.07	52.65		62.34	176.93	2.84	2.27	114.59	*
1555997_s_at	IGFBP5: insulin-like growth factor binding protein 5	BM128432	312.57	342.63	1.1	0.93	30.07		1663.65	4732.55	2.84	2.7	3068.9	*
207995_s_at	CLEC4M: C-type lectin domain family 4, member M	NM_014257	162.42	134.27	-1.21	-1.09	-28.15		95.46	270.35	2.83	1.74	174.89	*
235803_at	Hs.34574.0	AA843122	409.16	313.57	-1.3	-1.21	-95.59		61.76	174.91	2.83	2.36	113.15	*
236832_at	LOC221442: adenylate cyclase 10 pseudogene	AI674126	126.06	180.76	1.43	1.21	54.71		71.39	202.31	2.83	2.34	130.92	*
1560271_at	Hs2.375064.1	BC030757	458.88	308.53	-1.49	-1.36	-150.36		61.33	173.66	2.83	2.28	112.34	*
226808_at	ZNF862: zinc finger protein 862	AW771007	711.85	783.5	1.1	1.06	71.65		162.86	459.5	2.82	2.43	296.64	*
235891_at	Hs.131973.0	AI961147	1209.77	1768.69	1.46	1.4	558.93		770.1	2170.77	2.82	2.62	1400.67	*
207819_s_at	ABCB4: ATP-binding cassette, sub-family B (MDR/TAP), member 4	NM_000443	110.13	139.6	1.27	1.08	29.47		64.57	181.56	2.81	2.09	116.99	*
217757_at	A2M: alpha-2-macroglobulin	NM_000014	214.83	211.29	-1.02	-0.69	-3.54		177.83	499.13	2.81	1.9	321.3	*
227498_at	SOX6: SRY (sex determining region Y)-box 6	AI480314	359.21	388.41	1.08	0.96	29.19		147.1	411.51	2.8	2.28	264.41	*
228173_at	GNAS: GNAS complex locus	AA810695	400.2	409.18	1.02	0.93	8.99		85.23	238.45	2.8	2.35	153.22	*
231213_at	PDE1A: phosphodiesterase 1A, calmodulin-dependent	AU146305	23.48	48.92	2.08	1.5	25.44		111.21	310.98	2.8	2.58	199.77	*
1555860_x_at	LOC440944: hypothetical LOC440944	CA430188	496.54	579.85	1.17	1.1	83.31		165.36	463.21	2.8	2.51	297.85	*
207112_s_at	GAB1: GRB2-associated binding protein 1	NM_002039	160.05	148.75	-1.08	-0.92	-11.31		153.34	428.01	2.79	2.53	274.67	*
216994_s_at	RUNX2: runt-related transcription factor 2	L40992	95.95	117.68	1.23	1	21.73		65.65	182.56	2.78	2.26	116.91	*
227091_at	CCDC146: coiled-coil domain containing 146	AB040938	172.42	155.99	-1.11	-0.97	-16.43		112.92	313.45	2.78	2.19	200.52	*
230311_s_at	PRDM6: PR domain containing 6	AF272898	109.36	167.36	1.53	1.23	58		104.43	289.88	2.78	2.16	185.45	*
235716_at	Hs.194258.0	AW157450	1180.34	1097.08	-1.08	-1.02	-83.26		191.37	531.86	2.78	2.56	340.49	*
206302_s_at	NUDT4 /// NUDT4P1: nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	NM_019094	1788.42	1988.71	1.11	1.04	200.29		1599.37	4425.71	2.77	2.61	2826.34	*
232979_at	Hs.306410.0	AK000839	547.25	548.3	1	0.94	1.06		57.61	159.66	2.77	2.29	102.06	*
229694_at	BRWD2: bromodomain and WD repeat domain containing 2	BF062828	912.66	663.26	-1.38	-1.29	-249.4		107.63	296.27	2.75	2.2	188.65	*
238156_at	Hs.211198.0	AW205632	308.54	355.86	1.15	1.09	47.32		85.47	235.24	2.75	2.31	149.77	*
1556035_s_at	ZNF207: zinc finger protein 207	AI201248	1251.44	1006.14	-1.24	-1.17	-245.3		265.06	727.72	2.75	2.51	462.66	*
1556097_at	Hs2.68505.1	CA442342	467.25	498.58	1.07	0.99	31.33		313.96	863.38	2.75	2.57	549.42	*
1552670_a_at	PPP1R3B: protein phosphatase 1, regulatory (inhibitor) subunit 3B	NM_024607	218.59	217.24	-1.01	-0.85	-1.36		280.86	768.9	2.74	2.51	488.05	*
221919_at	HNRNPA1: heterogeneous nuclear ribonucleoprotein A1	AW450929	415.92	470.09	1.13	1.04	54.17		172.49	470.17	2.73	2.34	297.68	*
224965_at	GNG2: guanine nucleotide binding protein (G protein), gamma 2	AU118419	310.57	361.45	1.16	0.92	50.88		348.39	950.65	2.73	2.21	602.25	*
226366_at	SHPRH: SNF2 histone linker PHD RING helicase	AI828221	465.3	621.74	1.34	1.25	156.44		318	867.36	2.73	2.52	549.36	*
227946_at	OSBPL7: oxysterol binding protein-like 7	AI955239	301.1	462.83	1.54	1.43	161.73		200.24	547.03	2.73	2.36	346.79	*
233047_at	FRMD7: FERM domain containing 7	AL161984	55.54	59.83	1.08	0.61	4.28		177.04	483.13	2.73	2.45	306.1	*
218980_at	FHOD3: formin homology 2 domain containing 3	NM_025135	623.63	790.1	1.27	1.19	166.47		376.46	1024.86	2.72	2.53	648.4	*
213359_at	HNRNPD: Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	W74620	883.65	818.38	-1.08	-1.03	-65.28		256.16	695.18	2.71	2.4	439.02	*
223648_s_at	FGFRL1: fibroblast growth factor receptor-like 1	AF279689	70.46	164.1	2.33	1.97	93.64		70.1	189.66	2.71	2.3	119.56	*
227568_at	HECTD2: HECT domain containing 2	AF131793	864.09	1203.74	1.39	1.28	339.65		578.79	1568.26	2.71	2.5	989.46	*
219889_at	FRAT1: frequently rearranged in advanced T-cell lymphomas	NM_005479	137.89	161.19	1.17	0.98	23.3		61.28	165.39	2.7	2.18	104.11	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
230640_at	Hs.179838.0	AW027431	187.34	188.38	1.01	0.9	1.03		154.78	417.07	2.69	2.47	262.3	*
238750_at	Hs.218707.0	AW083576	65.41	130.2	1.99	1.64	64.79		130.28	349.9	2.69	2.36	219.63	*
240460_at	Hs.134215.0	AI190616	355.23	219.19	-1.62	-1.38	-136.04		490.48	1321.67	2.69	2.56	831.2	*
1557066_at	LUC7L: LUC7-like (S. cerevisiae)	AI744735	176.24	230.03	1.31	1.16	53.79		60.67	162.97	2.69	2.26	102.3	*
203817_at	GUCY1B3: guanylate cyclase 1, soluble, beta 3	W93728	103.63	171.86	1.66	1.2	68.23		330.33	883.88	2.68	2.5	553.55	*
211709_s_at	CLEC11A: C-type lectin domain family 11, member A	BC005810	2264.31	3228.51	1.43	1.24	964.21		3151.75	8439.5	2.68	2.45	5287.74	*
225191_at	CIRBP: cold inducible RNA binding protein	AL565767	1356.62	1383.87	1.02	0.94	27.25		467.09	1248.48	2.67	2.22	781.38	*
230180_at	Hs.6179.3	AA521056	3535.1	4504.89	1.27	1.23	969.8		461.57	1231.98	2.67	2.36	770.41	*
202342_s_at	TRIM2: tripartite motif-containing 2	NM_015271	969.44	1135.03	1.17	1.09	165.59		892.11	2371.13	2.66	2.54	1479.02	*
205348_s_at	DYNC1I1: dynein, cytoplasmic 1, intermediate chain 1	NM_004411	853.93	743.53	-1.15	-1.05	-110.4		1133.86	3003.76	2.65	2.49	1869.9	*
201418_s_at	SOX4: SRY (sex determining region Y)-box 4	NM_003107	1587.02	2181.18	1.37	1.29	594.16		992.52	2620.87	2.64	2.32	1628.35	*
204793_at	GPRASP1: G protein-coupled receptor associated sorting protein 1	NM_014710	299.84	361.54	1.21	1.11	61.7		141.58	373.49	2.64	2.3	231.91	*
225720_at	SYNPO2: synaptopodin 2	AW009747	1651.35	2118.36	1.28	1.16	467.01		1276.14	3372.68	2.64	2.37	2096.54	*
229479_at	Hs.152812.0	AI739132	1447.32	2025.16	1.4	1.32	577.84		1203	3158.94	2.63	2.44	1955.95	*
242767_at	LMCD1: LIM and cysteine-rich domains 1	N95437	443.14	676.49	1.53	1.38	233.35		530.44	1397.67	2.63	2.46	867.23	*
201287_s_at	SDC1: syndecan 1	NM_002997	716.57	792.11	1.11	0.99	75.54		820.29	2150.54	2.62	2.47	1330.25	*
206392_s_at	RARRES1: retinoic acid receptor responder (tazarotene induced) 1	NM_002888	210.52	267.21	1.27	1.13	56.69		127	332.36	2.62	2.27	205.36	*
206766_at	ITGA10: integrin, alpha 10	AF112345	233.42	340.7	1.46	1.23	107.28		350.29	919.16	2.62	2.37	568.87	*
219516_at	TRPV4: transient receptor potential cation channel, subfamily V, member 4	NM_021625	70.4	141.73	2.01	1.67	71.34		70.14	183.77	2.62	2.18	113.63	*
220462_at	CSRNP3: cysteine-serine-rich nuclear protein 3	NM_024969	81.74	37.52	-2.18	-1.77	-44.22		71.68	188.06	2.62	1.87	116.38	*
227452_at	Hs.236894.0	AI832118	326.62	332.02	1.02	0.93	5.4		192.28	504.67	2.62	2.38	312.38	*
232090_at	Hs.135159.0	AI761578	2421.51	3368.11	1.39	1.32	946.6		1562.43	4095.95	2.62	2.49	2533.52	*
206480_at	LTC4S: leukotriene C4 synthase	NM_000897	132.78	159.62	1.2	1.01	26.84		165.13	431.72	2.61	2.38	266.59	*
229371_at	Hs.119338.0	BF940010	283.97	363.44	1.28	1.15	79.46		223.93	582.16	2.6	2.37	358.23	*
230148_at	AHSA2: AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	AI831431	154.51	201.69	1.31	1.17	47.18		62.58	163	2.6	2.22	100.42	*
235064_s_at	C20orf196: chromosome 20 open reading frame 196	AA856721	48.25	105.55	2.19	1.3	57.3		78.91	204.92	2.6	1.82	126.01	*
224919_at	MRPS6: mitochondrial ribosomal protein S6	AL555227	1918.34	2072.74	1.08	0.98	154.4		2150.96	5561.42	2.59	2.4	3410.46	*
227368_at	Hs.182937.1	AW009630	174.02	239.24	1.37	1.23	65.22		114.51	296.88	2.59	2.28	182.38	*
242665_at	FMNL2: formin-like 2	AL042120	233.48	280.36	1.2	1.1	46.87		140.88	364.2	2.59	2.22	223.32	*
212468_at	SPAG9: sperm associated antigen 9	AK023512	1548.28	2363.5	1.53	1.44	815.23		983.7	2535.91	2.58	2.41	1552.22	*
227844_at	FMNL3: formin-like 3	AI089932	115.55	135.06	1.17	0.95	19.51		84.67	218.74	2.58	2.29	134.08	*
214753_at	N4BP2L2: NEDD4 binding protein 2-like 2	AW084068	1262.6	930.36	-1.36	-1.23	-332.24		93.56	240.07	2.57	1.95	146.51	*
215177_s_at	ITGA6: integrin, alpha 6	AV733308	97.32	85.72	-1.14	-0.75	-11.6		203.06	522.66	2.57	2.22	319.6	*
230233_at	Hs.170278.0	BF110534	138.41	237.49	1.72	1.51	99.08		173.69	447.15	2.57	2.38	273.45	*
231108_at	FUS: fusion (involved in t(12;16) in malignant liposarcoma)	H43040	445.92	421.1	-1.06	-0.98	-24.82		124.81	320.56	2.57	2.08	195.75	*
233986_s_at	PLEKHG2: pleckstrin homology domain containing, family G (with RhoGef domain) member 2	AK026111	407.22	536.98	1.32	1.22	129.76		313.77	807.56	2.57	2.3	493.79	*
206788_s_at	CBFB: core-binding factor, beta subunit	AF294326	763.97	1109.42	1.45	1.35	345.45		736.36	1888.72	2.56	2.41	1152.36	*
217478_s_at	HLA-DMA /// HLA-DMB: major histocompatibility complex, class II, DM alpha /// major histocompatibility complex, class II, DM beta	X76775	268.74	432.91	1.61	1.4	164.17		456.71	1167.71	2.56	2.3	711	*
221289_at	DLX6: distal-less homeobox 6	NM_005222	71.42	143.28	2.01	1.61	71.86		70.23	179.56	2.56	2.1	109.34	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
222662_at	PPP1R3B: protein phosphatase 1, regulatory (inhibitor) subunit 3B	W60806	589.82	714.42	1.21	1.1	124.6		723.13	1849.7	2.56	2.34	1126.57	*
230270_at	PRPF38B: PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	N32872	1276.6	1221.01	-1.05	-1.01	-55.6		260.5	666.84	2.56	2.35	406.34	*
232099_at	PCDHB16: protocadherin beta 16	AB046841	68.81	108.26	1.57	1.19	39.44		130.2	333.07	2.56	2.23	202.86	*
239432_at	FLJ31306: hypothetical LOC379025	AV729086	573.76	447.54	-1.28	-1.23	-126.23		108.69	278.63	2.56	2.13	169.94	*
209558_s_at	HIP1R /// LOC100294412: huntingtin interacting protein 1 related /// similar to KIAA0655 protein	AB013384	190.28	161.94	-1.17	-1.04	-28.34		126.03	321.05	2.55	2.02	195.02	*
205522_at	HOXD4: homeobox D4	NM_014621	208.6	238.12	1.14	1	29.52		73.99	188.2	2.54	2.18	114.21	*
215114_at	SENP3: SUMO1/sentrin/SMT3 specific peptidase 3	AK000923	229.41	251.16	1.09	1	21.75		70.63	179.58	2.54	2.18	108.94	*
228393_s_at	ZNF302: zinc finger protein 302	BF508739	357.96	407.63	1.14	1.04	49.67		138.48	351.3	2.54	2.19	212.82	*
238902_at	PCMTD1: Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	T85248	590.42	605.21	1.03	0.98	14.78		99	251.62	2.54	2.23	152.61	*
1558828_s_at	LOC728264: Hypothetical LOC728264	AL703532	750.86	627.22	-1.2	-1.07	-123.63		122.95	311.85	2.54	1.94	188.9	*
227510_x_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AL037917	1512.67	1878.17	1.24	1.19	365.5		341.44	863.75	2.53	2.13	522.31	*
228157_at	ZNF207: zinc finger protein 207	AI125646	665.23	776.28	1.17	1.1	111.06		200.19	507.18	2.53	2.34	306.99	*
203637_s_at	MID1: midline 1 (Opitz/BBB syndrome)	NM_000381	1041.39	1154.53	1.11	1.04	113.14		865.67	2184.58	2.52	2.36	1318.91	*
227838_at	UNC5C: unc-5 homolog C (C. elegans)	AW070250	553.64	635.18	1.15	1.04	81.55		525.8	1324.75	2.52	2.34	798.95	*
1570039_at	TMSB15B: thymosin beta 15B	BC029803	81.93	143.3	1.75	1.45	61.37		75.87	190.97	2.52	2.12	115.09	*
205911_at	PTH1R: parathyroid hormone 1 receptor	NM_000316	246.37	242.05	-1.02	-0.76	-4.31		235.81	592.84	2.51	1.89	357.03	*
226636_at	PLD1: phospholipase D1, phosphatidylcholine-specific	AI378587	153.8	142.05	-1.08	-0.88	-11.75		214.58	537.8	2.51	2.28	323.21	*
227155_at	LMO4: LIM domain only 4	R10289	144.82	225.78	1.56	1.41	80.97		84.18	211.3	2.51	2.12	127.11	*
1562415_a_at	SPOCD1: SPOC domain containing 1	AK096192	733.29	1139.1	1.55	1.44	405.81		314.9	791.14	2.51	2.28	476.24	*
209535_s_at	g5199315	AF127481	76.41	84.63	1.11	0.92	8.22		87.87	219.84	2.5	2.1	131.97	*
226218_at	IL7R: interleukin 7 receptor	BE217880	335.48	517.82	1.54	1.45	182.34		313.82	785.45	2.5	2.37	471.63	*
229795_at	Hs.48945.0	AI701591	628.21	859.04	1.37	1.21	230.83		559.2	1398.26	2.5	2.27	839.05	*
232463_at	NCRNA00107: non-protein coding RNA 107	T77995	331.85	329.93	-1.01	-0.9	-1.92		92.73	231.84	2.5	2.03	139.11	*
243629_x_at	Hs.128852.2	AI140985	589.68	891.23	1.51	1.43	301.55		355.4	889.97	2.5	2.27	534.57	*
210198_s_at	PLP1: proteolipid protein 1	BC002665	163.44	157.47	-1.04	-0.72	-5.97		134.03	333.25	2.49	1.74	199.22	*
223499_at	C1QTNF5 /// MFRP: C1q and tumor necrosis factor related protein 5 /// membrane frizzled-related protein	AF329841	1037.49	1402.45	1.35	1.22	364.97		1798.8	4474.04	2.49	2.34	2675.23	*
226192_at	Hs.76704.0	T68445	250.7	348.3	1.39	1.2	97.6		193.93	483.04	2.49	2.23	289.11	*
235377_at	C6orf142: chromosome 6 open reading frame 142	AI242549	54.88	37.13	-1.48	-1	-17.75		80.32	199.84	2.49	2.12	119.52	*
220650_s_at	SLC9A5: solute carrier family 9 (sodium/hydrogen exchanger), member 5	NM_004594	275.15	289.08	1.05	0.94	13.93		215.91	534.54	2.48	2.25	318.64	*
221768_at	SFPQ: Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	AV705803	1397.7	1448.99	1.04	0.99	51.3		329.23	816.13	2.48	2.29	486.9	*
225346_at	MTERFD3: MTERF domain containing 3	NM_025198	246.11	297.78	1.21	1.09	51.68		210.34	522.24	2.48	2.2	311.9	*
227283_at	EFR3B: EFR3 homolog B (S. cerevisiae)	AW138794	54.42	89.18	1.64	1.09	34.76		78.61	194.95	2.48	2.03	116.34	*
228582_x_at	Hs.6975.3	AI475544	1944.41	1647.99	-1.18	-1.07	-296.42		522.19	1294.22	2.48	2.22	772.03	*
1569312_at	Hs2.270347.1	BE383308	460.99	401.14	-1.15	-1.05	-59.86		104.14	258.31	2.48	2.16	154.18	*
205752_s_at	GSTM5: glutathione S-transferase mu 5	NM_000851	238.87	271.34	1.14	0.96	32.46		282.82	699.2	2.47	2.24	416.38	*
235926_at	Hs.155766.0	AI312527	526.64	583.44	1.11	1.04	56.8		114.76	283.85	2.47	2.07	169.09	*
1558486_at	ZNF493: zinc finger protein 493	BC022394	355.49	320.79	-1.11	-1.01	-34.7		70.41	174.21	2.47	1.67	103.8	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
228816_at	ATP6AP1L: ATPase, H+ transporting, lysosomal accessory protein 1-like	AK022625	265.57	399.41	1.5	1.35	133.84		338.72	834.49	2.46	2.22	495.77	*
232490_s_at	PRUNE: prune homolog (Drosophila)	U67085	124.98	127.84	1.02	0.89	2.86		119.49	294.34	2.46	2.02	174.85	*
204622_x_at	NR4A2: nuclear receptor subfamily 4, group A, member 2	NM_006186	122.63	139.82	1.14	0.93	17.19		96.75	237.21	2.45	2.12	140.46	*
224558_s_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AI446756	5042.96	4742.66	-1.06	-1.02	-300.3		1516.43	3716.76	2.45	2.29	2200.33	*
220952_s_at	PLEKHA5: pleckstrin homology domain containing, family A member 5	NM_019012	1939.49	2527.32	1.3	1.22	587.83		1511.89	3692.57	2.44	2.31	2180.68	*
221872_at	RARRES1: retinoic acid receptor responder (tazarotene induced) 1	AI669229	267.9	383.33	1.43	1.33	115.43		173	422.61	2.44	2.21	249.61	*
205739_x_at	ZNF107: zinc finger protein 107	NM_016220	141.65	199.08	1.41	1.25	57.44		167.72	406.74	2.43	2.18	239.02	*
225293_at	COL27A1: collagen, type XXVII, alpha 1	AK021957	314.24	263.63	-1.19	-1.02	-50.61		239.4	581.48	2.43	2.17	342.08	*
226419_s_at	FLJ44342: hypothetical LOC645460	AA046439	594.09	550.81	-1.08	-1.01	-43.28		89.77	218.5	2.43	2.01	128.73	*
231789_at	PCDHB15: protocadherin beta 15	AV722990	94.43	141.55	1.5	1.26	47.11		107.72	261.22	2.43	2.19	153.5	*
232991_at	ARL17: ADP-ribosylation factor-like 17	AK021675	289.74	226.06	-1.28	-1.1	-63.69		76.26	185.48	2.43	1.58	109.23	*
236987_at	Hs.24176.0	AI741514	225.29	136.83	-1.65	-1.16	-88.45		148.19	360.65	2.43	2.03	212.46	*
204861_s_at	NAIP: NLR family, apoptosis inhibitory protein	NM_004536	434.53	365.92	-1.19	-1.1	-68.61		152.42	368.54	2.42	2.1	216.11	*
226784_at	TWISTNB: TWIST neighbor	AA121481	534.24	627.72	1.17	1.1	93.48		493.15	1192.66	2.42	2.22	699.51	*
229004_at	Hs.64859.0	AI970797	98.58	146.43	1.49	1.19	47.85		71.16	171.98	2.42	1.93	100.82	*
238042_at	Hs.144967.0	AW134485	427.56	314.49	-1.36	-1.27	-113.07		118.82	287.18	2.42	2.07	168.36	*
242121_at	NCRNA00182: non-protein coding RNA 182	AW973232	1574.05	1047.55	-1.5	-1.43	-526.5		140.54	340.09	2.42	2.08	199.56	*
235511_at	Hs.128730.0	BE144058	201.79	263.35	1.31	1.17	61.56		102.28	246.15	2.41	2.16	143.87	*
213309_at	PLCL2: phospholipase C-like 2	AL117515	111.71	129.46	1.16	0.97	17.75		95.47	229.07	2.4	2.09	133.6	*
206303_s_at	NUDT4: nudix (nucleoside diphosphate linked moiety X)-type motif 4	AF191653	2035.44	1817.25	-1.12	-1.07	-218.19		1587.83	3788.06	2.39	2.19	2200.23	*
207329_at	MMP8: matrix metallopeptidase 8 (neutrophil collagenase)	NM_002424	22.91	31.59	1.38	0.92	8.68		120.46	287.68	2.39	2.12	167.22	*
205404_at	HSD11B1: hydroxysteroid (11-beta) dehydrogenase 1	NM_005525	103.84	137.28	1.32	1	33.44		272.79	648.27	2.38	2.11	375.48	*
212964_at	HIC2: hypermethylated in cancer 2	AI912206	141.16	201.55	1.43	1.19	60.39		112.06	266.18	2.38	1.94	154.13	*
230487_at	C6orf99 /// LOC100130967: chromosome 6 open reading frame 99 /// similar to Putative uncharacterized protein C6orf99	AA776715	42.93	31.99	-1.34	-0.84	-10.94		80.2	190.81	2.38	2.06	110.61	*
236133_x_at	ZNF254: zinc finger protein 254	AI983886	150.67	221.7	1.47	1.3	71.03		147.71	350.97	2.38	2.1	203.26	*
237640_at	C14orf138: chromosome 14 open reading frame 138	AW291389	275.36	251.77	-1.09	-1.02	-23.58		77.56	184.89	2.38	1.83	107.32	*
204440_at	CD83: CD83 molecule	NM_004233	113.18	110.1	-1.03	-0.87	-3.08		167.29	396.32	2.37	1.79	229.03	*
215017_s_at	FNBP1L: formin binding protein 1-like	AW270932	173.9	229.57	1.32	1.2	55.66		177.56	421.02	2.37	2.05	243.46	*
219287_at	KCNMB4: potassium large conductance calcium-activated channel, subfamily M, beta member 4	NM_014505	101.19	112.27	1.11	0.76	11.08		125.4	296.99	2.37	1.93	171.6	*
223458_at	SEZ6L2: seizure related 6 homolog (mouse)-like 2	BC000567	432.1	523.8	1.21	1.09	91.7		189.8	449.75	2.37	2.02	259.95	*
230424_at	C5orf13: chromosome 5 open reading frame 13	AU144860	788.6	1029.69	1.31	1.23	241.09		289.08	684.05	2.37	2.11	394.97	*
239638_at	Hs.134954.0	AI608696	187.01	121.72	-1.54	-1.18	-65.29		149.98	355.15	2.37	2.08	205.17	*
242852_at	LOC285147: hypothetical protein LOC285147	H23213	142.48	190.67	1.34	1.13	48.19		75.11	178.17	2.37	2.1	103.06	*
1555103_s_at	FGF7: fibroblast growth factor 7 (keratinocyte growth factor)	BC010956	1008.17	978.24	-1.03	-0.99	-29.94		167.25	396.84	2.37	1.96	229.59	*
221973_at	Hs.79732.5	AI983904	263.46	226.83	-1.16	-1.02	-36.63		97.14	229.04	2.36	1.85	131.9	*
229033_s_at	MUM1: melanoma associated antigen (mutated) 1	AA143060	388.94	472.95	1.22	1.1	84.01		92.25	217.32	2.36	1.7	125.07	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
235467_s_at	KCNC4: potassium voltage-gated channel, Shaw-related subfamily, member 4	BF969982	165.61	202.72	1.22	1.05	37.11		313.41	740.49	2.36	2.21	427.08	*
238751_at	Hs.156880.0	AI343000	637.12	646.05	1.01	0.96	8.92		326.97	770.29	2.36	2.19	443.31	*
238823_at	FMNL3: formin-like 3	AA481044	230.87	250.54	1.09	0.97	19.67		226.13	534.02	2.36	2.12	307.89	*
211700_s_at	TRO: trophinin	AF349719	413.78	545.68	1.32	1.22	131.9		328.85	774.06	2.35	2.14	445.21	*
222307_at	LOC282997: hypothetical protein LOC282997	AI695595	48.37	102.44	2.12	1.46	54.08		76.55	179.92	2.35	2.07	103.37	*
226651_at	HOMER1: homer homolog 1 (Drosophila)	AW052119	645.17	764.76	1.19	1.09	119.59		457.84	1076.36	2.35	2.26	618.52	*
231904_at	U2AF1: U2 small nuclear RNA auxiliary factor 1	AU122448	324.78	285.78	-1.14	-0.99	-39		76.39	179.64	2.35	1.65	103.25	*
236241_at	MED31: mediator complex subunit 31	BF593977	424.4	451.33	1.06	0.97	26.92		109.91	258.25	2.35	1.84	148.34	*
238501_at	Hs.121655.0	AA992936	86.76	121.92	1.41	1.12	35.16		83.37	196.12	2.35	1.84	112.75	*
244075_at	Hs.192152.0	BF224218	410.47	408.2	-1.01	-0.94	-2.28		132.61	311.88	2.35	1.97	179.27	*
202744_at	SLC20A2: solute carrier family 20 (phosphate transporter), member 2	NM_006749	617.74	537.06	-1.15	-1.09	-80.69		537.66	1255.64	2.34	2.19	717.98	*
203425_s_at	IGFBP5: insulin-like growth factor binding protein 5	NM_000599	269.82	234.56	-1.15	-0.72	-35.26		652.06	1522.83	2.34	2.13	870.77	*
213170_at	GPX7: glutathione peroxidase 7	AA406605	1110.83	1725.84	1.55	1.45	615		1612.59	3773.17	2.34	2.23	2160.59	*
214769_at	CLCN4: chloride channel 4	AF052117	147.15	220.86	1.5	1.22	73.71		197.09	460.74	2.34	2.12	263.65	*
219594_at	NINJ2: ninjurin 2	NM_016533	155.1	249.84	1.61	1.3	94.75		275.44	644.74	2.34	2.13	369.3	*
230712_at	NBPF1 /// NBPF3 /// NBPF8: neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8	AI634549	550.97	454.86	-1.21	-1.13	-96.12		168.84	395.1	2.34	1.86	226.26	*
206492_at	FHIT: fragile histidine triad gene	NM_002012	57.04	71.12	1.25	0.84	14.08		76.78	178.91	2.33	1.79	102.13	*
219142_at	RASL11B: RAS-like, family 11, member B	NM_023940	84.48	134.85	1.6	1.13	50.37		109.69	256.13	2.33	1.74	146.43	*
230876_at	LOC169834: hypothetical protein LOC169834	AI827906	116.28	206.41	1.78	1.43	90.13		129.05	300.32	2.33	2	171.27	*
235571_at	Hs.195641.0	AW300953	946.57	1029.57	1.09	1.06	83		300.83	700.68	2.33	2.18	399.86	*
206189_at	UNC5C: unc-5 homolog C (C. elegans)	NM_003728	114.72	151.62	1.32	1.1	36.9		141.58	327.87	2.32	2.04	186.29	*
209897_s_at	SLIT2: slit homolog 2 (Drosophila)	AF055585	2442.09	3530.27	1.45	1.39	1088.18		1967.82	4572.82	2.32	2.18	2605	*
214059_at	IFI44: Interferon-induced protein 44	BE049439	174.65	163.51	-1.07	-0.94	-11.14		99.75	231.25	2.32	2.02	131.49	*
209204_at	LMO4: LIM domain only 4	AI824831	321.5	422.96	1.32	1.15	101.46		146.23	337.57	2.31	1.76	191.34	*
225341_at	MTERFD3: MTERF domain containing 3	BF697312	349.15	378.47	1.08	0.96	29.32		302.84	700.92	2.31	2.12	398.08	*
226041_at	NAPEPLD: N-acyl phosphatidylethanolamine phospholipase D	BF382393	359.85	490.99	1.36	1.2	131.14		461.73	1068.35	2.31	2.13	606.61	*
240221_at	CSNK1A1: Casein kinase 1, alpha 1	AV704610	683.29	528.93	-1.29	-1.18	-154.36		116.96	269.61	2.31	1.95	152.65	*
213653_at	METTL3: methyltransferase like 3	AW069290	287.94	327.52	1.14	1.05	39.58		101.76	233.98	2.3	2	132.22	*
230885_at	SPG7: spastic paraplegia 7 (pure and complicated autosomal recessive)	BE670386	373.2	278.02	-1.34	-1.22	-95.18		82.79	190.61	2.3	1.93	107.82	*
238540_at	LOC401320: hypothetical LOC401320	AA933883	435.05	371.77	-1.17	-1.1	-63.28		85.19	195.78	2.3	1.85	110.59	*
201506_at	TGFBI: transforming growth factor, beta-induced, 68kDa	NM_000358	10479.33	16186.34	1.54	1.4	5707.02		5047.02	11558.69	2.29	2.03	6511.67	*
219683_at	FZD3: frizzled homolog 3 (Drosophila)	NM_017412	131.59	94.93	-1.39	-1.06	-36.67		84.9	194.02	2.29	1.87	109.12	*
226204_at	C22orf29: chromosome 22 open reading frame 29	AI832193	427.34	662.32	1.55	1.44	234.97		339.3	778.02	2.29	2.09	438.72	*
239804_at	Hs.58698.0	AI057404	335.19	239.7	-1.4	-1.23	-95.48		89.94	205.89	2.29	1.72	115.95	*
1552477_a_at	IRF6: interferon regulatory factor 6	BC014852	48.18	58.87	1.22	0.78	10.7		90.13	206.09	2.29	1.97	115.97	*
223327_x_at	LOC727751 /// LOC727849 /// LOC80154: hypothetical LOC727751 /// similar to cis-Golgi matrix protein GM130 /// hypothetical LOC80154	AF316855	705.34	795.15	1.13	1.05	89.81		232.18	529.68	2.28	1.92	297.5	*
238794_at	C10orf78: chromosome 10 open reading frame 78	N23586	317.35	442.26	1.39	1.23	124.91		370.78	846.17	2.28	2.14	475.38	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
242587_at	SLC9A9: solute carrier family 9 (sodium/hydrogen exchanger), member 9	AA029791	92.54	92	-1.01	-0.81	-0.54		100.2	228.4	2.28	1.93	128.2	*
228519_x_at	CIRBP: cold inducible RNA binding protein	AW027567	1525.15	1863.7	1.22	1.17	338.54		476.31	1080.3	2.27	2.14	603.99	*
238320_at	NEAT1: nuclear paraspeckle assembly transcript 1 (non-protein coding)	AV659198	1901.14	1506.77	-1.26	-1.19	-394.37		416.57	943.99	2.27	2.02	527.42	*
238756_at	GAS2L3: Growth arrest-specific 2 like 3	AI860012	76.05	83.52	1.1	0.84	7.47		265.84	604.56	2.27	2.1	338.71	*
1564963_x_at	ZNF92: zinc finger protein 92	M61872	45.84	98.54	2.15	1.71	52.7		83.18	188.83	2.27	1.98	105.65	*
205932_s_at	MSX1: msh homeobox 1	NM_002448	576.83	756.84	1.31	1.22	180		691.74	1566.62	2.26	2.15	874.87	*
213517_at	PCBP2: poly(rC) binding protein 2	AW103422	746.06	885.78	1.19	1.12	139.72		168.42	381.37	2.26	1.99	212.96	*
214276_at	KLF12: Kruppel-like factor 12	N49268	467.54	563.13	1.2	1.05	95.58		392.65	886.61	2.26	2.09	493.95	*
232347_x_at	Hs.200113.0	AK021441	407.19	272.84	-1.49	-1.34	-134.35		88.19	199.44	2.26	1.84	111.24	*
243514_at	Hs.143056.0	AI475902	772.36	494.44	-1.56	-1.47	-277.92		91.55	207.03	2.26	1.86	115.49	*
201137_s_at	HLA-DPB1: major histocompatibility complex, class II, DP beta 1	NM_002121	229.35	361.85	1.58	1.38	132.5		204.1	459.01	2.25	1.91	254.91	*
222924_at	SLMAP: sarcolemma associated protein	BF526855	303.81	361.76	1.19	1.09	57.94		253.28	568.71	2.25	1.98	315.42	*
230733_at	Hs.190086.0	H98113	578.5	672.54	1.16	1.06	94.04		109.67	246.9	2.25	1.72	137.23	*
238549_at	CBFA2T2: core-binding factor, runt domain, alpha subunit 2; translocated to, 2	AI420611	484.33	481.02	-1.01	-0.93	-3.31		117.93	264.86	2.25	1.64	146.93	*
205382_s_at	CFD: complement factor D (adipsin)	NM_001928	209.78	225.62	1.08	0.9	15.84		384.27	860.76	2.24	2.12	476.49	*
223645_s_at	CYorf15B: chromosome Y open reading frame 15B	BF062193	738.25	592.84	-1.25	-1.21	-145.41		259.72	581.99	2.24	2.05	322.27	*
229272_at	FNBP4: formin binding protein 4	AI083506	340.5	355.42	1.04	0.97	14.91		91.27	204.28	2.24	1.82	113.01	*
239577_at	Hs.54245.0	AV699781	578.02	407.84	-1.42	-1.34	-170.17		111.14	248.45	2.24	1.88	137.31	*
244371_at	Hs.292986.0	AW085142	34.93	15.06	-2.32	-0.77	-19.87		94.61	211.98	2.24	2.02	117.37	*
212448_at	NEDD4L: neural precursor cell expressed, developmentally down-regulated 4-like	AB007899	233.32	322.15	1.38	1.27	88.83		219.84	490.22	2.23	2.09	270.38	*
226002_at	GAB1: GRB2-associated binding protein 1	AK022142	419.37	493.48	1.18	1.09	74.1		460.77	1025.55	2.23	2.07	564.78	*
227300_at	TMEM119: transmembrane protein 119	AL521682	1722.92	1153.15	-1.49	-1.33	-569.78		2963.52	6594.59	2.23	2.09	3631.06	*
228242_at	N4BP2: NEDD4 binding protein 2	BF055201	224.62	336.35	1.5	1.33	111.73		184.37	410.66	2.23	2.03	226.3	*
230653_at	Hs.170698.0	AI469960	548.74	594.79	1.08	1.03	46.05		208.2	463.98	2.23	1.93	255.79	*
226464_at	C3orf58: chromosome 3 open reading frame 58	BE348597	884.48	811.42	-1.09	-0.97	-73.06		863.99	1920.45	2.22	2.1	1056.47	*
228507_at	Hs.24305.0	AI742043	135.75	198.69	1.46	1.25	62.95		98.33	218.09	2.22	1.85	119.76	*
242725_at	Hs.269956.0	BG026159	743.5	671.03	-1.11	-1.04	-72.48		184.27	408.72	2.22	1.79	224.46	*
212249_at	PIK3R1: phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	AI934473	203.13	279.85	1.38	1.25	76.73		183.55	405.73	2.21	2.01	222.18	*
213113_s_at	SLC43A3: solute carrier family 43, member 3	AI630178	363.94	510.54	1.4	1.26	146.6		373.38	824.4	2.21	1.98	451.02	*
222853_at	FLRT3: fibronectin leucine rich transmembrane protein 3	N71923	115.7	156.72	1.35	1.11	41.02		143.63	317.46	2.21	1.95	173.83	*
228144_at	ZNF300: zinc finger protein 300	N49841	345	355.87	1.03	0.97	10.87		243.1	536.23	2.21	2.01	293.14	*
229234_at	ZC3H12B: zinc finger CCCH-type containing 12B	AW007160	49.91	126.13	2.53	1.89	76.23		98.92	218.46	2.21	1.89	119.54	*
209301_at	CA2: carbonic anhydrase II	M36532	107.79	153.14	1.42	1.15	45.35		105.45	231.91	2.2	1.61	126.46	*
224568_x_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AW005982	9301.03	8995.03	-1.03	-0.99	-306.01		2426.88	5330.47	2.2	1.93	2903.59	*
227260_at	ANKRD10: Ankyrin repeat domain 10	AV724266	677.57	997.01	1.47	1.38	319.44		293.08	646.19	2.2	1.83	353.1	*
206263_at	FMO4: flavin containing monooxygenase 4	NM_002022	195.5	275.15	1.41	1.23	79.66		252.02	551.75	2.19	1.88	299.73	*
211590_x_at	TBXA2R: thromboxane A2 receptor	U11271	70.68	135.37	1.92	1.6	64.69		108.68	237.78	2.19	1.7	129.1	*
212470_at	SPAG9: sperm associated antigen 9	AB011088	2319.45	3534.5	1.52	1.45	1215.05		2213.1	4839.78	2.19	2.09	2626.68	*
213939_s_at	RUFY3: RUN and FYVE domain containing 3	AI871641	1265.78	1213.43	-1.04	-1	-52.35		371.48	813.33	2.19	2.02	441.85	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
231098_at	Hs.10263.0	BF939996	459.22	740.98	1.61	1.49	281.75		659.74	1446.03	2.19	2.09	786.29	*
236649_at	DTWD1: DTW domain containing 1	AA907927	828.89	614.95	-1.35	-1.28	-213.93		149.85	327.54	2.19	1.9	177.7	*
1558680_s_at	PDE1A: phosphodiesterase 1A, calmodulin-dependent	BQ894022	62.31	141.11	2.26	1.56	78.8		393.41	863.06	2.19	2.04	469.65	*
212239_at	PIK3R1: phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	AI680192	749.49	1007.32	1.34	1.24	257.83		728.48	1586.89	2.18	2.05	858.41	*
226431_at	FAM117B: family with sequence similarity 117, member B	AK025007	383.92	445.5	1.16	1.03	61.59		354.96	775.18	2.18	2.04	420.22	*
228772_at	HNMT: histamine N-methyltransferase	AU157303	767.59	1000.03	1.3	1.21	232.43		914.27	1992.04	2.18	2.08	1077.78	*
209682_at	CBLB: Cas-Br-M (murine) ecotropic retroviral transforming sequence b	U26710	2439.72	3372.21	1.38	1.33	932.49		1099.73	2389.41	2.17	2.08	1289.68	*
216894_x_at	CDKN1C: cyclin-dependent kinase inhibitor 1C (p57, Kip2)	D64137	69.15	102.62	1.48	1.19	33.47		98.58	214.38	2.17	1.86	115.8	*
229114_at	GAB1: GRB2-associated binding protein 1	AW237741	457.18	521.17	1.14	1.06	63.99		432.98	938.07	2.17	2.08	505.08	*
1555348_at	TFAP2E: transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)	BC041175	227.26	313.77	1.38	1.21	86.51		89.54	194.44	2.17	1.66	104.9	*
1567213_at	PNN: pinin, desmosome associated protein	U59479	176.08	210.12	1.19	1.08	34.04		122.26	265.09	2.17	1.84	142.83	*
202887_s_at	DDIT4: DNA-damage-inducible transcript 4	NM_019058	7836.23	7961.64	1.02	0.98	125.42		1001.73	2160.83	2.16	1.77	1159.1	*
211071_s_at	MLLT11: myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	BC006471	3353.91	4696.92	1.4	1.32	1343.01		4501.61	9704.37	2.16	2.05	5202.77	*
211701_s_at	TRO: trophinin	AF349720	401.79	545.01	1.36	1.28	143.22		373.84	805.72	2.16	2.02	431.88	*
229537_at	LMO4: LIM domain only 4	AI694521	264.51	317.73	1.2	1.11	53.23		111.46	240.54	2.16	1.92	129.08	*
1554483_at	TMEM37: transmembrane protein 37	AF361356	121.98	186.74	1.53	1.19	64.76		121.27	261.63	2.16	1.72	140.36	*
201656_at	ITGA6: integrin, alpha 6	NM_000210	351.08	369.77	1.05	0.97	18.69		650.17	1395.5	2.15	2.02	745.33	*
202948_at	IL1R1: interleukin 1 receptor, type I	NM_000877	2437.35	3572.11	1.47	1.37	1134.76		3393.76	7285.97	2.15	2.06	3892.21	*
203685_at	BCL2: B-cell CLL/lymphoma 2	NM_000633	206.56	117.21	-1.76	-1.51	-89.36		157.67	338.85	2.15	1.92	181.18	*
212240_s_at	PIK3R1: phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	AI679268	611.91	789.42	1.29	1.19	177.51		564.08	1213.19	2.15	2.03	649.1	*
229111_at	Hs.83938.0	AA033699	558.06	631.39	1.13	1.03	73.33		170.13	364.94	2.15	1.85	194.82	*
229422_at	NRD1: nardilysin (N-arginine dibasic convertase)	AA448346	740.27	601.87	-1.23	-1.16	-138.41		197.38	425.25	2.15	1.92	227.87	*
230713_at	Hs.182185.0	BF115786	468.83	380.36	-1.23	-1.14	-88.47		109.92	235.92	2.15	1.79	125.99	*
1554250_s_at	TRIM73: tripartite motif-containing 73	BC033812	350.63	339.34	-1.03	-0.95	-11.29		101.55	218.83	2.15	1.75	117.28	*
1556744_a_at	Hs2.118758.1	AI732587	583.39	566.44	-1.03	-0.98	-16.95		161.83	348.28	2.15	1.91	186.45	*
209599_s_at	PRUNE: prune homolog (Drosophila)	AI762105	158.48	218.72	1.38	1.22	60.24		197.53	423.15	2.14	1.97	225.62	*
210357_s_at	SMOX: spermine oxidase	BC000669	672.94	591.01	-1.14	-1.07	-81.93		532.83	1141.21	2.14	1.85	608.38	*
229667_s_at	HOXB8: homeobox B8	AI277015	224.9	148.78	-1.51	-1.27	-76.12		163.66	350.8	2.14	1.92	187.13	*
232931_at	SNRNP200: small nuclear ribonucleoprotein 200kDa (U5)	AK021583	376.99	343.24	-1.1	-1.07	-33.75		91.8	196.09	2.14	1.81	104.29	*
208798_x_at	GOLGA8A: golgi autoantigen, golgin subfamily a, 8A	AF204231	2812.82	3021.55	1.07	1.04	208.73		616.29	1311.5	2.13	1.92	695.2	*
213689_x_at	FAM69A: family with sequence similarity 69, member A	AL137958	1622.26	1619.01	-1	-0.91	-3.25		2775.79	5904.87	2.13	2.02	3129.08	*
213870_at	COL11A2: collagen, type XI, alpha 2	AL031228	82.04	71.88	-1.14	-0.82	-10.17		92.76	197.92	2.13	1.65	105.16	*
228551_at	DENND5B: DENN/MADD domain containing 5B	AL137364	572.81	812	1.42	1.35	239.18		613.08	1304.34	2.13	2.01	691.26	*
229517_at	PTPDC1: protein tyrosine phosphatase domain containing 1	BE046919	901.78	833.03	-1.08	-1	-68.76		365.05	776.87	2.13	1.94	411.82	*
236953_s_at	NHLRC3: NHL repeat containing 3	N25548	442.84	376.45	-1.18	-1.11	-66.39		94.46	201.5	2.13	1.79	107.04	*
177_at	PLD1: phospholipase D1, phosphatidylcholine-specific	U38545	194.08	148.99	-1.3	-1.15	-45.09		212.09	449.09	2.12	2	237	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
210882_s_at	TRO: trophinin	U04811	175.65	207.1	1.18	1.03	31.45		198.19	419.96	2.12	1.93	221.77	*
214631_at	ZBTB33: zinc finger and BTB domain containing 33	BG391005	127.84	193.79	1.52	1.38	65.94		136.42	289.49	2.12	1.95	153.07	*
227062_at	NEAT1: nuclear paraspeckle assembly transcript 1 (non-protein coding)	AU155361	3171.58	2244.55	-1.41	-1.31	-927.03		371.76	786.86	2.12	1.74	415.1	*
236251_at	Hs.115122.0	AA228366	671.82	693.47	1.03	0.97	21.65		130.69	276.65	2.12	1.7	145.96	*
216563_at	ANKRD12: Ankyrin repeat domain 12	X80821	210.77	282.66	1.34	1.21	71.89		106.9	225.14	2.11	1.72	118.24	*
223646_s_at	CYorf15B: chromosome Y open reading frame 15B	AF332225	337.32	342.77	1.02	0.93	5.46		127.54	269.08	2.11	1.88	141.55	*
225735_at	ANKRD50: ankyrin repeat domain 50	AL110131	296.69	427.03	1.44	1.31	130.34		295.99	625.81	2.11	1.97	329.82	*
234723_x_at	Hs.306716.0	AK024881	848.57	636.6	-1.33	-1.28	-211.97		120.77	254.31	2.11	1.86	133.55	*
241708_at	DOCK1: dedicator of cytokinesis 1	AA599017	119.31	186.61	1.56	1.4	67.3		130.62	275.12	2.11	1.88	144.5	*
1556827_at	LOC339929: hypothetical protein LOC339929	BC042414	90.46	154.81	1.71	1.34	64.35		123.08	259.69	2.11	1.89	136.6	*
219113_x_at	HSD17B14: hydroxysteroid (17-beta) dehydrogenase 14	NM_016246	112.99	138.6	1.23	1.01	25.61		113.6	238.54	2.1	1.79	124.94	*
225601_at	HMGB3: high-mobility group box 3	AI806853	361.81	325.87	-1.11	-1.05	-35.94		279.87	587.19	2.1	1.96	307.32	*
226232_at	GDF11: growth differentiation factor 11	AI889093	141.98	130.4	-1.09	-0.89	-11.58		172.84	363.51	2.1	1.88	190.67	*
229966_at	EWSR1: Ewing sarcoma breakpoint region 1	AW089574	701.19	771.74	1.1	1.05	70.55		164.24	344.93	2.1	1.66	180.7	*
207316_at	HAS1: hyaluronan synthase 1	NM_001523	132.57	167.1	1.26	0.9	34.53		558.1	1164.41	2.09	1.96	606.31	*
210954_s_at	TSC22D2: TSC22 domain family, member 2	AF201292	220.95	201.87	-1.09	-1.02	-19.08		178.41	373.16	2.09	1.96	194.75	*
213212_x_at	FLJ40113 /// LOC440295: golgi autoantigen, golgin subfamily a-like pseudogene /// golgi autoantigen, golgin subfamily a, 6D-like	AI632181	2042.61	2265.63	1.11	1.06	223.02		597.25	1250.08	2.09	2.01	652.83	*
225998_at	GAB1: GRB2-associated binding protein 1	AK022142	453.73	497.25	1.1	0.99	43.51		463.43	967.48	2.09	1.92	504.05	*
209542_x_at	IGF1: insulin-like growth factor 1 (somatomedin C)	M29644	1458.39	1429.1	-1.02	-0.8	-29.29		1681.87	3492.64	2.08	1.7	1810.77	*
209568_s_at	RGL1: ral guanine nucleotide dissociation stimulator-like 1	AF186779	1403.44	2054.49	1.46	1.38	651.05		1132.76	2339.48	2.07	1.92	1206.72	*
209586_s_at	PRUNE: prune homolog (Drosophila)	AF123539	922.88	1002.68	1.09	1	79.8		896.4	1854.22	2.07	1.9	957.82	*
210988_s_at	PRUNE: prune homolog (Drosophila)	AF123538	335.76	389.29	1.16	1.06	53.53		347.01	717.24	2.07	1.86	370.23	*
214805_at	EIF4A1: Eukaryotic translation initiation factor 4A, isoform 1	U79273	591.44	520.65	-1.14	-1.09	-70.79		165.85	343.06	2.07	1.95	177.2	*
216044_x_at	FAM69A: family with sequence similarity 69, member A	AK027146	1561.24	1749	1.12	1.01	187.75		2814.9	5829.28	2.07	1.97	3014.38	*
223571_at	C1QTNF6: C1q and tumor necrosis factor related protein 6	AF329842	288.14	429.1	1.49	1.31	140.97		563.04	1166.05	2.07	1.96	603.02	*
226670_s_at	PABPC1L: poly(A) binding protein, cytoplasmic 1-like	AL109839	1050.35	932.05	-1.13	-1.04	-118.31		192.84	398.54	2.07	1.66	205.7	*
227628_at	GPX8: glutathione peroxidase 8 (putative)	AL571557	7906.01	8078.67	1.02	0.76	172.66		9899.01	20500.49	2.07	1.66	10601.49	*
235595_at	ARHGEF2: Rho/Rac guanine nucleotide exchange factor (GEF) 2	AW299534	1339.23	1108.97	-1.21	-1.17	-230.25		114.81	238.12	2.07	1.69	123.31	*
206022_at	NDP: Norrie disease (pseudoglioma)	NM_000266	101.91	32.29	-3.16	-2.12	-69.61		126.58	260.94	2.06	1.83	134.36	*
210751_s_at	RGN: regucalcin (senescence marker protein-30)	D31815	269.83	289.85	1.07	0.98	20.03		237.91	491.28	2.06	1.87	253.37	*
220786_s_at	SLC38A4: solute carrier family 38, member 4	NM_018018	47.7	47.93	1	0.73	0.23		112.32	231.23	2.06	1.87	118.91	*
225571_at	LIFR: leukemia inhibitory factor receptor alpha	AA701657	194.82	219.67	1.13	1.01	24.85		106.66	219.22	2.06	1.79	112.56	*
236027_at	C10orf78: chromosome 10 open reading frame 78	N23587	736.69	918.76	1.25	1.13	182.07		876.84	1809.21	2.06	1.98	932.37	*
236525_at	FBXO36: F-box protein 36	BG479112	146.87	165.26	1.13	0.96	18.39		113.2	232.92	2.06	1.8	119.72	*
1558522_at	Hs2.362871.1	BC013077	148.36	163.06	1.1	0.94	14.7		147.61	303.46	2.06	1.88	155.85	*
232113_at	Hs.50150.0	N90870	4018.79	4762.03	1.18	1.13	743.24		1000.76	2049.36	2.05	1.87	1048.59	*
239151_at	RP11-144G6.7: hypothetical LOC399753	BG427809	642.1	407.2	-1.58	-1.43	-234.89		109.31	224.6	2.05	1.68	115.28	*
1557348_at	Hs2.363526.1	AI915861	287.94	304.39	1.06	1	16.45		127.81	261.85	2.05	1.84	134.04	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
210087_s_at	MPZL1: myelin protein zero-like 1	AF095727	1801.85	2826.83	1.57	1.49	1024.98		2233.43	4548.59	2.04	1.97	2315.16	*
213146_at	KDM6B: lysine (K)-specific demethylase 6B	AA521267	362.42	491.4	1.36	1.25	128.98		167.2	340.28	2.04	1.82	173.09	*
215470_at	GTF2H2B: general transcription factor IIH, polypeptide 2B	U21915	719.34	508.41	-1.41	-1.31	-210.93		133.84	273.42	2.04	1.53	139.58	*
221139_s_at	CSAD: cysteine sulfinic acid decarboxylase	NM_015989	1327.53	1291.86	-1.03	-0.97	-35.67		370.8	756.19	2.04	1.9	385.4	*
239735_at	Hs.264622.0	N67106	1524.86	1008.93	-1.51	-1.42	-515.92		201.27	410.31	2.04	1.78	209.04	*
201867_s_at	TBL1X: transducin (beta)-like 1X-linked	AW968555	507.52	679.32	1.34	1.24	171.8		210.43	426.36	2.03	1.72	215.93	*
203504_s_at	ABCA1: ATP-binding cassette, sub-family A (ABC1), member 1	NM_005502	355.42	322.96	-1.1	-1	-32.45		154.87	314.75	2.03	1.76	159.88	*
226197_at	Hs.76704.0	AW173504	265.16	371.07	1.4	1.21	105.92		206.4	419.62	2.03	1.63	213.22	*
232480_at	LOC400931: hypothetical LOC400931	AA758934	507.73	444.42	-1.14	-1.05	-63.31		98.76	200.84	2.03	1.54	102.08	*
235902_at	Hs.135223.0	AI090764	464.07	564.64	1.22	1.15	100.57		195.42	396.74	2.03	1.76	201.32	*
242919_at	ZNF253: zinc finger protein 253	AV683221	193.35	246.2	1.27	1.2	52.85		201.4	408.97	2.03	1.85	207.57	*
1560622_at	Hs2.116468.1	AK000203	924.92	697.36	-1.33	-1.28	-227.57		143.74	291.22	2.03	1.72	147.49	*
203903_s_at	HEPH: hephaestin	NM_014799	2549.72	3896.24	1.53	1.43	1346.52		2980.51	6010.26	2.02	1.93	3029.75	*
217080_s_at	HOMER2: homer homolog 2 (Drosophila)	Y19026	226.36	180.92	-1.25	-1.04	-45.44		197.36	398.34	2.02	1.77	200.98	*
225575_at	LIFR: leukemia inhibitory factor receptor alpha	AI680541	729.04	817	1.12	1.06	87.96		491.56	995	2.02	1.91	503.44	*
226360_at	ZNRF3: zinc and ring finger 3	AK022809	377.26	545.37	1.45	1.38	168.11		332.76	670.87	2.02	1.9	338.11	*
226408_at	TEAD2: TEA domain family member 2	AA905942	736.76	1087.52	1.48	1.38	350.76		922.96	1866.59	2.02	1.92	943.64	*
227771_at	LIFR: leukemia inhibitory factor receptor alpha	AW592684	377.66	349	-1.08	-0.99	-28.66		256.59	517.66	2.02	1.82	261.08	*
235363_at	Hs.28360.0	BF108778	77.24	90.82	1.18	0.79	13.58		151.71	305.86	2.02	1.74	154.15	*
215723_s_at	PLD1: phospholipase D1, phosphatidylcholine-specific	AJ276230	148.15	109.73	-1.35	-1.14	-38.42		178.13	358.28	2.01	1.86	180.16	*
223588_at	THAP2: THAP domain containing, apoptosis associated protein 2	AL136607	217.71	339.63	1.56	1.39	121.92		135.04	271.91	2.01	1.73	136.87	*
229327_s_at	Hs.30250.2	BE674528	84.11	89.4	1.06	0.79	5.28		147.46	295.96	2.01	1.79	148.49	*
235190_at	Hs.127453.0	BF591288	2162.8	1855.67	-1.17	-1.1	-307.13		532.05	1068.12	2.01	1.82	536.07	*
238142_at	Hs.191952.0	AW029203	382.3	329.38	-1.16	-1.08	-52.91		120.2	241.35	2.01	1.72	121.15	*
243338_at	Hs.293668.0	AI674461	467.24	405.76	-1.15	-1.08	-61.48		131.46	264.38	2.01	1.79	132.92	*
203723_at	ITPKB: inositol 1,4,5-trisphosphate 3-kinase B	NM_002221	209.16	238.98	1.14	0.99	29.82		264.36	528.97	2	1.76	264.61	*
229511_at	SMARCE1: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	AA195255	208.21	244.94	1.18	1.02	36.73		251.77	504.73	2	1.87	252.95	*
1554411_at	CTNNB1: catenin (cadherin-associated protein), beta 1, 88kDa	AB062292	587.96	603.3	1.03	0.96	15.33		676.22	1350.8	2	1.93	674.58	*
202597_at	IRF6: interferon regulatory factor 6	AU144284	153.42	128.1	-1.2	-0.97	-25.32		161.13	320.93	1.99	1.72	159.8	*
212637_s_at	WWP1: WW domain containing E3 ubiquitin protein ligase 1	AU155187	765.47	1061.76	1.39	1.31	296.29		801.77	1595.27	1.99	1.88	793.51	*
217525_at	OLFML1: olfactomedin-like 1	AW305097	29.84	39.14	1.31	0.68	9.29		257.01	511.98	1.99	1.85	254.97	*
223464_at	OSBPL5: oxysterol binding protein-like 5	AL136918	304.16	335.5	1.1	0.96	31.34		326.96	649.55	1.99	1.78	322.6	*
235658_at	Hs.151444.0	AW058580	230.19	279.68	1.22	1.1	49.49		273.81	544.42	1.99	1.87	270.61	*
244455_at	KCNT2: potassium channel, subfamily T, member 2	AI732637	927.39	1228.61	1.32	1.27	301.23		285.43	567.39	1.99	1.74	281.97	*
213523_at	CCNE1: cyclin E1	AI671049	232.86	368.09	1.58	1.42	135.24		438.1	867.42	1.98	1.86	429.32	*
217606_at	Hs.196555.0	AI653960	89.48	107.31	1.2	0.95	17.83		116.92	232	1.98	1.69	115.08	*
219055_at	SRBD1: S1 RNA binding domain 1	NM_018079	703.62	795.06	1.13	1.05	91.43		890.37	1765.88	1.98	1.87	875.51	*
219815_at	GAL3ST4: galactose-3-O-sulfotransferase 4	NM_024637	494.53	801.46	1.62	1.43	306.94		794.46	1573.9	1.98	1.89	779.44	*
224901_at	SCD5: stearoyl-CoA desaturase 5	AL571375	662.77	603.77	-1.1	-1.03	-59		777.5	1538.37	1.98	1.9	760.87	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
226436_at	RASSF4: Ras association (RalGDS/AF-6) domain family member 4	N49935	268.4	278.42	1.04	0.93	10.02		316.73	627.87	1.98	1.77	311.14	*
227663_at	Hs.44898.2	BE674006	1000.34	1045.47	1.05	0.99	45.12		351.32	694.34	1.98	1.87	343.02	*
229344_x_at	RIMKLB: ribosomal modification protein rimK-like family member B	AW135012	1151.21	1321.5	1.15	1.12	170.29		513.13	1015.08	1.98	1.79	501.95	*
243134_at	Hs.271019.0	AW190862	972.66	659.19	-1.48	-1.43	-313.47		152.83	303.08	1.98	1.71	150.26	*
204418_x_at	GSTM2: glutathione S-transferase mu 2 (muscle)	NM_000848	1357.38	1822.99	1.34	1.24	465.6		1620.81	3188.38	1.97	1.89	1567.56	*
210963_s_at	GYG2: glycogenin 2	U94363	124.03	159.4	1.29	1.02	35.37		149.73	295.71	1.97	1.56	145.98	*
213650_at	GOLGA8A /// GOLGA8B: golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B	AW006438	1890.72	1665.06	-1.14	-1.09	-225.66		295.98	583.77	1.97	1.79	287.79	*
215333_x_at	GSTM1: glutathione S-transferase mu 1	X08020	1181.51	1692.54	1.43	1.32	511.03		1401.61	2760.06	1.97	1.85	1358.45	*
210594_x_at	MPZL1: myelin protein zero-like 1	AF239756	1823.11	2624.98	1.44	1.34	801.87		2140.28	4201.09	1.96	1.88	2060.82	*
225633_at	DPY19L3: dpy-19-like 3 (C. elegans)	BF057717	1110.15	1656.28	1.49	1.42	546.13		1533.07	3011.42	1.96	1.9	1478.35	*
226612_at	FLJ25076: probable ubiquitin-conjugating enzyme E2 FLJ25076	H17038	596.99	1071.32	1.79	1.43	474.33		853.23	1671.7	1.96	1.62	818.47	*
227976_at	LOC644538: hypothetical protein LOC644538	AW242009	96.03	141.97	1.48	1.18	45.93		123.15	241.5	1.96	1.71	118.35	*
229648_at	RICS: Rho GTPase-activating protein	AW025358	108.69	82.82	-1.31	-1.09	-25.88		119.06	233.59	1.96	1.7	114.53	*
239443_at	PCDHB6: protocadherin beta 6	AI821557	121.23	183.34	1.51	1.26	62.11		173.12	339.01	1.96	1.79	165.9	*
204154_at	CDO1: cysteine dioxygenase, type I	NM_001801	224.04	259.35	1.16	0.99	35.31		430.46	839.74	1.95	1.81	409.28	*
204550_x_at	GSTM1: glutathione S-transferase mu 1	NM_000561	1463.59	1741.75	1.19	1.07	278.16		1583	3085.93	1.95	1.86	1502.93	*
212719_at	PHLPP1: PH domain and leucine rich repeat protein phosphatase 1	AB011178	297.84	277.2	-1.07	-0.95	-20.64		340.29	662.54	1.95	1.81	322.25	*
218093_s_at	ANKRD10: ankyrin repeat domain 10	NM_017664	1422.25	1934.3	1.36	1.32	512.04		722.23	1411.29	1.95	1.85	689.06	*
219355_at	CXorf57: chromosome X open reading frame 57	NM_018015	145.62	146.9	1.01	0.9	1.29		127.81	248.93	1.95	1.67	121.12	*
228906_at	TET1: tet oncogene 1	AI968175	124.51	223.84	1.8	1.55	99.33		141.43	276.43	1.95	1.73	135	*
231936_at	HOXC9: homeobox C9	AK000445	760.58	1075.43	1.41	1.26	314.85		446.71	868.85	1.95	1.78	422.14	*
231937_at	Hs.185707.0	AU153281	286.33	385.06	1.34	1.19	98.73		125.93	245.91	1.95	1.65	119.98	*
232052_at	LOC440944: hypothetical LOC440944	AL110136	359.11	392.31	1.09	1.01	33.2		156.73	304.88	1.95	1.64	148.16	*
211958_at	IGFBP5: insulin-like growth factor binding protein 5	R73554	1329.22	1213.3	-1.1	-0.93	-115.92		4741.24	9183.09	1.94	1.82	4441.86	*
213761_at	MDM1: Mdm1 nuclear protein homolog (mouse)	AW664850	933.96	937.76	1	0.95	3.81		374.38	726.13	1.94	1.77	351.75	*
226225_at	MCC: mutated in colorectal cancers	BE967311	548.88	672.76	1.23	1.11	123.89		592.43	1147.93	1.94	1.82	555.5	*
228087_at	CCDC126: coiled-coil domain containing 126	AK026684	564.57	660.12	1.17	1.08	95.55		562.11	1088.27	1.94	1.83	526.16	*
231738_at	PCDHB7: protocadherin beta 7	NM_018940	231.5	380.28	1.64	1.48	148.78		436.79	847.62	1.94	1.81	410.82	*
1556007_s_at	Hs2.438760.1	AI377389	956.59	845.45	-1.13	-1.07	-111.15		143.77	278.33	1.94	1.74	134.56	*
202600_s_at	NRIP1: nuclear receptor interacting protein 1	AI824012	1027.84	1060.88	1.03	0.98	33.03		531.25	1025.68	1.93	1.81	494.43	*
202830_s_at	SLC37A4: solute carrier family 37 (glucose-6-phosphate transporter), member 4	NM_001467	243.44	210.29	-1.16	-1.02	-33.15		263.91	508.88	1.93	1.75	244.97	*
219885_at	SLFN12: schlafen family member 12	NM_018042	471.52	449.4	-1.05	-0.97	-22.11		535.22	1034.25	1.93	1.82	499.03	*
223827_at	TNFRSF19: tumor necrosis factor receptor superfamily, member 19	AF246998	410.48	352.5	-1.16	-1.07	-57.97		427.22	826.17	1.93	1.81	398.95	*
201294_s_at	WSB1: WD repeat and SOCS box-containing 1	N24643	2320.56	2526.31	1.09	1.03	205.75		579.14	1114.45	1.92	1.72	535.31	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
223435_s_at	PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2: protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	AI268404	112.86	170.36	1.51	1.19	57.5		163.44	317.12	1.94	1.68	153.68	*
203214_x_at	CDC2: cell division cycle 2, G1 to S and G2 to M	NM_001786	78.99	85.29	1.08	0.78	6.3		294.99	565.62	1.92	1.79	270.63	*
204294_at	AMT: aminomethyltransferase	NM_000481	644.39	710.67	1.1	1	66.28		257.89	495.3	1.92	1.57	237.41	*
221899_at	N4BP2L2: NEDD4 binding protein 2-like 2	AI809961	2930.67	2415.62	-1.21	-1.15	-515.05		486.73	933.46	1.92	1.7	446.74	*
234731_at	Hs.53478.0	AK022428	529.8	485.34	-1.09	-1.05	-44.46		133.69	256.85	1.92	1.71	123.16	*
200783_s_at	STMN1: stathmin 1	NM_005563	391.94	356.25	-1.1	-0.88	-35.69		379.3	722.58	1.91	1.65	343.28	*
213649_at	SFRS7: splicing factor, arginine/serine-rich 7, 35kDa	AA524053	1502.26	1494.58	-1.01	-0.95	-7.69		487.32	928.51	1.91	1.75	441.19	*
219274_at	TSPAN12: tetraspanin 12	NM_012338	64.6	73.23	1.13	0.78	8.64		116.7	223.16	1.91	1.65	106.47	*
228238_at	GAS5: growth arrest-specific 5 (non-protein coding)	AW105301	806.11	961.36	1.19	1.13	155.25		295.05	563.74	1.91	1.74	268.69	*
242490_at	Hs.193682.0	AA564255	384.15	294.03	-1.31	-1.2	-90.12		140.38	268.8	1.91	1.65	128.42	*
203505_at	ABCA1: ATP-binding cassette, sub-family A (ABC1), member 1	AF285167	592.74	586.05	-1.01	-0.97	-6.69		295.1	560.72	1.9	1.78	265.62	*
209442_x_at	ANK3: ankyrin 3, node of Ranvier (ankyrin G)	AL136710	214.83	221.88	1.03	0.9	7.05		272.61	514.84	1.89	1.72	242.23	*
209596_at	MXRA5: matrix-remodelling associated 5	AF245505	914.31	695.39	-1.31	-1.08	-218.92		3236.03	6106.18	1.89	1.79	2870.15	*
226047_at	MRVI1: murine retrovirus integration site 1 homolog	N66571	284.1	259.67	-1.09	-0.93	-24.43		428.35	809.97	1.89	1.64	381.62	*
228713_s_at	HSD17B14: hydroxysteroid (17-beta) dehydrogenase 14	AI742586	241.19	210.63	-1.15	-1.04	-30.56		278.57	526.38	1.89	1.73	247.81	*
201869_s_at	TBL1X: transducin (beta)-like 1X-linked	BF593932	444.99	619.91	1.39	1.29	174.92		240.08	450.66	1.88	1.65	210.58	*
218731_s_at	VWA1: von Willebrand factor A domain containing 1	NM_022834	120.25	162.19	1.35	1.13	41.94		249.27	468.59	1.88	1.68	219.33	*
222653_at	PNPO: pyridoxamine 5'-phosphate oxidase	AA005137	517.07	518.31	1	0.89	1.24		752.73	1411.42	1.88	1.79	658.68	*
228737_at	TOX2: TOX high mobility group box family member 2	AA211909	1123.72	1308.99	1.16	1.11	185.27		227.28	427.07	1.88	1.58	199.79	*
229434_at	Hs.9403.0	AA865357	652.28	532.89	-1.22	-1.14	-119.39		119.28	224.69	1.88	1.58	105.41	*
235170_at	ZNF92: zinc finger protein 92	T52999	391.22	467.86	1.2	1.08	76.65		424.44	797.76	1.88	1.78	373.32	*
213326_at	VAMP1: vesicle-associated membrane protein 1 (synaptobrevin 1)	AU150319	301.78	456.92	1.51	1.35	155.14		266.9	499.62	1.87	1.7	232.72	*
233364_s_at	Hs.50150.1	AK021804	3253.71	4149.28	1.28	1.21	895.57		952.91	1778.33	1.87	1.66	825.42	*
235094_at	Hs.137526.0	AI972661	2104.31	1699.09	-1.24	-1.16	-405.21		407.55	760.42	1.87	1.71	352.87	*
238547_at	HEXIM2: hexamthylene bis-acetamide inducible 2	AI972367	248.95	356.49	1.43	1.31	107.53		277.11	518.52	1.87	1.78	241.41	*
222108_at	AMIGO2: adhesion molecule with Ig-like domain 2	AC004010	8635.82	12444.8	1.44	1.37	3808.97		4818.23	8943.53	1.86	1.72	4125.3	*
223667_at	FKBP7: FK506 binding protein 7	AF092137	161.55	250.82	1.55	1.31	89.27		360.24	671.25	1.86	1.74	311	*
232150_at	Hs.36093.0	AA134418	738.86	606.44	-1.22	-1.16	-132.42		147.42	274.85	1.86	1.62	127.43	*
1559957_a_at	LOC642852: hypothetical LOC642852	BG396868	500.81	517.09	1.03	0.98	16.28		191.38	356.5	1.86	1.68	165.12	*
204381_at	LRP3: low density lipoprotein receptor-related protein 3	NM_002333	1185.09	1544.87	1.3	1.21	359.78		1308.19	2416.05	1.85	1.78	1107.86	*
213367_at	ZNF783: zinc finger family member 783	AF035281	498.91	551.97	1.11	1.01	53.07		179.44	331.48	1.85	1.56	152.04	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
223533_at	LRRC8C: leucine rich repeat containing 8 family, member C	AL136919	127.36	104.33	-1.22	-0.96	-23.03		166.48	308.46	1.85	1.67	141.98	*
225627_s_at	CACHD1: cache domain containing 1	AK024256	389.17	367.05	-1.06	-0.93	-22.12		394.94	731.08	1.85	1.64	336.14	*
241400_at	Hs.160316.0	AI860360	3098.03	2788.48	-1.11	-1.1	-309.55		188.1	347.35	1.85	1.66	159.25	*
212148_at	PBX1: pre-B-cell leukemia homeobox 1	AL049381	350.77	421.18	1.2	1.09	70.41		510.66	938.1	1.84	1.75	427.44	*
223251_s_at	ANKRD10: ankyrin repeat domain 10	BC001727	926.11	1080.34	1.17	1.12	154.24		379.05	696.41	1.84	1.65	317.36	*
224494_x_at	HSD17B14: hydroxysteroid (17-beta) dehydrogenase 14	BC006283	121.54	93.36	-1.3	-1.04	-28.17		121.18	223.36	1.84	1.55	102.18	*
227517_s_at	GAS5: growth arrest-specific 5 (non-protein coding)	AI056992	1648.62	1822.9	1.11	1.04	174.29		560.89	1032.04	1.84	1.7	471.15	*
242033_at	RNF180: ring finger protein 180	BE672684	164.71	243.43	1.48	1.31	78.72		208.36	382.6	1.84	1.72	174.24	*
202242_at	TSPAN7: tetraspanin 7	NM_004615	132.08	66.52	-1.99	-1.32	-65.56		308.54	564.49	1.83	1.73	255.94	*
205345_at	BARD1: BRCA1 associated RING domain 1	NM_000465	122.78	137.46	1.12	0.95	14.67		148.91	273.01	1.83	1.65	124.1	*
209348_s_at	MAF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	AF055376	1383.51	1026.17	-1.35	-1.24	-357.33		2143.49	3923.12	1.83	1.75	1779.63	*
210880_s_at	EFS: embryonal Fyn-associated substrate	AB001467	332.84	489.73	1.47	1.31	156.89		477.48	873.64	1.83	1.67	396.15	*
213645_at	ENOSF1: enolase superfamily member 1	AF305057	747.59	466.36	-1.6	-1.44	-281.23		141.01	257.37	1.83	1.55	116.37	*
214595_at	KCNG1: potassium voltage-gated channel, subfamily G, member 1	AI332979	667.95	799.13	1.2	1.13	131.18		217.72	397.71	1.83	1.71	179.99	*
226234_at	GDF11: growth differentiation factor 11	D80983	207.59	230.07	1.11	1	22.48		388.14	709.12	1.83	1.72	320.98	*
226925_at	ACPL2: acid phosphatase-like 2	AW069729	550.53	820.14	1.49	1.31	269.61		1386.11	2538.62	1.83	1.76	1152.51	*
227350_at	HELLS: helicase, lymphoid-specific	AI889959	110.03	158.85	1.44	1.26	48.82		148.21	271.71	1.83	1.66	123.5	*
238493_at	ZNF506: zinc finger protein 506	AI559570	184.23	235.83	1.28	1.11	51.59		206.32	377.14	1.83	1.7	170.81	*
203438_at	STC2: stanniocalcin 2	AI435828	5945.36	8942.73	1.5	1.44	2997.37		819.61	1494.74	1.82	1.62	675.13	*
205046_at	CENPE: centromere protein E, 312kDa	NM_001813	26.99	36.77	1.36	0.7	9.78		128.5	233.98	1.82	1.57	105.48	*
205104_at	SNPH: syntaphilin	NM_014723	459.46	462.66	1.01	0.92	3.2		478.06	867.91	1.82	1.73	389.86	*
218789_s_at	C11orf71: chromosome 11 open reading frame 71	NM_019021	108.41	132.9	1.23	1.02	24.49		143.77	262.03	1.82	1.61	118.26	*
221427_s_at	CCNL2: cyclin L2	NM_030937	1959.17	1743.42	-1.12	-1.06	-215.75		597.84	1087.67	1.82	1.61	489.83	*
223940_x_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AF132202	10500.73	10539.05	1	0.96	38.32		3802.69	6911.66	1.82	1.6	3108.97	*
229700_at	ZNF738: zinc finger protein 738	BE966267	462.52	546.3	1.18	1.08	83.77		758.78	1380.9	1.82	1.77	622.12	*
232511_at	Hs.35982.1	AK022838	572.44	464.28	-1.23	-1.14	-108.16		130.66	238.16	1.82	1.52	107.49	*
238508_at	DBF4B: DBF4 homolog B (S. cerevisiae)	BG026951	129.62	166.13	1.28	1.15	36.5		156.61	285.57	1.82	1.65	128.96	*
203301_s_at	DMTF1: cyclin D binding myb-like transcription factor 1	NM_021145	1791.69	1884.94	1.05	1	93.26		794.43	1438.74	1.81	1.72	644.3	*
235123_at	Hs.210761.0	AI951144	595.3	493.17	-1.21	-1.13	-102.14		213.99	387.8	1.81	1.61	173.82	*
205138_s_at	UST: uronyl-2-sulfotransferase	AW418882	216.81	214	-1.01	-0.81	-2.81		319.72	574.16	1.8	1.68	254.44	*
210129_s_at	TTLL3: tubulin tyrosine ligase-like family, member 3	AF078842	253.32	366.95	1.45	1.31	113.63		136.48	245.54	1.8	1.59	109.06	*
238841_at	PTPDC1: protein tyrosine phosphatase domain containing 1	AA651920	512.29	411.52	-1.24	-1.15	-100.77		192.89	346.38	1.8	1.53	153.49	*
210609_s_at	TP53I3: tumor protein p53 inducible protein 3	BC000474	1786.13	1753.33	-1.02	-0.94	-32.81		1991.07	3558.59	1.79	1.69	1567.52	*
215913_s_at	GULP1: GULP, engulfment adaptor PTB domain containing 1	AK023668	678.42	852.33	1.26	1.18	173.92		290.68	520.19	1.79	1.62	229.51	*
227647_at	KCNE3: potassium voltage-gated channel, Isk-related family, member 3	AI692703	136.51	146.67	1.07	0.86	10.16		147.94	264.8	1.79	1.61	116.86	*
231848_x_at	ZNF207: zinc finger protein 207	AW192569	1763.15	1455.62	-1.21	-1.16	-307.53		454.06	814.2	1.79	1.55	360.14	*
201449_at	TIA1: TIA1 cytotoxic granule-associated RNA binding protein	AL567227	552.49	694.33	1.26	1.18	141.83		273.02	487.34	1.78	1.59	214.32	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
203146_s_at	GABBR1: gamma-aminobutyric acid (GABA) B receptor, 1	NM_001470	771.9	704.73	-1.1	-0.99	-67.18		311.58	555.01	1.78	1.51	243.43	*
204813_at	MAPK10: mitogen-activated protein kinase 10	NM_002753	331.45	385.78	1.16	1.06	54.32		399.02	708.5	1.78	1.63	309.48	*
207030_s_at	CSRP2: cysteine and glycine-rich protein 2	NM_001321	3342.45	3147.43	-1.06	-0.99	-195.01		4135.71	7364.46	1.78	1.68	3228.75	*
211126_s_at	CSRP2: cysteine and glycine-rich protein 2	U46006	1387.55	1366.01	-1.02	-0.91	-21.54		1783.96	3182.3	1.78	1.68	1398.34	*
214016_s_at	SFPQ: splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	AL558875	1869.68	1966.71	1.05	1.01	97.03		677.2	1206.58	1.78	1.63	529.38	*
218162_at	OLFML3: olfactomedin-like 3	NM_020190	3271.35	4226.38	1.29	1.13	955.03		6245.18	11118.02	1.78	1.68	4872.83	*
242191_at	NBPF10: neuroblastoma breakpoint family, member 10	AI701905	1354.5	1059.17	-1.28	-1.21	-295.32		336.2	599.92	1.78	1.66	263.72	*
1552278_a_at	SLC46A1: solute carrier family 46 (folate transporter), member 1	NM_080669	54.72	38.7	-1.41	-0.9	-16.02		135.77	241.33	1.78	1.62	105.56	*
1555894_s_at	MTSS1L: metastasis suppressor 1-like	AA829283	171.34	176.38	1.03	0.86	5.04		252.02	448.35	1.78	1.62	196.33	*
221589_s_at	ALDH6A1: aldehyde dehydrogenase 6 family, member A1	AW612403	706.18	764.35	1.08	1	58.18		839.69	1482.13	1.77	1.65	642.45	*
41856_at	UNC5B: Unc-5 homolog B (C. elegans)	AL049370	3063.75	3202.63	1.05	1	138.88		1445.57	2555.23	1.77	1.6	1109.66	*
225380_at	SGK493: protein kinase-like protein SgK493	BF528878	126.63	109.56	-1.16	-0.92	-17.08		136.87	242.85	1.77	1.53	105.98	*
227556_at	NME7: non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	AI094580	626.32	832.78	1.33	1.21	206.46		875.61	1549.81	1.77	1.68	674.2	*
228959_at	Hs.296031.0	AI676241	335.86	382.26	1.14	0.89	46.41		554.12	980.27	1.77	1.63	426.14	*
230720_at	RNF182: ring finger protein 182	AI884906	227.81	330.09	1.45	1.27	102.28		336.41	597.01	1.77	1.63	260.6	*
231234_at	CTSC: cathepsin C	AV699565	138.66	156.01	1.13	0.97	17.35		199.07	351.43	1.77	1.61	152.36	*
235834_at	CALD1: Caldesmon 1	BF063186	2796.07	1800.15	-1.55	-1.49	-995.92		338.9	598.87	1.77	1.55	259.97	*
200879_s_at	EPAS1: endothelial PAS domain protein 1	NM_001430	1262.57	1457.87	1.15	1.09	195.3		867.92	1531.02	1.76	1.67	663.09	*
204235_s_at	GULP1: GULP, engulfment adaptor PTB domain containing 1	AF200715	1222.82	1466.54	1.2	1.14	243.73		491.89	864.81	1.76	1.63	372.92	*
37996_s_at	DMPK: dystrophia myotonica-protein kinase	L08835	461.36	401.23	-1.15	-1.01	-60.13		256.02	451.3	1.76	1.6	195.28	*
1567214_a_at	PNN: pinin, desmosome associated protein	U59479	1207.86	1427.83	1.18	1.13	219.97		561.05	986.05	1.76	1.62	425	*
1556039_s_at	GPR173: G protein-coupled receptor 173	AW150212	402.96	353.05	-1.14	-1.08	-49.92		169.7	298.73	1.76	1.54	129.03	*
201196_s_at	AMD1: adenosylmethionine decarboxylase 1	M21154	1027.37	1474.99	1.44	1.31	447.62		1421.36	2484.98	1.75	1.66	1063.62	*
210653_s_at	BCKDHB: branched chain keto acid dehydrogenase E1, beta polypeptide	M55575	373.84	490.31	1.31	1.19	116.47		497.09	868.62	1.75	1.63	371.52	*
221957_at	PDK3: pyruvate dehydrogenase kinase, isozyme 3	BF939522	108.65	127.46	1.17	0.91	18.82		178.28	312.43	1.75	1.58	134.15	*
202963_at	RFX5: regulatory factor X, 5 (influences HLA class II expression)	AW027312	814.88	949.51	1.17	1.09	134.63		956.34	1661.89	1.74	1.65	705.55	*
212177_at	SFRS18: splicing factor, arginine/serine-rich 18	AW081113	3084.76	3276.82	1.06	1.04	192.07		1096.23	1902.65	1.74	1.65	806.42	*
213046_at	PABPN1: poly(A) binding protein, nuclear 1	AI130920	1143.63	1045.85	-1.09	-1.04	-97.77		411.75	715.06	1.74	1.61	303.31	*
213998_s_at	DDX17: DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	AW188131	2336.46	2642.83	1.13	1.09	306.38		478.26	833.19	1.74	1.59	354.93	*
49306_at	RASSF4: Ras association (RalGDS/AF-6) domain family member 4	AI890191	185.63	167.44	-1.11	-1.01	-18.19		196.18	342.1	1.74	1.58	145.92	*
231726_at	PCDHB14: protocadherin beta 14	NM_018934	233.62	308.83	1.32	1.09	75.21		338.3	590.33	1.74	1.62	252.03	*
201295_s_at	WSB1: WD repeat and SOCS box-containing 1	BF111821	1693.71	1912.26	1.13	1.08	218.55		551.99	955.69	1.73	1.56	403.7	*
205876_at	LIFR: leukemia inhibitory factor receptor alpha	NM_002310	119.66	153.26	1.28	1.07	33.6		148.96	258.03	1.73	1.54	109.07	*
209948_at	KCNMB1: potassium large conductance calcium-activated channel, subfamily M, beta member 1	U61536	345.03	347.45	1.01	0.79	2.42		829.44	1435.65	1.73	1.62	606.21	*
214748_at	N4BP2L2: NEDD4 binding protein 2-like 2	U50529	1150.74	991.89	-1.16	-1.11	-158.85		356.41	618.32	1.73	1.62	261.91	*
219978_s_at	NUSAP1: nucleolar and spindle associated protein 1	NM_018454	31.65	26.66	-1.19	-0.48	-4.99		212.56	366.68	1.73	1.58	154.12	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
224477_s_at	NUDT16L1: nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	BC006223	587.31	771.25	1.31	1.23	183.94		732.8	1267.85	1.73	1.65	535.05	*
204237_at	GULP1: GULP, engulfment adaptor PTB domain containing 1	NM_016315	1589.59	2081.1	1.31	1.25	491.51		675.73	1159.67	1.72	1.62	483.94	*
204773_at	IL11RA: interleukin 11 receptor, alpha	NM_004512	1009.11	1430.71	1.42	1.37	421.6		1623.61	2791.73	1.72	1.64	1168.12	*
219627_at	ZNF767: zinc finger family member 767	NM_024910	450.89	480.89	1.07	0.99	30		193.12	332.4	1.72	1.51	139.28	*
225178_at	TTC14: tetratricopeptide repeat domain 14	W73788	1252.58	1151.7	-1.09	-0.99	-100.88		512.94	882.16	1.72	1.57	369.22	*
229487_at	EBF1: early B-cell factor 1	W73890	551.6	903.39	1.64	1.49	351.79		917.69	1582.17	1.72	1.63	664.48	*
231881_at	CALD1: caldesmon 1	AU145225	1634.86	1295.07	-1.26	-1.2	-339.79		189.02	325.18	1.72	1.51	136.16	*
234675_x_at	Hs.306914.0	AK027219	1331.97	1364.23	1.02	0.97	32.26		566.99	977.67	1.72	1.62	410.68	*
1566989_at	ARID1B: AT rich interactive domain 1B (SWI1-like)	Y08266	733.31	1142.72	1.56	1.49	409.4		424.96	731.63	1.72	1.62	306.66	*
206102_at	GINS1: GINS complex subunit 1 (Psf1 homolog)	NM_021067	63.77	78.58	1.23	0.95	14.81		209.57	359.03	1.71	1.56	149.45	*
211062_s_at	CPZ: carboxypeptidase Z	BC006393	441.51	326.41	-1.35	-1.19	-115.1		557.7	951.97	1.71	1.6	394.27	*
214850_at	LOC100170939: glucuronidase, beta pseudogene	X75940	548.84	574.18	1.05	0.98	25.34		169.21	288.66	1.71	1.55	119.45	*
219239_s_at	ZNF654: zinc finger protein 654	NM_018293	678.79	840.16	1.24	1.18	161.37		358.91	613.14	1.71	1.56	254.22	*
227226_at	MRAP2: melanocortin 2 receptor accessory protein 2	AA418816	47.1	87.4	1.86	1.18	40.29		199.65	341.91	1.71	1.58	142.26	*
1552287_s_at	AFG3L1: AFG3 ATPase family gene 3-like 1 (S. cerevisiae)	NM_001132	696.29	613.91	-1.13	-1.08	-82.38		259.96	444.43	1.71	1.54	184.47	*
1569150_x_at	PDLIM7: PDZ and LIM domain 7 (enigma)	BC023629	766.53	489.8	-1.57	-1.44	-276.74		186.19	317.46	1.71	1.55	131.28	*
228703_at	P4HA3: prolyl 4-hydroxylase, alpha polypeptide III	AW665086	412.64	577.27	1.4	1.23	164.63		797.17	1355.98	1.7	1.62	558.8	*
232125_at	Hs.202577.0	AU147419	525.84	481.37	-1.09	-1.03	-44.47		210.7	358.59	1.7	1.53	147.88	*
1556564_at	HHIPL1: HHIP-like 1	AK095603	80.83	93.35	1.15	0.85	12.51		203.6	346.17	1.7	1.53	142.57	*
205909_at	POLE2: polymerase (DNA directed), epsilon 2 (p59 subunit)	NM_002692	82.33	157.8	1.92	1.45	75.47		234.81	396.06	1.69	1.56	161.26	*
206993_at	ATP5S: ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	NM_015684	191.03	235.22	1.23	1.08	44.19		243.17	411.67	1.69	1.56	168.5	*
220602_s_at	LOC388152 /// LOC727751 /// LOC727849 /// LOC80154: hypothetical LOC388152 /// hypothetical LOC727751 /// similar to cis-Golgi matrix protein GM130 /// hypothetical LOC80154	NM_025084	563.61	601.66	1.07	1.01	38.05		212.53	359.94	1.69	1.51	147.4	*
227444_at	ARMCX4: Armadillo repeat containing, X-linked 4	AW519141	526.92	644.34	1.22	1.11	117.42		1026.15	1734.66	1.69	1.64	708.5	*
227752_at	SPTLC3: serine palmitoyltransferase, long chain base subunit 3	AA005105	171.27	190.72	1.11	0.98	19.45		348.01	586.89	1.69	1.64	238.88	*
229271_x_at	COL11A1: collagen, type XI, alpha 1	BG028597	584.62	689.75	1.18	1.08	105.13		722.31	1218.18	1.69	1.57	495.87	*
234135_x_at	Hs.306609.0	AK021652	1744.13	1270.5	-1.37	-1.32	-473.63		323.61	548.37	1.69	1.54	224.76	*
206059_at	ZNF91: zinc finger protein 91	NM_003430	913.25	745.21	-1.23	-1.14	-168.03		352.68	593.49	1.68	1.5	240.81	*
210559_s_at	CDC2: cell division cycle 2, G1 to S and G2 to M	D88357	91.69	78.64	-1.17	-0.88	-13.05		401.41	670.3	1.67	1.57	268.89	*
212686_at	PPM1H: protein phosphatase 1H (PP2C domain containing)	AB032983	556.22	551.33	-1.01	-0.92	-4.9		847.87	1419.85	1.67	1.6	571.98	*
216860_s_at	GDF11: growth differentiation factor 11	AF028333	422.26	404.65	-1.04	-0.94	-17.61		635.18	1061.82	1.67	1.58	426.64	*
226507_at	PAK1: p21 protein (Cdc42/Rac)-activated kinase 1	AU154408	479.94	432.12	-1.11	-0.99	-47.82		580.47	967.17	1.67	1.51	386.7	*
242300_at	Hs.104580.0	BF432276	351.66	412.11	1.17	1.05	60.45		517.61	865.08	1.67	1.57	347.47	*
1552737_s_at	WWP2: WW domain containing E3 ubiquitin protein ligase 2	NM_007014	147.5	107.3	-1.37	-1.18	-40.2		196.79	329.06	1.67	1.53	132.27	*
201896_s_at	PSRC1: proline/serine-rich coiled-coil 1	BC001425	184.07	202.22	1.1	0.96	18.15		239.95	398.99	1.66	1.58	159.04	*
202107_s_at	MCM2: minichromosome maintenance complex component 2	NM_004526	180.81	173.74	-1.04	-0.87	-7.06		274.52	452.18	1.65	1.51	177.66	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
212151_at	PBX1: pre-B-cell leukemia homeobox 1	BF967998	500.34	647.74	1.29	1.17	147.4		644.73	1063.36	1.65	1.53	418.63	*
238955_at	RFTN2: raftlin family member 2	BG535419	213.32	280.7	1.32	1.14	67.38		357.45	589.91	1.65	1.55	232.46	*
241698_at	RFTN2: raftlin family member 2	AI206317	378.54	549.97	1.45	1.33	171.43		574.56	950.51	1.65	1.57	375.94	*
202894_at	EPHB4: EPH receptor B4	NM_004444	537.71	622.41	1.16	1.03	84.71		721.36	1181.04	1.64	1.52	459.68	*
203744_at	HMGB3: high-mobility group box 3	NM_005342	1435.28	1162.62	-1.23	-1.18	-272.66		1448.31	2368.42	1.64	1.58	920.11	*
209615_s_at	PAK1: p21 protein (Cdc42/Rac)-activated kinase 1	U51120	169.91	162.09	-1.05	-0.9	-7.81		235.7	385.81	1.64	1.51	150.12	*
218625_at	NRN1: neuritin 1	NM_016588	1019.07	1370.05	1.34	1.25	350.98		1496.12	2451.48	1.64	1.58	955.36	*
228762_at	LFNG: LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	AW151924	984.37	721.99	-1.36	-1.23	-262.37		1406.7	2302.29	1.64	1.54	895.59	*
205884_at	ITGA4: integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	NM_000885	120.67	220.15	1.82	1.57	99.48		295.45	481.77	1.63	1.51	186.32	*
219648_at	MREG: melanoregulin	NM_018000	164.78	191.6	1.16	1.06	26.82		219.85	357.93	1.63	1.5	138.08	*
222036_s_at	MCM4: minichromosome maintenance complex component 4	AI859865	339.25	436.5	1.29	1.15	97.26		819.69	1339.74	1.63	1.56	520.05	*
228471_at	ANKRD44: ankyrin repeat domain 44	AA744636	582.82	742.65	1.27	1.2	159.83		235.26	383.1	1.63	1.51	147.84	*
225646_at	CTSC: cathepsin C	AI246687	919.28	878.11	-1.05	-1	-41.17		1335.02	2161.55	1.62	1.55	826.54	*
226287_at	CCDC34: coiled-coil domain containing 34	AI458313	589.09	633.58	1.08	0.98	44.5		861.68	1383.64	1.61	1.52	521.96	*
217714_x_at	STMN1: stathmin 1	AV756729	1081.08	1291.67	1.19	1.12	210.59		2034.05	3241.41	1.59	1.54	1207.36	*
227812_at	TNFRSF19: tumor necrosis factor receptor superfamily, member 19	BF432648	1399.78	1230.82	-1.14	-1.06	-168.96		1552.27	2470.85	1.59	1.53	918.58	*
202345_s_at	FABP5: fatty acid binding protein 5 (psoriasis-associated)	NM_001444	1991.29	1819.24	-1.09	-1.03	-172.05		3047.72	4801.51	1.58	1.52	1753.79	*
212915_at	PDZRN3: PDZ domain containing ring finger 3	AL569804	901.94	925.09	1.03	0.96	23.15		1374.69	2175.67	1.58	1.51	800.97	*

Appendix 1.4 Down-Regulated Genes in Response to 20nM BMP6

Down-Regulated Genes at Both Days in Response to 20nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
209496_at	RARRES2: retinoic acid receptor responder (tazarotene induced) 2	BC000069	1237.61	79.66	-15.54	-11.34	-1157.95	*	2392.06	37.6	-63.61	-43.56	-2354.46	*
229580_at	Hs.7413.0	R71596	251.83	9.34	-26.97	-15.05	-242.49	*	450.01	9.66	-46.57	-24.53	-440.35	*
211518_s_at	BMP4: bone morphogenetic protein 4	D30751	1146.8	111.41	-10.29	-8.03	-1035.39	*	2341.4	51.78	-45.22	-34.86	-2289.62	*
203716_s_at	DPP4: dipeptidyl-peptidase 4	M80536	862.03	33.59	-25.66	-14.8	-828.44	*	594.15	16.98	-34.99	-16.83	-577.17	*
238778_at	MPP7: membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	AI244661	282.34	53.82	-5.25	-4.32	-228.52	*	371.05	16.33	-22.72	-14.92	-354.72	*
211478_s_at	DPP4: dipeptidyl-peptidase 4	M74777	1080.68	67.61	-15.99	-13.01	-1013.07	*	736.96	47.66	-15.46	-11.88	-689.3	*
221211_s_at	C21orf7: chromosome 21 open reading frame 7	NM_020152	3537.36	372.15	-9.51	-8.62	-3165.21	*	4069.16	265.14	-15.35	-13.69	-3804.02	*
208075_s_at	CCL7: chemokine (C-C motif) ligand 7	NM_006273	456.89	19.23	-23.76	-15.74	-437.66	*	1176.14	84.17	-13.97	-11.51	-1091.97	*
230831_at	FRMD5: FERM domain containing 5	AW294986	237.68	48.01	-4.95	-3.74	-189.67	*	271.85	20.24	-13.43	-9.31	-251.6	*
204933_s_at	TNFRSF11B: tumor necrosis factor receptor superfamily, member 11b	NM_002546	11834.82	3853.99	-3.07	-2.79	-7980.83	*	9957.11	763.05	-13.05	-11.02	-9194.07	*
1553147_at	RANBP3L: RAN binding protein 3-like	NM_145000	367.28	126.79	-2.9	-2.65	-240.49	*	579.29	45.44	-12.75	-11.06	-533.85	*
228335_at	CLDN11: claudin 11	AW264204	3595.88	1565.49	-2.3	-2.15	-2030.4	*	2140.45	168.52	-12.7	-10.9	-1971.93	*
1554685_a_at	KIAA1199: KIAA1199	BC020256	2790.73	254.27	-10.98	-8.89	-2536.46	*	2697.29	217.16	-12.42	-10.13	-2480.13	*
201596_x_at	KRT18: keratin 18	NM_000224	6204.7	2567.21	-2.42	-2.32	-3637.49	*	1398.45	118.87	-11.76	-8.59	-1279.58	*
205082_s_at	AOX1: aldehyde oxidase 1	AB046692	1423.04	333.42	-4.27	-3.86	-1089.62	*	1503.32	128.07	-11.74	-9.08	-1375.24	*
1558378_a_at	AHNAK2: AHNAK nucleoprotein 2	BC004283	361.33	75.96	-4.76	-3.32	-285.37	*	372.03	32.15	-11.57	-7.03	-339.88	*
206614_at	GDF5: growth differentiation factor 5	NM_000557	623.98	46.34	-13.47	-10.19	-577.64	*	899.84	82.27	-10.94	-9.43	-817.57	*
202687_s_at	TNFSF10: tumor necrosis factor (ligand) superfamily, member 10	U57059	260	15.92	-16.33	-8.91	-244.08	*	235.18	21.57	-10.9	-5.8	-213.61	*
217767_at	C3: complement component 3	NM_000064	1329.19	505.26	-2.63	-2.4	-823.92	*	3862.5	364.22	-10.6	-9.79	-3498.28	*
238125_at	ADAMTS16: ADAM metallopeptidase with thrombospondin type 1 motif, 16	AI740544	289.34	39.72	-7.28	-5.84	-249.62	*	571.91	55.91	-10.23	-8.09	-516	*
203477_at	COL15A1: collagen, type XV, alpha 1	NM_001855	7554.48	1918.18	-3.94	-3.55	-5636.3	*	7563.92	740.17	-10.22	-9.09	-6823.75	*
233658_at	Hs.332765.0	AK022413	335.08	84.51	-3.96	-2.46	-250.57	*	120.25	12.05	-9.98	-4.02	-108.19	*
204879_at	PDPN: podoplanin	NM_006474	583.49	55.72	-10.47	-7.87	-527.77	*	611.9	61.45	-9.96	-7.18	-550.45	*
216598_s_at	CCL2: chemokine (C-C motif) ligand 2	S69738	6526.2	710.08	-9.19	-8.04	-5816.12	*	9508.03	968.35	-9.82	-8.73	-8539.68	*
221111_at	IL26: interleukin 26	NM_018402	858.35	212.32	-4.04	-3.59	-646.02	*	221.5	23.1	-9.59	-5.52	-198.4	*
203717_at	DPP4: dipeptidyl-peptidase 4	NM_001935	1993.17	180.58	-11.04	-9.49	-1812.59	*	1320.15	137.81	-9.58	-7.89	-1182.34	*
221898_at	PDPN: podoplanin	AU154455	361.63	57	-6.34	-4.99	-304.63	*	381.23	40.43	-9.43	-6.24	-340.8	*
221371_at	TNFSF18: tumor necrosis factor (ligand) superfamily, member 18	NM_005092	183.46	50.69	-3.62	-2.54	-132.78	*	306.26	34.75	-8.81	-5.65	-271.51	*
230418_s_at	GALNTL1: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	AI097463	362.54	43.55	-8.33	-5.64	-318.99	*	1722.56	207.49	-8.3	-6.95	-1515.07	*
205083_at	AOX1: aldehyde oxidase 1	NM_001159	2164.96	602.34	-3.59	-3.22	-1562.62	*	2045.68	264.01	-7.75	-6.66	-1781.67	*
206969_at	KRT34: keratin 34	NM_021013	1346.17	783.18	-1.72	-1.56	-562.99	*	1347.42	178.18	-7.56	-5.92	-1169.24	*
201743_at	CD14: CD14 molecule	NM_000591	1108.63	371.54	-2.98	-2.78	-737.1	*	957.85	127.46	-7.52	-6.08	-830.39	*
223623_at	C2orf40: chromosome 2 open reading frame 40	AF325503	148.72	38.48	-3.87	-2.78	-110.24	*	1053.96	140.24	-7.52	-6.79	-913.72	*
228780_at	Hs.47448.0	AW149422	493.18	85.05	-5.8	-4.56	-408.13	*	351.22	47.7	-7.36	-4.8	-303.52	*
212942_s_at	KIAA1199: KIAA1199	AB033025	9762.9	1642.97	-5.94	-4.84	-8119.93	*	9713.01	1319.98	-7.36	-6.17	-8393.03	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
210471_s_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	U33428	1140.47	334.08	-3.41	-3.17	-806.39	*	1236.37	169.28	-7.3	-6.31	-1067.09	*
202912_at	ADM: adrenomedullin	NM_001124	3820.54	920.9	-4.15	-3.97	-2899.64	*	2165.9	299.35	-7.24	-6.54	-1866.55	*
230417_at	GALNTL1: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	AI097463	266.35	54.6	-4.88	-3.43	-211.75	*	1116.17	155.49	-7.18	-5.73	-960.68	*
230121_at	C1orf133: chromosome 1 open reading frame 133	BF508679	281.99	92.07	-3.06	-2.44	-189.92	*	868.4	122.2	-7.11	-5.91	-746.2	*
206932_at	CH25H: cholesterol 25-hydroxylase	NM_003956	455.9	139.32	-3.27	-2.54	-316.58	*	775.71	109.04	-7.11	-5.74	-666.67	*
210106_at	RDH5: retinol dehydrogenase 5 (11-cis/9-cis)	U43559	994.3	264.97	-3.75	-3.02	-729.33	*	2048.18	289	-7.09	-5.97	-1759.18	*
205302_at	IGFBP1: insulin-like growth factor binding protein 1	NM_000596	831.51	110.02	-7.56	-6.39	-721.5	*	180.98	25.68	-7.05	-4.94	-155.3	*
220639_at	TM4SF20: transmembrane 4 L six family member 20	NM_024795	245.96	43.13	-5.7	-3.48	-202.83	*	254.19	36.54	-6.96	-4.36	-217.65	*
209850_s_at	CDC42EP2: CDC42 effector protein (Rho GTPase binding) 2	BC005406	376.89	113.54	-3.32	-2.47	-263.36	*	363.85	53.35	-6.82	-4.56	-310.5	*
215020_at	NRXN3: neurexin 3	AF123462	515.31	132.32	-3.89	-3.21	-382.99	*	394.15	58.54	-6.73	-4.81	-335.61	*
212992_at	AHNAK2: AHNAK nucleoprotein 2	AI935123	869.46	182.11	-4.77	-4.11	-687.36	*	1800.36	273.35	-6.59	-6.05	-1527.01	*
210121_at	B3GALT2: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	AF288390	825.45	214.31	-3.85	-3.4	-611.14	*	467.94	72.21	-6.48	-5.21	-395.73	*
229566_at	LOC645638: similar to WDNM1-like protein	AA149250	2651.94	1123.95	-2.36	-2.18	-1527.99	*	4232.46	661.72	-6.4	-5.75	-3570.74	*
201042_at	TGM2: transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	AL031651	3254.33	1514.66	-2.15	-1.95	-1739.67	*	1020.09	161.57	-6.31	-4.4	-858.53	*
244280_at	Hs.103070.0	W46364	536.33	266.01	-2.02	-1.89	-270.32	*	845.08	134.7	-6.27	-5.64	-710.38	*
227749_at	Hs.15085.0	AI703496	415.25	85.01	-4.88	-3.98	-330.24	*	471.75	75.67	-6.23	-5.41	-396.08	*
230660_at	SERTAD4: SERTA domain containing 4	AU146709	254.07	91.78	-2.77	-2.26	-162.29	*	625.34	101.78	-6.14	-5.25	-523.56	*
204932_at	TNFRSF11B: tumor necrosis factor receptor superfamily, member 11b	BF433902	10329.04	6030.78	-1.71	-1.62	-4298.26	*	10241.18	1701.96	-6.02	-5.44	-8539.21	*
218451_at	CDCP1: CUB domain containing protein 1	NM_022842	813.62	242.72	-3.35	-3	-570.9	*	496.73	82.5	-6.02	-4.85	-414.23	*
207375_s_at	IL15RA: interleukin 15 receptor, alpha	NM_002189	206.74	83.54	-2.47	-1.81	-123.21	*	176.74	29.43	-6.01	-3.84	-147.31	*
210078_s_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	L39833	2036.38	698.15	-2.92	-2.69	-1338.23	*	2163.88	366.31	-5.91	-5.43	-1797.57	*
1558847_at	Hs2.353773.1	BQ576193	453.93	229.95	-1.97	-1.74	-223.98	*	521.25	89.79	-5.81	-4.55	-431.46	*
229674_at	SERTAD4: SERTA domain containing 4	AL035414	615	222.9	-2.76	-2.51	-392.1	*	1257.43	219.04	-5.74	-5.24	-1038.39	*
202668_at	EFNB2: ephrin-B2	BF001670	1104.13	292.92	-3.77	-3.15	-811.21	*	1267.82	221.98	-5.71	-4.73	-1045.85	*
209546_s_at	APOL1: apolipoprotein L, 1	AF323540	1098.35	654.83	-1.68	-1.57	-443.52	*	1014.75	179.53	-5.65	-4.75	-835.23	*
217452_s_at	B3GALT2: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	Y15014	855.57	238.58	-3.59	-3.39	-617	*	561.58	101.87	-5.51	-4.77	-459.71	*
206702_at	TEK: TEK tyrosine kinase, endothelial	NM_000459	841.23	395.68	-2.13	-2	-445.55	*	965.17	176.33	-5.47	-4.98	-788.84	*
229121_at	CMKLR1: chemokine-like receptor 1	BE857553	1724.64	249.66	-6.91	-6.42	-1474.98	*	2407.61	443.01	-5.43	-5.14	-1964.6	*
1556427_s_at	LRRN4CL: LRRN4 C-terminal like	AL834319	646.3	177.04	-3.65	-3.02	-469.26	*	1444.87	266.54	-5.42	-4.91	-1178.33	*
205249_at	EGR2: early growth response 2	NM_000399	1436.25	213.91	-6.71	-6.18	-1222.34	*	754.08	139.58	-5.4	-4.47	-614.5	*
222717_at	SDPR: serum deprivation response (phosphatidylserine binding protein)	BF982174	324.34	97.75	-3.32	-2.91	-226.59	*	554.72	104.38	-5.31	-4.83	-450.34	*
202986_at	ARNT2: aryl-hydrocarbon receptor nuclear translocator 2	NM_014862	975.41	200.85	-4.86	-4.42	-774.56	*	1128.23	213.45	-5.29	-4.85	-914.77	*
221029_s_at	WNT5B: wingless-type MMTV integration site family, member 5B	NM_030775	2437.24	843.07	-2.89	-2.65	-1594.17	*	2587.77	496.62	-5.21	-4.58	-2091.15	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
209781_s_at	KHDRBS3: KH domain containing, RNA binding, signal transduction associated 3	AF069681	538.19	310.3	-1.73	-1.6	-227.89	*	644.12	127.17	-5.07	-4.58	-516.95	*
205767_at	EREG: epiregulin	NM_001432	339.83	60.81	-5.59	-4.29	-279.02	*	145.93	28.76	-5.07	-3.63	-117.16	*
230112_at	MARCH4: membrane-associated ring finger (C3HC4) 4	AB037820	751.19	341.07	-2.2	-1.9	-410.12	*	599.26	119.69	-5.01	-3.79	-479.56	*
235337_at	Hs.88143.0	AI276403	384.64	220.32	-1.75	-1.66	-164.32	*	926.96	185.6	-4.99	-4.46	-741.36	*
232102_at	METTL6: methyltransferase like 6	AK027185	168.9	62.91	-2.68	-1.57	-105.98	*	194.61	39.08	-4.98	-2.84	-155.52	*
210818_s_at	BACH1: BTB and CNC homology 1, basic leucine zipper transcription factor 1	AF026199	420.85	144.34	-2.92	-2.56	-276.51	*	367.17	74.46	-4.93	-3.67	-292.71	*
209369_at	ANXA3: annexin A3	M63310	446.68	83.99	-5.32	-4.49	-362.69	*	351.36	72.32	-4.86	-4.28	-279.03	*
223734_at	C4orf49: chromosome 4 open reading frame 49	AF329088	2792.35	866.11	-3.22	-3.02	-1926.23	*	2298.97	478.89	-4.8	-4.34	-1820.08	*
207571_x_at	C1orf38: chromosome 1 open reading frame 38	NM_004848	274.23	89.67	-3.06	-2.49	-184.56	*	221.58	46.32	-4.78	-3.43	-175.26	*
206298_at	ARHGAP22: Rho GTPase activating protein 22	NM_021226	2097.45	587.83	-3.57	-3.08	-1509.62	*	2260.85	488.44	-4.63	-4.18	-1772.41	*
208161_s_at	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_020037	1046.81	394.33	-2.65	-2.53	-652.48	*	360.44	78.33	-4.6	-3.53	-282.11	*
238462_at	UBASH3B: ubiquitin associated and SH3 domain containing, B	AI418293	1195.56	649.56	-1.84	-1.72	-545.99	*	931.37	204.51	-4.55	-4	-726.87	*
207652_s_at	CMKLR1: chemokine-like receptor 1	NM_004072	327.19	53.56	-6.11	-4.65	-273.63	*	377.8	83.66	-4.52	-3.57	-294.14	*
52651_at	COL8A2: collagen, type VIII, alpha 2	AI806793	2615.48	603.73	-4.33	-3.89	-2011.76	*	4004.32	893.47	-4.48	-4.2	-3110.85	*
210571_s_at	CMAH: cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	AF074480	2436.58	1408.58	-1.73	-1.66	-1028	*	1260.02	281.59	-4.47	-3.94	-978.43	*
233485_at	Hs.210297.0	AK001128	186.99	56.22	-3.33	-2.68	-130.77	*	224.76	50.29	-4.47	-3.69	-174.47	*
201474_s_at	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	NM_002204	2766.77	1526.91	-1.81	-1.7	-1239.86	*	2372.44	532.27	-4.46	-4.11	-1840.17	*
202357_s_at	C2 /// CFB: complement component 2 /// complement factor B	NM_001710	2481.06	1102.42	-2.25	-2.03	-1378.64	*	3065.45	688.7	-4.45	-3.86	-2376.75	*
230090_at	LOC100287032: similar to hCG2006445	AW296078	1573.44	473.58	-3.32	-3.02	-1099.86	*	891.08	201.85	-4.41	-3.82	-689.23	*
205795_at	NRXN3: neurexin 3	NM_004796	1423.89	410.7	-3.47	-2.99	-1013.19	*	1047.15	240.76	-4.35	-3.52	-806.39	*
227051_at	Hs.43047.0	AU157716	4069.64	1005.7	-4.05	-3.67	-3063.94	*	3666.04	845.59	-4.34	-4.02	-2820.46	*
203910_at	ARHGAP29: Rho GTPase activating protein 29	NM_004815	850.78	307.54	-2.77	-2.52	-543.24	*	1821.81	426.8	-4.27	-4.06	-1395.01	*
211596_s_at	LRIG1: leucine-rich repeats and immunoglobulin-like domains 1	AB050468	871.29	193.1	-4.51	-4.17	-678.19	*	1219.34	285.53	-4.27	-3.98	-933.82	*
232122_s_at	VEPH1: ventricular zone expressed PH domain homolog 1 (zebrafish)	AK022666	1618.47	852.1	-1.9	-1.8	-766.38	*	978.64	230.93	-4.24	-3.64	-747.72	*
223537_s_at	WNT5B: wingless-type MMTV integration site family, member 5B	AW007350	522.13	179.15	-2.91	-2.49	-342.98	*	504.73	119.26	-4.23	-3.58	-385.47	*
231986_at	RIMS1: regulating synaptic membrane exocytosis 1	AL035633	706.22	367.44	-1.92	-1.74	-338.78	*	699.77	166.9	-4.19	-3.6	-532.86	*
204803_s_at	RRAD: Ras-related associated with diabetes	NM_004165	1245.47	271.14	-4.59	-4.21	-974.33	*	512.85	122.35	-4.19	-3.55	-390.5	*
227340_s_at	RGMB: RGM domain family, member B	AL117590	1832.37	1094.37	-1.67	-1.53	-738	*	2242	541.07	-4.14	-3.7	-1700.93	*
214319_at	FRY: furry homolog (Drosophila)	W58342	178.96	42.84	-4.18	-3.09	-136.12	*	200.11	48.34	-4.14	-3.15	-151.77	*
220049_s_at	PDCD1LG2: programmed cell death 1 ligand 2	NM_025239	349.43	175.66	-1.99	-1.79	-173.77	*	423.57	103.1	-4.11	-3.3	-320.47	*
208608_s_at	SNTB1: syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	NM_021021	267.13	123.89	-2.16	-2.01	-143.24	*	167.32	40.74	-4.11	-2.76	-126.59	*
204326_x_at	MT1X: metallothionein 1X	NM_002450	1515	594.57	-2.55	-2.37	-920.43	*	1439.75	352.66	-4.08	-3.33	-1087.08	*
225817_at	CGNL1: cingulin-like 1	AB051536	540.05	225.05	-2.4	-2.04	-315	*	1757.89	432.35	-4.07	-3.65	-1325.54	*
211668_s_at	PLAU: plasminogen activator, urokinase	K03226	2565.63	763.85	-3.36	-3.05	-1801.77	*	4823.09	1198.33	-4.02	-3.83	-3624.76	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
204224_s_at	GCH1: GTP cyclohydrolase 1	NM_000161	765.75	343.24	-2.23	-2.04	-422.51	*	305.87	77.14	-3.97	-3.22	-228.73	*
214797_s_at	PCTK3: PCTAIRE protein kinase 3	BC000281	228.64	79.91	-2.86	-2.58	-148.73	*	221.35	55.71	-3.97	-3.33	-165.64	*
238587_at	UBASH3B: ubiquitin associated and SH3 domain containing, B	AI927919	774.99	279.75	-2.77	-2.5	-495.24	*	497.17	125.41	-3.96	-3.2	-371.75	*
209212_s_at	KLF5: Kruppel-like factor 5 (intestinal)	AB030824	717.43	217.08	-3.3	-2.88	-500.35	*	564.46	143.41	-3.94	-3.53	-421.05	*
212938_at	COL6A1: collagen, type VI, alpha 1	M20776	2389.64	719.71	-3.32	-3.03	-1669.93	*	3658.28	927.46	-3.94	-3.72	-2730.82	*
227339_at	RGMB: RGM domain family, member B	BE206621	1263.93	735.11	-1.72	-1.62	-528.82	*	1417.59	363.88	-3.9	-3.39	-1053.71	*
219602_s_at	FAM38B: family with sequence similarity 38, member B	NM_022068	870.99	297.25	-2.93	-2.69	-573.74	*	672.04	173.13	-3.88	-3.57	-498.91	*
210659_at	CMKLR1: chemokine-like receptor 1	U79526	240.79	50.37	-4.78	-3.41	-190.43	*	301.9	78.2	-3.86	-2.81	-223.7	*
210261_at	KCNK2: potassium channel, subfamily K, member 2	AF004711	1412.66	355.6	-3.97	-3.59	-1057.06	*	2664.52	705.63	-3.78	-3.51	-1958.89	*
212940_at	COL6A1: collagen, type VI, alpha 1	BE350145	1678.3	742.41	-2.26	-2.07	-935.88	*	2977.34	789.62	-3.77	-3.45	-2187.71	*
239582_at	PML: promyelocytic leukemia	AW514654	360.92	140.55	-2.57	-2.16	-220.37	*	358.33	95.93	-3.74	-3.04	-262.39	*
1553142_at	C13orf31: chromosome 13 open reading frame 31	NM_153218	829.9	233.76	-3.55	-3.17	-596.14	*	401.64	108.88	-3.69	-3.22	-292.76	*
210079_x_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	U16953	415.67	155.36	-2.68	-2.36	-260.31	*	384.32	104.49	-3.68	-3.03	-279.82	*
204105_s_at	NRCAM: neuronal cell adhesion molecule	NM_005010	217.81	31.47	-6.92	-5.03	-186.35	*	327.5	89.3	-3.67	-3.14	-238.2	*
209211_at	KLF5: Kruppel-like factor 5 (intestinal)	AF132818	639.86	154.93	-4.13	-3.69	-484.93	*	504.21	139.52	-3.61	-3.31	-364.69	*
208116_s_at	MAN1A1: mannosidase, alpha, class 1A, member 1	NM_005907	847.37	393.28	-2.15	-2.01	-454.09	*	2240.21	624.76	-3.59	-3.39	-1615.45	*
202688_at	TNFSF10: tumor necrosis factor (ligand) superfamily, member 10	NM_003810	428.24	88.45	-4.84	-3.55	-339.79	*	383	106.59	-3.59	-2.79	-276.41	*
227320_at	FAM101A: family with sequence similarity 101, member A	AW264333	732.28	373.8	-1.96	-1.67	-358.49	*	841.15	236.04	-3.56	-2.72	-605.11	*
1553141_at	C13orf31: chromosome 13 open reading frame 31	BC035749	902.33	189	-4.77	-4.39	-713.33	*	339.66	95.33	-3.56	-2.78	-244.33	*
213802_at	Hs.22404.1	AI810767	642.26	347.31	-1.85	-1.64	-294.94	*	780.7	221.2	-3.53	-3.16	-559.5	*
201079_at	SYNGR2: synaptogyrin 2	NM_004710	857.69	468.47	-1.83	-1.52	-389.23	*	978.3	277.59	-3.52	-3.09	-700.71	*
217995_at	SQRDL: sulfide quinone reductase-like (yeast)	NM_021199	3288.32	1889.86	-1.74	-1.64	-1398.46	*	3159.26	906.43	-3.49	-3.27	-2252.83	*
211456_x_at	MT1P2: metallothionein 1 pseudogene 2	AF333388	1857.18	848.7	-2.19	-1.98	-1008.48	*	1825.1	524.85	-3.48	-2.89	-1300.25	*
204881_s_at	UGCG: UDP-glucose ceramide glucosyltransferase	NM_003358	5285.88	3316.86	-1.59	-1.53	-1969.03	*	2817.05	812.29	-3.47	-3.27	-2004.76	*
212937_s_at	COL6A1: collagen, type VI, alpha 1	M20776	4046.19	1342.86	-3.01	-2.65	-2703.33	*	5805.38	1692.43	-3.43	-3.15	-4112.95	*
226989_at	RGMB: RGM domain family, member B	BE855765	3623.21	2149.03	-1.69	-1.6	-1474.18	*	3898.31	1138.86	-3.42	-3.07	-2759.45	*
205479_s_at	PLAU: plasminogen activator, urokinase	NM_002658	3162.35	1059.11	-2.99	-2.67	-2103.25	*	5446.96	1594.88	-3.42	-3.18	-3852.08	*
227607_at	STAMBPL1: STAM binding protein-like 1	AI638611	646.6	360.06	-1.8	-1.63	-286.53	*	636.6	188.41	-3.38	-3.04	-448.18	*
205515_at	PRSS12: protease, serine, 12 (neurotrypsin, motopsin)	NM_003619	347.02	163.41	-2.12	-1.84	-183.6	*	481.25	142.54	-3.38	-2.77	-338.7	*
228635_at	PCDH10: protocadherin 10	AI640307	1313	775.8	-1.69	-1.59	-537.19	*	947.89	282.48	-3.36	-3.14	-665.41	*
208581_x_at	MT1X: metallothionein 1X	NM_005952	2078	890.07	-2.33	-2.1	-1187.93	*	1935.53	577.85	-3.35	-2.86	-1357.69	*
201650_at	KRT19: keratin 19	NM_002276	585.36	354.69	-1.65	-1.51	-230.67	*	986.96	296.62	-3.33	-3.12	-690.34	*
206914_at	CRTAM: cytotoxic and regulatory T cell molecule	NM_019604	262.93	87.49	-3.01	-2.52	-175.44	*	185.15	56.26	-3.29	-2.59	-128.89	*
213338_at	TMEM158: transmembrane protein 158	BF062629	3390.81	1129.74	-3	-2.67	-2261.07	*	3447.02	1064.6	-3.24	-2.89	-2382.42	*
225868_at	TRIM47: tripartite motif-containing 47	AW249467	845.81	460.69	-1.84	-1.66	-385.13	*	1616.93	504.09	-3.21	-2.94	-1112.84	*
229649_at	NRXN3: neurexin 3	AI129949	1844.57	662.68	-2.78	-2.54	-1181.9	*	1656.23	516.12	-3.21	-2.84	-1140.11	*
204802_at	RRAD: Ras-related associated with diabetes	NM_004165	833.96	189.26	-4.41	-3.74	-644.7	*	334.38	104.04	-3.21	-2.72	-230.34	*
210785_s_at	C1orf38: chromosome 1 open reading frame 38	AB035482	313.87	111.29	-2.82	-2.21	-202.57	*	246.28	77.29	-3.19	-2.59	-168.99	*
205832_at	CPA4: carboxypeptidase A4	NM_016352	787.94	449.2	-1.75	-1.62	-338.74	*	451.8	142.3	-3.17	-2.4	-309.5	*
228937_at	C13orf31: chromosome 13 open reading frame 31	AI659800	3092.13	917.02	-3.37	-3.15	-2175.11	*	1487.46	470.07	-3.16	-2.86	-1017.39	*
227145_at	LOXL4: lysyl oxidase-like 4	AW190565	4331.77	991.41	-4.37	-4.06	-3340.36	*	3297.9	1042.51	-3.16	-2.73	-2255.39	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
1558105_a_at	Hs2.91389.1	AK096921	1348.78	798.47	-1.69	-1.55	-550.31	*	981.6	312.79	-3.14	-2.9	-668.81	*
208078_s_at	SIK1: salt-inducible kinase 1	NM_030751	665.83	312.25	-2.13	-1.99	-353.57	*	279.82	89.82	-3.12	-2.48	-190	*
214708_at	SNTB1: syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	BG484314	361.04	165.63	-2.18	-1.91	-195.4	*	229.81	73.81	-3.11	-2.63	-156	*
206432_at	HAS2: hyaluronan synthase 2	NM_005328	3026.97	823.02	-3.68	-3.45	-2203.95	*	3262.97	1050.96	-3.1	-2.87	-2212	*
222908_at	FAM38B: family with sequence similarity 38, member B	AW269818	357.57	167.47	-2.14	-1.77	-190.1	*	356.48	115.43	-3.09	-2.42	-241.06	*
212185_x_at	MT2A: metallothionein 2A	NM_005953	5496.26	2826.86	-1.94	-1.82	-2669.4	*	4912.14	1595.74	-3.08	-2.88	-3316.4	*
230372_at	HAS2: Hyaluronan synthase 2	AI374739	4185.98	1309.52	-3.2	-3.05	-2876.46	*	4613.01	1501.71	-3.07	-2.93	-3111.3	*
229759_s_at	VEPH1: ventricular zone expressed PH domain homolog 1 (zebrafish)	AA988323	3176.58	1971.02	-1.61	-1.55	-1205.56	*	1433.43	469.12	-3.06	-2.62	-964.31	*
216336_x_at	MT1E /// MT1H /// MT1M: metallothionein 1E /// metallothionein 1H /// metallothionein 1M	AL031602	826.81	384.21	-2.15	-2	-442.6	*	734.62	243.2	-3.02	-2.58	-491.43	*
1566402_at	SNORA68: small nucleolar RNA, H/ACA box 68	Y11162	338.79	171.54	-1.98	-1.71	-167.25	*	567.36	189.95	-2.99	-2.62	-377.42	*
205266_at	LIF: leukemia inhibitory factor (cholinergic differentiation factor)	NM_002309	1044.1	409.6	-2.55	-2.32	-634.5	*	643.32	217.45	-2.96	-2.51	-425.87	*
212543_at	AIM1: absent in melanoma 1	U83115	799.35	263.03	-3.04	-2.78	-536.32	*	1063.09	359.35	-2.96	-2.71	-703.75	*
228910_at	Hs.164261.0	AI870617	543.96	309.1	-1.76	-1.56	-234.86	*	1003.1	341.39	-2.94	-2.66	-661.71	*
212472_at	MICAL2: microtubule associated monoxygenase, calponin and LIM domain containing 2	BE965029	6217.17	3274.91	-1.9	-1.8	-2942.26	*	4655	1584.81	-2.94	-2.73	-3070.19	*
239468_at	MKX: mohawk homeobox	AW023227	314.38	154.96	-2.03	-1.74	-159.42	*	342.88	116.73	-2.94	-2.58	-226.15	*
203828_s_at	IL32: interleukin 32	NM_004221	386.01	80.06	-4.82	-3.74	-305.95	*	1002.01	340.89	-2.94	-2.65	-661.12	*
206275_s_at	MICAL2: microtubule associated monoxygenase, calponin and LIM domain containing 2	NM_014632	452.92	258.65	-1.75	-1.57	-194.27	*	389.84	133.25	-2.93	-2.44	-256.6	*
212859_x_at	MT1E: metallothionein 1E	BF217861	1195.47	598.48	-2	-1.8	-596.99	*	1237.34	421.7	-2.93	-2.48	-815.64	*
219477_s_at	THSD1 /// THSD1P: thrombospondin, type I, domain containing 1 /// thrombospondin, type I, domain containing 1 pseudogene	NM_018676	2189.13	826.02	-2.65	-2.44	-1363.12	*	1827.61	624.44	-2.93	-2.6	-1203.17	*
235723_at	BNC2: basonuclin 2	AA843242	365.68	191.14	-1.91	-1.67	-174.54	*	331.83	113.45	-2.92	-2.5	-218.39	*
216184_s_at	RIMS1: regulating synaptic membrane exocytosis 1	AF263310	228.47	107.43	-2.13	-1.56	-121.03	*	221.54	75.86	-2.92	-2.31	-145.69	*
212977_at	CXCR7: chemokine (C-X-C motif) receptor 7	AI817041	396	126.19	-3.14	-2.74	-269.81	*	514.87	177.63	-2.9	-2.52	-337.23	*
217998_at	LOC100289208 /// PHLDA1: hypothetical protein LOC100289208 /// pleckstrin homology-like domain, family A, member 1	NM_007350	1203.33	494.09	-2.44	-2.18	-709.24	*	781.17	270.37	-2.89	-2.31	-510.8	*
219949_at	LRRC2: leucine rich repeat containing 2	NM_024512	244.8	125.97	-1.94	-1.58	-118.83	*	299.08	103.75	-2.88	-2.48	-195.34	*
216080_s_at	FADS3: fatty acid desaturase 3	AC004770	4472.19	2503.15	-1.79	-1.69	-1969.04	*	3362.23	1171.78	-2.87	-2.57	-2190.45	*
241902_at	MKX: mohawk homeobox	R59304	698.48	288.57	-2.42	-2.28	-409.91	*	574.35	200.33	-2.87	-2.59	-374.02	*
215021_s_at	NRXN3: neurexin 3	AF123462	480.16	176.73	-2.72	-2.52	-303.42	*	329.72	114.84	-2.87	-2.22	-214.88	*
204194_at	BACH1: BTB and CNC homology 1, basic leucine zipper transcription factor 1	NM_001186	5812.76	2951.48	-1.97	-1.82	-2861.28	*	4678.83	1635.75	-2.86	-2.62	-3043.08	*
228885_at	MAMDC2: MAM domain containing 2	AI862120	1214.75	329.1	-3.69	-3.31	-885.65	*	2010.72	703.08	-2.86	-2.67	-1307.64	*
205236_x_at	SOD3: superoxide dismutase 3, extracellular	NM_003102	431.03	188.17	-2.29	-2.01	-242.86	*	624.4	219.05	-2.85	-2.39	-405.35	*
202566_s_at	SVIL: supervillin	AF051851	1695.11	702.26	-2.41	-2.27	-992.86	*	1763.59	622.84	-2.83	-2.58	-1140.76	*
224399_at	PDCD1LG2: programmed cell death 1 ligand 2	AF329193	265.78	150.52	-1.77	-1.51	-115.26	*	343.07	121.8	-2.82	-2.25	-221.27	*
227061_at	Hs.7882.0	AI088063	10074.14	3906.38	-2.58	-2.36	-6167.76	*	9523.62	3389.13	-2.81	-2.49	-6134.49	*
233335_at	Hs.56027.0	AL117454	2258.89	1214.13	-1.86	-1.76	-1044.76	*	752.24	268.65	-2.8	-2.42	-483.58	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
218543_s_at	PARP12: poly (ADP-ribose) polymerase family, member 12	NM_022750	1033.42	518.78	-1.99	-1.89	-514.64	*	641.82	228.83	-2.8	-2.37	-412.99	*
209290_s_at	NFIB: nuclear factor I/B	BC001283	1633.32	980.94	-1.67	-1.6	-652.38	*	1424.31	510.61	-2.79	-2.59	-913.7	*
209663_s_at	ITGA7: integrin, alpha 7	AF072132	3111.9	1536.72	-2.03	-1.86	-1575.18	*	3404.53	1221.79	-2.79	-2.54	-2182.74	*
229942_at	BNC2: basonuclin 2	AW024890	933.08	420.18	-2.22	-2.09	-512.9	*	792.32	287.03	-2.76	-2.49	-505.29	*
243864_at	CCDC80: coiled-coil domain containing 80	AA994712	3767.47	1464.11	-2.57	-2.46	-2303.36	*	3193.55	1162.39	-2.75	-2.54	-2031.16	*
217999_s_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	NM_007350	1264.1	481.85	-2.62	-2.4	-782.25	*	603.93	219.83	-2.75	-2.4	-384.1	*
204072_s_at	FRY: furry homolog (Drosophila)	NM_023037	2253.45	825.1	-2.73	-2.52	-1428.35	*	2169.3	788.67	-2.75	-2.54	-1380.63	*
1555904_at	Hs2.380934.1	BM975756	481.93	114.16	-4.22	-3.73	-367.77	*	413.51	150.53	-2.75	-2.52	-262.98	*
213056_at	FRMD4B: FERM domain containing 4B	AU145019	381.54	132.99	-2.87	-2.52	-248.55	*	494.47	180.78	-2.74	-2.36	-313.69	*
210875_s_at	ZEB1: zinc finger E-box binding homeobox 1	U12170	1266.55	729.5	-1.74	-1.67	-537.05	*	1387.82	508.11	-2.73	-2.56	-879.71	*
238419_at	PHLDB2: pleckstrin homology-like domain, family B, member 2	T68150	717.48	345.65	-2.08	-1.88	-371.82	*	400.66	146.92	-2.73	-2.44	-253.73	*
236140_at	GCLM: glutamate-cysteine ligase, modifier subunit	AI753488	1742.78	810.58	-2.15	-2	-932.19	*	1445.91	533.01	-2.71	-2.33	-912.9	*
217867_x_at	BACE2: beta-site APP-cleaving enzyme 2	NM_012105	4937.66	2239.99	-2.2	-2.04	-2697.67	*	5254.31	1942.25	-2.71	-2.46	-3312.06	*
206825_at	OXTR: oxytocin receptor	NM_000916	1008.41	540.02	-1.87	-1.71	-468.39	*	1193.06	442.14	-2.7	-2.55	-750.93	*
227606_s_at	STAMBPL1: STAM binding protein-like 1	AI638611	329.9	164.18	-2.01	-1.88	-165.73	*	366.59	136.29	-2.69	-2.36	-230.3	*
225722_at	Hs.95734.0	BF246937	756.06	352.14	-2.15	-1.97	-403.92	*	780.99	291.76	-2.68	-2.43	-489.23	*
212091_s_at	COL6A1: collagen, type VI, alpha 1	AI141603	7863.1	3578.32	-2.2	-2.04	-4284.78	*	9034.7	3379.59	-2.67	-2.49	-5655.11	*
209774_x_at	CXCL2: chemokine (C-X-C motif) ligand 2	M57731	290.04	141.15	-2.05	-1.71	-148.9	*	216.94	81.55	-2.66	-2.05	-135.39	*
244561_at	Hs.170481.0	BG289443	658.7	410.04	-1.61	-1.5	-248.66	*	525.27	198.37	-2.65	-2.39	-326.9	*
208213_s_at	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1	NM_003471	513.84	177	-2.9	-2.32	-336.84	*	443.12	167.56	-2.64	-2.23	-275.56	*
229307_at	ANKRD28: ankyrin repeat domain 28	N32051	1122.89	498.5	-2.25	-2.17	-624.39	*	619.75	235.23	-2.63	-2.46	-384.51	*
213006_at	CEBPD: CCAAT/enhancer binding protein (C/EBP), delta	AV655640	274.64	111.63	-2.46	-2.03	-163.01	*	176.9	67.28	-2.63	-2.19	-109.62	*
239066_at	Hs.173921.0	AW364675	1252.77	421.2	-2.97	-2.67	-831.56	*	987.66	375.18	-2.63	-2.47	-612.49	*
213906_at	MYBL1: v-myb myeloblastosis viral oncogene homolog (avian)-like 1	AW592266	914.24	410.46	-2.23	-2.01	-503.78	*	1971.77	755.55	-2.61	-2.48	-1216.21	*
209825_s_at	UCK2: uridine-cytidine kinase 2	BC002906	2452.33	998.16	-2.46	-2.29	-1454.17	*	2356.41	907.09	-2.6	-2.4	-1449.32	*
227550_at	GFRA1: GDNF family receptor alpha 1	AW242720	422.49	91.16	-4.63	-3.34	-331.33	*	755.31	292.58	-2.58	-2.38	-462.72	*
219230_at	TMEM100: transmembrane protein 100	NM_018286	145.35	441.57	3.04	2.62	296.23	*	521.07	203.67	-2.56	-2.24	-317.4	*
202286_s_at	TACSTD2: tumor-associated calcium signal transducer 2	J04152	752.47	363.4	-2.07	-1.87	-389.07	*	798.84	311.76	-2.56	-2.32	-487.09	*
1560821_at	ARHGAP22: Rho GTPase activating protein 22	BG122789	293.66	75.64	-3.88	-3.43	-218.02	*	282.54	110.92	-2.55	-2.24	-171.63	*
218802_at	CCDC109B: coiled-coil domain containing 109B	NM_017918	1408.75	626.36	-2.25	-2.05	-782.39	*	1652.7	650.92	-2.54	-2.36	-1001.77	*
221900_at	COL8A2: collagen, type VIII, alpha 2	AI806793	5773.04	2285.86	-2.53	-2.16	-3487.19	*	7206.2	2834.16	-2.54	-2.23	-4372.04	*
209789_at	CORO2B: coronin, actin binding protein, 2B	BF939649	737.49	437.56	-1.69	-1.53	-299.93	*	763.42	301.86	-2.53	-2.3	-461.56	*
220272_at	BNC2: basonuclin 2	NM_017637	985.64	491.73	-2	-1.84	-493.91	*	634.52	250.36	-2.53	-2.16	-384.16	*
202575_at	CRABP2: cellular retinoic acid binding protein 2	NM_001878	3478.06	412.41	-8.43	-7.41	-3065.65	*	9552.27	3794.31	-2.52	-2.34	-5757.96	*
213029_at	NFIB: nuclear factor I/B	BG478428	1229.34	683.13	-1.8	-1.68	-546.21	*	967.25	387.42	-2.5	-2.21	-579.83	*
230722_at	BNC2: basonuclin 2	AI377043	1663.3	726.65	-2.29	-2.12	-936.65	*	1105.17	442.6	-2.5	-2.18	-662.57	*
235542_at	TET3: tet oncogene family member 3	BF675754	525.04	271.81	-1.93	-1.79	-253.23	*	208.34	84.14	-2.48	-2.09	-124.2	*
210538_s_at	BIRC3: baculoviral IAP repeat-containing 3	U37546	351.21	108.75	-3.23	-2.75	-242.46	*	190.19	76.86	-2.47	-1.99	-113.33	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
225842_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	AK026181	2741.44	1267.62	-2.16	-2.08	-1473.82	*	1253.72	515.63	-2.43	-2.12	-738.09	*
211067_s_at	GAS7: growth arrest-specific 7	BC006454	481.95	70.15	-6.87	-6.34	-411.8	*	354.96	146.53	-2.42	-2	-208.42	*
238478_at	BNC2: basonuclin 2	H97386	1530.87	677.99	-2.26	-2.15	-852.88	*	1075.24	446.22	-2.41	-2.21	-629.02	*
223058_at	FAM107B: family with sequence similarity 107, member B	AL136885	1910.66	1058.69	-1.8	-1.68	-851.97	*	1446.07	601.54	-2.4	-2.21	-844.53	*
1555929_s_at	Hs2.145725.1	BM873997	813.47	476.84	-1.71	-1.61	-336.63	*	255.83	108.79	-2.35	-1.95	-147.05	*
205157_s_at	KRT17: keratin 17	NM_000422	447.75	242.19	-1.85	-1.58	-205.56	*	829.95	353.37	-2.35	-2.14	-476.59	*
226769_at	FIBIN: fin bud initiation factor homolog (zebrafish)	AI802391	2640.9	1028.46	-2.57	-2.31	-1612.44	*	2516.22	1069.05	-2.35	-2.2	-1447.17	*
37512_at	HSD17B6: hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	U89281	901.48	485.6	-1.86	-1.77	-415.88	*	1160.67	497.91	-2.33	-2.18	-662.76	*
203037_s_at	MTSS1: metastasis suppressor 1	NM_014751	756.03	266.77	-2.83	-2.45	-489.26	*	375	162.21	-2.31	-1.73	-212.79	*
207119_at	PRKG1: protein kinase, cGMP-dependent, type I	NM_006258	323.72	152.47	-2.12	-1.81	-171.25	*	320.74	139.21	-2.3	-2.01	-181.53	*
41037_at	TEAD4: TEA domain family member 4	U63824	320.06	149.9	-2.14	-1.86	-170.16	*	339.9	148.35	-2.29	-2.04	-191.55	*
225436_at	FAM108C1: family with sequence similarity 108, member C1	AI339710	669.17	284.78	-2.35	-2.08	-384.39	*	811.73	355.08	-2.29	-2.05	-456.64	*
205376_at	INPP4B: inositol polyphosphate-4-phosphatase, type II, 105kDa	NM_003866	335.28	167.32	-2	-1.82	-167.96	*	396.68	174.08	-2.28	-1.98	-222.6	*
218815_s_at	TMEM51: transmembrane protein 51	NM_018022	326.89	134.87	-2.42	-2.12	-192.03	*	421.37	184.59	-2.28	-2.16	-236.78	*
203185_at	RASSF2: Ras association (RalGDS/AF-6) domain family member 2	NM_014737	222.11	81.05	-2.74	-1.97	-141.07	*	390.57	171.81	-2.27	-1.96	-218.75	*
212236_x_at	KRT17: keratin 17	Z19574	1127.46	492.17	-2.29	-1.86	-635.29	*	1796.99	795.7	-2.26	-2.05	-1001.29	*
203896_s_at	PLCB4: phospholipase C, beta 4	NM_000933	2471.9	1401.33	-1.76	-1.67	-1070.57	*	1663.57	743.22	-2.24	-2.09	-920.35	*
225387_at	TSPAN5: tetraspanin 5	AA059445	2098.88	844.71	-2.48	-2.31	-1254.17	*	1946.43	867.92	-2.24	-2.09	-1078.52	*
236599_at	Hs.38449.0	AA703280	3082.91	687.4	-4.48	-4.05	-2395.51	*	388.21	173.61	-2.24	-1.72	-214.61	*
213071_at	DPT: dermatopontin	AL049798	212.36	40.61	-5.23	-2.92	-171.76	*	1817.27	813.81	-2.23	-2.12	-1003.46	*
239909_at	ADAMTSL1: ADAMTS-like 1	AI937348	602.27	319.92	-1.88	-1.75	-282.36	*	481.34	217.1	-2.22	-1.97	-264.24	*
215223_s_at	SOD2: superoxide dismutase 2, mitochondrial	W46388	4275.26	1492.74	-2.86	-2.63	-2782.52	*	5294.17	2383.27	-2.22	-2.02	-2910.91	*
211506_s_at	IL8: interleukin 8	AF043337	244.15	516.98	2.12	1.87	272.83	*	379.26	172.03	-2.2	-1.91	-207.24	*
209184_s_at	IRS2: insulin receptor substrate 2	BF700086	764.79	355.47	-2.15	-2.01	-409.32	*	311.33	141.55	-2.2	-1.92	-169.79	*
221747_at	TNS1: tensin 1	AL046979	1611.26	853.93	-1.89	-1.77	-757.33	*	1534.11	699.11	-2.19	-2.05	-835	*
234986_at	Hs.315562.0	AA630626	1073.89	548.2	-1.96	-1.8	-525.69	*	1004.75	458.48	-2.19	-2.03	-546.27	*
219566_at	PLEKHF1: pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024310	1818.75	908.94	-2	-1.86	-909.81	*	1163.01	530.57	-2.19	-2	-632.45	*
209890_at	TSPAN5: tetraspanin 5	AF065389	2157.23	1061.32	-2.03	-1.92	-1095.91	*	1729.25	789.79	-2.19	-2.04	-939.46	*
209969_s_at	STAT1: signal transducer and activator of transcription 1, 91kDa	BC002704	1496.03	815.21	-1.84	-1.77	-680.82	*	889.12	407.57	-2.18	-1.98	-481.55	*
218000_s_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	NM_007350	1219.57	649.88	-1.88	-1.76	-569.69	*	579.83	265.48	-2.18	-1.85	-314.36	*
205397_x_at	SMAD3: SMAD family member 3	U76622	294.18	156.99	-1.87	-1.62	-137.18	*	308.04	141.68	-2.17	-1.79	-166.36	*
216971_s_at	PLEC1: plectin 1, intermediate filament binding protein 500kDa	Z54367	1089.7	542.03	-2.01	-1.86	-547.67	*	1083.52	500.02	-2.17	-2.01	-583.5	*
209185_s_at	IRS2: insulin receptor substrate 2	AF073310	1320.43	719.84	-1.83	-1.72	-600.58	*	869.69	403.41	-2.16	-1.72	-466.29	*
206417_at	CNGA1: cyclic nucleotide gated channel alpha 1	NM_000087	283.01	151.08	-1.87	-1.69	-131.93	*	215.65	100.03	-2.16	-1.8	-115.62	*
223059_s_at	FAM107B: family with sequence similarity 107, member B	BC004872	1625.79	862.12	-1.89	-1.72	-763.67	*	1174.21	546.67	-2.15	-1.88	-627.54	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
201369_s_at	ZFP36L2: zinc finger protein 36, C3H type-like 2	NM_006887	313.75	138.2	-2.27	-1.99	-175.55	*	472.63	219.97	-2.15	-1.99	-252.66	*
201465_s_at	JUN: jun oncogene	BC002646	744.14	302.52	-2.46	-2.14	-441.62	*	954.78	443.1	-2.15	-2.01	-511.68	*
201136_at	PLP2: proteolipid protein 2 (colonic epithelium-enriched)	NM_002668	5416.22	3371.01	-1.61	-1.52	-2045.21	*	6754.48	3155.94	-2.14	-2	-3598.54	*
205341_at	EHD2: EH-domain containing 2	NM_014601	606.14	345.37	-1.76	-1.57	-260.77	*	670.45	314.03	-2.14	-1.89	-356.43	*
237411_at	ADAMTS6: ADAM metallopeptidase with thrombospondin type 1 motif, 6	N71063	1043.63	331.9	-3.14	-2.87	-711.73	*	517.17	243.2	-2.13	-1.8	-273.97	*
216831_s_at	RUNX1T1: runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	AF018283	375.8	102.49	-3.67	-2.91	-273.32	*	239.89	113.93	-2.11	-1.81	-125.96	*
225166_at	ARHGAP18: Rho GTPase activating protein 18	AU158022	377.31	166.88	-2.26	-1.99	-210.43	*	302.87	144.21	-2.1	-1.88	-158.66	*
204789_at	FMNL1: formin-like 1	NM_005892	193.04	18.87	-10.23	-4.99	-174.18	*	217.4	103.49	-2.1	-1.73	-113.91	*
216841_s_at	SOD2: superoxide dismutase 2, mitochondrial	X15132	2626.18	947.88	-2.77	-2.49	-1678.3	*	3421.47	1649.68	-2.07	-1.95	-1771.79	*
218608_at	ATP13A2: ATPase type 13A2	NM_022089	471.3	165.67	-2.84	-2.32	-305.63	*	444.04	215.02	-2.07	-1.9	-229.02	*
205543_at	HSPA4L: heat shock 70kDa protein 4-like	NM_014278	598.72	288.71	-2.07	-1.85	-310	*	471.57	229.91	-2.05	-1.86	-241.66	*
228728_at	C7orf58: chromosome 7 open reading frame 58	BF724137	732.75	321.82	-2.28	-2.03	-410.93	*	978.28	478.26	-2.05	-1.91	-500.02	*
212758_s_at	ZEB1: zinc finger E-box binding homeobox 1	AI373166	2697.68	1294.8	-2.08	-2	-1402.88	*	1923.86	943.5	-2.04	-1.89	-980.37	*
228186_s_at	RSPO3: R-spondin 3 homolog (Xenopus laevis)	BF589322	555.75	320.14	-1.74	-1.54	-235.61	*	1053.39	518.14	-2.03	-1.91	-535.25	*
217419_x_at	AGRN: agrin	AK021586	1056.6	517.54	-2.04	-1.98	-539.06	*	899.77	446.05	-2.02	-1.89	-453.72	*
205528_s_at	RUNX1T1: runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	X79990	1906.96	661.15	-2.88	-2.79	-1245.81	*	1119.14	555.47	-2.01	-1.92	-563.67	*
203788_s_at	SEMA3C: sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	AI962897	4351.48	2475.38	-1.76	-1.64	-1876.1	*	6322.18	3168.08	-2	-1.91	-3154.1	*
212338_at	MYO1D: myosin ID	AA621962	1913.23	802.21	-2.38	-2.18	-1111.02	*	1980.77	989.6	-2	-1.9	-991.17	*
1554474_a_at	MOXD1: monooxygenase, DBH-like 1	BC018756	693.43	370.23	-1.87	-1.7	-323.2	*	1366.33	685.6	-1.99	-1.89	-680.74	*
205130_at	RAGE: renal tumor antigen	NM_014226	1614.52	550.05	-2.94	-2.63	-1064.47	*	827.36	415.06	-1.99	-1.67	-412.3	*
209676_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	J03225	2218.34	4012.4	1.81	1.7	1794.06	*	2713.14	1369.52	-1.98	-1.89	-1343.62	*
202995_s_at	FBLN1: fibulin 1	NM_006486	422.29	716.89	1.7	1.56	294.6	*	1359.52	690.58	-1.97	-1.84	-668.94	*
201367_s_at	ZFP36L2: zinc finger protein 36, C3H type-like 2	AI356398	383.18	201.14	-1.91	-1.62	-182.04	*	635.95	322.06	-1.97	-1.86	-313.89	*
226907_at	PPP1R14C: protein phosphatase 1, regulatory (inhibitor) subunit 14C	N32557	546.01	930.08	1.7	1.6	384.08	*	583.24	299.5	-1.95	-1.69	-283.74	*
228396_at	PRKG1: protein kinase, cGMP-dependent, type I	AW274503	1327.07	601.01	-2.21	-2.06	-726.06	*	1417.54	726.94	-1.95	-1.88	-690.61	*
225171_at	ARHGAP18: Rho GTPase activating protein 18	BE644830	2761.13	1237.78	-2.23	-2.12	-1523.35	*	2227.38	1151.96	-1.93	-1.83	-1075.42	*
227609_at	EPSTI1: epithelial stromal interaction 1 (breast)	AA633203	1700.85	497.51	-3.42	-3.06	-1203.34	*	1206.72	626.11	-1.93	-1.74	-580.61	*
226438_at	SNTB1: syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	AK025100	491.98	291.78	-1.69	-1.56	-200.2	*	249.18	129.8	-1.92	-1.62	-119.38	*
235174_s_at	LOC100128822: hypothetical LOC100128822	AW952781	222.59	111.2	-2	-1.71	-111.4	*	244.2	126.9	-1.92	-1.68	-117.3	*
229581_at	ELFN1: extracellular leucine-rich repeat and fibronectin type III domain containing 1	AI694118	408.71	205.7	-1.99	-1.66	-203.02	*	548.96	289.57	-1.9	-1.73	-259.4	*
213258_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	BF511231	3371.7	5679.97	1.68	1.61	2308.28	*	3740.26	1978.3	-1.89	-1.76	-1761.96	*
224674_at	TTYH3: tweety homolog 3 (Drosophila)	AI934753	1103.8	639.72	-1.73	-1.52	-464.08	*	1392.42	738.55	-1.89	-1.75	-653.87	*
221840_at	PTPRE: protein tyrosine phosphatase, receptor type, E	AA775177	793.62	376.66	-2.11	-1.96	-416.96	*	591.2	312.8	-1.89	-1.77	-278.4	*
221477_s_at	SOD2: superoxide dismutase 2, mitochondrial	BF575213	4244.29	1979.68	-2.14	-2.03	-2264.61	*	5801.09	3068.88	-1.89	-1.77	-2732.21	*
225173_at	ARHGAP18: Rho GTPase activating protein 18	BE501862	2806.45	1166.69	-2.41	-2.25	-1639.76	*	1878.09	994.95	-1.89	-1.72	-883.14	*
209193_at	PIM1: pim-1 oncogene	M24779	1197.76	372.63	-3.21	-2.76	-825.13	*	765.41	404.25	-1.89	-1.68	-361.17	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
202086_at	MX1: myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	NM_002462	586.34	131.04	-4.47	-3.43	-455.3	*	733.2	388.64	-1.89	-1.64	-344.56	*
205700_at	HSD17B6: hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	NM_003725	1468.33	799.96	-1.84	-1.68	-668.37	*	1862.58	988.83	-1.88	-1.77	-873.75	*
217996_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	AA576961	3162.51	1905.91	-1.66	-1.53	-1256.6	*	2104.46	1124.29	-1.87	-1.71	-980.17	*
241869_at	APOL6: apolipoprotein L, 6	AW026509	1133.52	628.72	-1.8	-1.73	-504.8	*	408.41	218.96	-1.87	-1.65	-189.45	*
205381_at	LRRC17: leucine rich repeat containing 17	NM_005824	1295.09	571.4	-2.27	-2.03	-723.69	*	3959.58	2168.02	-1.83	-1.73	-1791.56	*
225564_at	C1QTNF9 /// SPATA13: C1q and tumor necrosis factor related protein 9 /// spermatogenesis associated 13	AW269397	1346.33	534.58	-2.52	-2.16	-811.74	*	2181.93	1201.7	-1.82	-1.73	-980.23	*
244623_at	KCNQ5: potassium voltage-gated channel, KQT-like subfamily, member 5	BF513800	789.06	251.19	-3.14	-2.88	-537.87	*	415.54	228.68	-1.82	-1.61	-186.85	*
227727_at	MRGPRF: MAS-related GPR, member F	H15920	1959.62	1132.17	-1.73	-1.6	-827.46	*	3346.8	1855.65	-1.8	-1.73	-1491.15	*
202440_s_at	ST5: suppression of tumorigenicity 5	NM_005418	1394.38	483.03	-2.89	-2.6	-911.35	*	1031.58	573.9	-1.8	-1.64	-457.68	*
210664_s_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AF021834	2474.27	5025.97	2.03	1.9	2551.7	*	3218.17	1833.43	-1.76	-1.68	-1384.74	*
225167_at	FRMD4A: FERM domain containing 4A	AW515645	2455.69	1541.26	-1.59	-1.51	-914.43	*	1467.63	838.46	-1.75	-1.61	-629.17	*
204967_at	SHROOM2: shroom family member 2	NM_001649	1302.09	230.79	-5.64	-4.97	-1071.31	*	1024.65	593.14	-1.73	-1.58	-431.52	*
232031_s_at	KIAA1632: KIAA1632	AK023817	456.82	269.09	-1.7	-1.52	-187.74	*	291.29	169.91	-1.71	-1.53	-121.38	*
1553559_at	TMEM171: transmembrane protein 171	NM_173490	217.73	94.06	-2.31	-1.98	-123.66	*	253.44	148.27	-1.71	-1.51	-105.17	*
207977_s_at	DPT: dermatopontin	NM_001937	246.34	35	-7.04	-3.24	-211.34	*	2213.96	1293.55	-1.71	-1.64	-920.41	*
217997_at	PHLDA1: pleckstrin homology-like domain, family A, member 1	AI795908	1240.4	523.97	-2.37	-2.18	-716.43	*	656.54	386.44	-1.7	-1.51	-270.09	*
203835_at	LRRC32: leucine rich repeat containing 32	NM_005512	506.95	1448.94	2.86	2.64	941.99	*	776.69	458.41	-1.69	-1.51	-318.28	*
209708_at	MOXD1: monooxygenase, DBH-like 1	AY007239	665.83	313.74	-2.12	-1.83	-352.08	*	1220.32	722.38	-1.69	-1.57	-497.94	*
205822_s_at	HMGCS1: 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NM_002130	926.58	237.3	-3.9	-3.22	-689.28	*	3246.31	1933.16	-1.68	-1.61	-1313.15	*
204255_s_at	VDR: vitamin D (1,25- dihydroxyvitamin D3) receptor	AA772285	2040.75	612.11	-3.33	-3.17	-1428.64	*	1610.52	965.25	-1.67	-1.58	-645.27	*
202994_s_at	FBLN1: fibulin 1	Z95331	343.48	755.79	2.2	2.04	412.31	*	1065.49	645.82	-1.65	-1.59	-419.67	*
229441_at	PRSS23: Protease, serine, 23	AI569872	3810.94	2082.23	-1.83	-1.65	-1728.72	*	5792.24	3505.46	-1.65	-1.55	-2286.78	*
219572_at	CADPS2: Ca++-dependent secretion activator 2	NM_017954	423.64	238.13	-1.78	-1.66	-185.51	*	728	442.68	-1.64	-1.56	-285.32	*
219501_at	ENOX1: ecto-NOX disulfide-thiol exchanger 1	NM_017993	1380.14	346.06	-3.99	-3.6	-1034.08	*	892.86	543.23	-1.64	-1.53	-349.63	*
225325_at	MFSD6: major facilitator superfamily domain containing 6	AA133311	1093.16	607.45	-1.8	-1.65	-485.72	*	1590.47	978.43	-1.63	-1.57	-612.04	*
235821_at	Hs.131329.0	AI917494	796.55	478.12	-1.67	-1.53	-318.44	*	2060.21	1280.79	-1.61	-1.5	-779.42	*
204359_at	FLRT2: fibronectin leucine rich transmembrane protein 2	NM_013231	2846.81	1081.87	-2.63	-2.5	-1764.94	*	3538.84	2222.85	-1.59	-1.53	-1315.99	*
229116_at	CNKSR2: connector enhancer of kinase suppressor of Ras 2	AI670947	901.94	262.87	-3.43	-3.09	-639.07	*	498.02	811.78	1.63	1.54	313.76	*
241981_at	FAM20A: family with sequence similarity 20, member A	AW291369	393.68	142.13	-2.77	-2.57	-251.55	*	317.36	570.53	1.8	1.69	253.18	*
243221_at	FAM20A: family with sequence similarity 20, member A	AA579773	235.54	86.15	-2.73	-2.34	-149.4	*	270.47	468.25	1.73	1.63	197.78	*
227911_at	ARHGAP28: Rho GTPase activating protein 28	AI935647	405.25	157.2	-2.58	-2	-248.05	*	841.24	1492.09	1.77	1.7	650.85	*
235028_at	Hs.173830.0	BG288330	2063.41	909.92	-2.27	-2.13	-1153.49	*	109.62	263.86	2.41	2.04	154.23	*
232098_at	DST: dystonin	AK025142	937.87	437.5	-2.14	-2.03	-500.37	*	144.25	262.24	1.82	1.58	118	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
215506_s_at	DIRAS3: DIRAS family, GTP-binding RAS-like 3	AK021882	488.66	235.1	-2.08	-1.74	-253.56	*	558.93	1224.96	2.19	2.09	666.03	*
224559_at	MALAT1: metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AF001540	8643.56	4209.27	-2.05	-1.84	-4434.29	*	2107.31	5488.95	2.6	2.23	3381.64	*
203435_s_at	MME: membrane metallo-endopeptidase	NM_007287	246.04	121.27	-2.03	-1.79	-124.77	*	476.47	1886.58	3.96	3.32	1410.1	*
218974_at	SOBP: sine oculis binding protein homolog (Drosophila)	NM_018013	274.13	142.5	-1.92	-1.63	-131.63	*	444.05	800.3	1.8	1.73	356.25	*
219681_s_at	RAB11FIP1: RAB11 family interacting protein 1 (class I)	NM_025151	276.23	148.9	-1.86	-1.58	-127.33	*	278.78	698.19	2.5	2.31	419.42	*
225177_at	RAB11FIP1: RAB11 family interacting protein 1 (class I)	AA143793	677.72	366.93	-1.85	-1.65	-310.8	*	745.64	1771.59	2.38	2.25	1025.95	*
221176_x_at	WBSCR23: Williams-Beuren syndrome chromosome region 23	NM_025042	765.08	420.01	-1.82	-1.68	-345.08	*	100.84	205.43	2.04	1.76	104.59	*
232889_at	Hs.283742.0	AU147591	1068.9	598.24	-1.79	-1.69	-470.66	*	96.6	232.18	2.4	1.9	135.58	*
1557543_at	Hs2.376974.1	AL832672	428.39	239.1	-1.79	-1.67	-189.29	*	40.79	141.16	3.46	2.47	100.37	*
227576_at	Hs.14947.0	AW003140	1101.67	621.21	-1.77	-1.69	-480.46	*	101.78	221.72	2.18	1.55	119.94	*
205525_at	CALD1: caldesmon 1	NM_018495	3260.05	1852.48	-1.76	-1.66	-1407.57	*	394.55	694.7	1.76	1.57	300.15	*
228623_at	Hs.181195.2	AI224133	906.98	516.51	-1.76	-1.65	-390.47	*	26.71	133.86	5.01	3.29	107.15	*
1553186_x_at	RASEF: RAS and EF-hand domain containing	NM_152573	1120.82	646.29	-1.73	-1.68	-474.52	*	155.98	295.02	1.89	1.66	139.04	*
242405_at	Hs.266701.0	BF358386	602.64	348.83	-1.73	-1.63	-253.82	*	75.31	196.46	2.61	1.9	121.15	*
239251_at	Hs.269339.0	AW963634	1752.74	1021.02	-1.72	-1.6	-731.72	*	194.68	424.9	2.18	1.79	230.23	*
1553185_at	RASEF: RAS and EF-hand domain containing	NM_152573	1146.36	708.91	-1.62	-1.51	-437.45	*	158.88	309.93	1.95	1.69	151.06	*
228793_at	JMJD1C: jumonji domain containing 1C	BF002296	570.21	354.39	-1.61	-1.52	-215.82	*	128.48	303.34	2.36	1.94	174.85	*
220940_at	ANKRD36B: ankyrin repeat domain 36B	NM_025190	1105.75	701.31	-1.58	-1.5	-404.44	*	170.26	416.33	2.45	2.08	246.07	*
1560445_x_at	ARHGEF1: Rho guanine nucleotide exchange factor (GEF) 1	AK026781	749.54	478.45	-1.57	-1.52	-271.1	*	142.79	245.41	1.72	1.54	102.61	*

Down-Regulated Genes at Day 4 in Response to 20nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
218723_s_at	C13orf15: chromosome 13 open reading frame 15	NM_014059	195.41	14.05	-13.91	-7.43	-181.36	*	489.11	595.05	1.22	1.18	105.94	
1562836_at	Hs2.271541.1	AK021715	564.66	55.54	-10.17	-7.03	-509.11	*	566.34	573.09	1.01	0.88	6.75	
1561064_a_at	Hs2.286666.1	BC015159	233.81	24.91	-9.39	-7.21	-208.9	*	139.22	46.81	-2.97	-2.14	-92.41	
223551_at	PKIB: protein kinase (cAMP-dependent, catalytic) inhibitor beta	AF225513	217.09	27.33	-7.94	-5.76	-189.76	*	81.08	39.57	-2.05	-1.71	-41.51	
1569512_at	Hs2.382226.1	BC022883	389.84	58.83	-6.63	-5.48	-331.01	*	43.15	14.39	-3	-1.3	-28.75	
222561_at	LANCL2: LanC lantibiotic synthetase component C-like 2 (bacterial)	AJ278245	919.03	141.4	-6.5	-4.54	-777.63	*	483.52	308.43	-1.57	-1.25	-175.09	
237891_at	MDM2: Mdm2 p53 binding protein homolog (mouse)	AI274906	173.64	26.92	-6.45	-3.4	-146.72	*	14.03	24.34	1.73	0.5	10.3	
204774_at	EVI2A: ecotropic viral integration site 2A	NM_014210	643.11	99.97	-6.43	-4.23	-543.15	*	964.36	706.38	-1.37	-1.28	-257.97	
215813_s_at	PTGS1: prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	S36219	159.87	27.38	-5.84	-3.99	-132.49	*	50.13	28.07	-1.79	-1.15	-22.06	
230250_at	PTPRB: protein tyrosine phosphatase, receptor type, B	AI670852	151.47	27.92	-5.42	-3.26	-123.55	*	81.15	51.62	-1.57	-1.17	-29.54	
214953_s_at	APP: amyloid beta (A4) precursor protein	X06989	6111.67	1141.7	-5.35	-4.53	-4969.97	*	5644.36	6339.87	1.12	1.07	695.52	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
225119_at	CHMP4B: chromatin modifying protein 4B	AW299290	1167.75	226.7	-5.15	-4.49	-941.05	*	1530.79	1240.92	-1.23	-1.19	-289.87	
242541_at	ABCA9: ATP-binding cassette, sub-family A (ABC1), member 9	AV692159	238.64	46.3	-5.15	-4.27	-192.34	*	99.86	22.31	-4.48	-2.6	-77.54	
227427_at	GEFT: RhoA/RAC/CDC42 exchange factor	AI677902	194.54	38.04	-5.11	-3.5	-156.5	*	229.73	198.65	-1.16	-1.06	-31.08	
203423_at	RBP1: retinol binding protein 1, cellular	NM_002899	436.92	86.22	-5.07	-4.13	-350.7	*	87.85	123.11	1.4	1.18	35.26	
222319_at	Hs.269403.0	AW970948	142.64	28.25	-5.05	-3.66	-114.4	*	21.84	32.69	1.5	0.72	10.85	
241060_x_at	Hs.52897.0	H37807	182.94	36.88	-4.96	-3.58	-146.06	*	11.8	11.87	1.01	0.26	0.07	
242794_at	MAML3: mastermind-like 3 (Drosophila)	AI569476	180.26	36.97	-4.88	-3.87	-143.29	*	120.25	143.42	1.19	0.99	23.17	
213068_at	DPT: dermatopontin	AI146848	199.35	41.06	-4.85	-2.87	-158.29	*	2183.86	1392.72	-1.57	-1.48	-791.14	
215874_at	Hs.287730.0	AK026820	140.29	30.27	-4.63	-2.77	-110.02	*	92.96	80.22	-1.16	-0.97	-12.74	
219249_s_at	FKBP10: FK506 binding protein 10, 65 kDa	NM_021939	3522.5	791.83	-4.45	-3.85	-2730.66	*	3821.44	4039.22	1.06	1.01	217.79	
202827_s_at	MMP14: matrix metallopeptidase 14 (membrane-inserted)	AU149305	1505.31	343.01	-4.39	-3.89	-1162.3	*	1799.7	1831.21	1.02	0.95	31.52	
205069_s_at	ARHGAP26: Rho GTPase activating protein 26	NM_015071	287.55	66.68	-4.31	-3.39	-220.87	*	31.22	49	1.57	0.97	17.79	
239979_at	Hs.201875.0	BE645480	264.19	62.17	-4.25	-3.25	-202.02	*	27.66	34.5	1.25	0.65	6.84	
213247_at	SVEP1: sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	AA716107	1259.81	297.32	-4.24	-3.39	-962.49	*	1169.16	1136.15	-1.03	-0.97	-33.01	
209032_s_at	CADM1: cell adhesion molecule 1	AF132811	319.49	77.28	-4.13	-2.98	-242.21	*	200.36	107.92	-1.86	-1.49	-92.45	
208241_at	NRG1: neuregulin 1	NM_004495	493.32	120.32	-4.1	-3.4	-373	*	93.69	76.94	-1.22	-0.82	-16.74	
1563414_at	Hs2.384566.1	AF087981	156.87	38.22	-4.1	-3.28	-118.65	*	13.18	41.23	3.13	1.93	28.05	
212843_at	NCAM1: neural cell adhesion molecule 1	AA126505	950.33	232.82	-4.08	-3.59	-717.5	*	358.92	284.69	-1.26	-1.11	-74.23	
226762_at	PURB: purine-rich element binding protein B	AV709094	1059.63	259.86	-4.08	-3.61	-799.77	*	970.18	1156.73	1.19	1.11	186.55	
218219_s_at	LANCL2: LanC lantibiotic synthetase component C-like 2 (bacterial)	NM_018697	1585.49	391.37	-4.05	-3.59	-1194.12	*	976.73	617.68	-1.58	-1.49	-359.05	
210587_at	INHBE: inhibin, beta E	BC005161	871.17	217.49	-4.01	-3.55	-653.68	*	10.92	18.04	1.65	0.67	7.12	
224576_at	ERGIC1: endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	AK000752	3610.74	905.36	-3.99	-3.54	-2705.38	*	3378.91	3128.66	-1.08	-1.02	-250.24	
215137_at	Hs.270010.0	H92070	151.83	38.55	-3.94	-2.93	-113.27	*	31.47	33.01	1.05	0.62	1.54	
1561631_at	Hs2.384146.1	AF147415	176.27	44.94	-3.92	-2.96	-131.34	*	6.25	40.16	6.42	2.12	33.9	
210872_x_at	GAS7: growth arrest-specific 7	BC001152	193.13	49.33	-3.91	-3.19	-143.8	*	146.57	66.96	-2.19	-1.9	-79.62	
1562389_at	Hs2.434306.1	BC040219	156.81	40.22	-3.9	-2.83	-116.59	*	99.22	26.94	-3.68	-2.54	-72.28	
209031_at	CADM1: cell adhesion molecule 1	AL519710	1625.38	419.68	-3.87	-3.49	-1205.69	*	1039.67	764.56	-1.36	-1.28	-275.11	
205195_at	AP1S1: adaptor-related protein complex 1, sigma 1 subunit	NM_001283	937.53	244.55	-3.83	-3.12	-692.98	*	1090.12	1071.05	-1.02	-0.98	-19.06	
209635_at	AP1S1: adaptor-related protein complex 1, sigma 1 subunit	BC003561	1759.49	459.11	-3.83	-3.47	-1300.38	*	1926.02	1837.32	-1.05	-1	-88.7	
219552_at	SVEP1: sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	NM_024500	169.89	45.17	-3.76	-3.05	-124.72	*	96.94	111.51	1.15	0.96	14.57	
230179_at	LOC285812: hypothetical protein LOC285812	N52572	182.26	49.17	-3.71	-3.07	-133.09	*	145.21	61.6	-2.36	-1.78	-83.61	
240259_at	FLRT2: Fibronectin leucine rich transmembrane protein 2	AI188161	217.86	59.02	-3.69	-2.76	-158.84	*	121.14	90.23	-1.34	-1.11	-30.91	
227394_at	NCAM1: neural cell adhesion molecule 1	W94001	1560.11	424.05	-3.68	-3.33	-1136.06	*	657.8	450.77	-1.46	-1.32	-207.03	
238617_at	Hs.143134.0	AW207243	560.72	154.73	-3.62	-3.2	-405.99	*	190.86	174.92	-1.09	-0.91	-15.94	
232935_at	Hs.298055.0	AA569225	427.22	118.38	-3.61	-3.24	-308.83	*	61.32	56.55	-1.08	-0.45	-4.77	
215163_at	Hs.203349.0	AK022211	158.27	43.97	-3.6	-2.63	-114.3	*	9.44	16.7	1.77	0.47	7.25	
1558430_at	Hs2.431319.1	R08650	516.39	143.54	-3.6	-3.31	-372.86	*	46	34.59	-1.33	-0.67	-11.41	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
202840_at	TAF15: TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	NM_003487	668.34	186.76	-3.58	-2.54	-481.58	*	513.63	515.55	1	0.92	1.92	
235783_at	MRTO4: mRNA turnover 4 homolog (S. cerevisiae)	BG107419	487.54	136.45	-3.57	-3	-351.09	*	511.66	431.03	-1.19	-1.11	-80.63	
217704_x_at	SUZ12P: Suppressor of zeste 12 homolog pseudogene	AI820796	173.84	48.91	-3.55	-2.75	-124.93	*	7.9	21.99	2.78	0.87	14.08	
232473_at	PRPF18: PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	AU144329	234.44	67.07	-3.5	-3.01	-167.37	*	20.31	23.45	1.15	0.47	3.14	
226804_at	FAM20A: family with sequence similarity 20, member A	AI632223	547.67	157.15	-3.48	-2.84	-390.51	*	542.83	768.98	1.42	1.33	226.14	
232568_at	MGC24103: hypothetical MGC24103	AU145658	564.67	162.29	-3.48	-3.04	-402.38	*	26.79	34.9	1.3	0.55	8.11	
239448_at	Hs.36915.0	AI475033	365.68	107.94	-3.39	-2.74	-257.74	*	23.94	40.64	1.7	1.16	16.7	
217279_x_at	MMP14: matrix metallopeptidase 14 (membrane-inserted)	X83535	672.79	198.95	-3.38	-2.54	-473.84	*	847.14	1031.68	1.22	1.14	184.54	
236558_at	Hs.189900.0	AA699809	236.53	70.68	-3.35	-2.78	-165.85	*	12.69	11.19	-1.13	-0.41	-1.5	
235701_at	Hs.132947.0	AW592510	147.87	44.37	-3.33	-2.55	-103.49	*	28.37	29.52	1.04	0.33	1.16	
232898_at	DAB2: disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	R79120	1552.39	473.38	-3.28	-2.95	-1079.01	*	199.54	105.41	-1.89	-1.48	-94.13	
204916_at	RAMP1: receptor (G protein-coupled) activity modifying protein 1	NM_005855	1069	331.12	-3.23	-2.99	-737.88	*	718.69	437.92	-1.64	-1.45	-280.76	
205196_s_at	AP1S1: adaptor-related protein complex 1, sigma 1 subunit	NM_001283	1059.37	330.24	-3.21	-2.91	-729.13	*	1266.57	1179.6	-1.07	-1.02	-86.97	
219773_at	NOX4: NADPH oxidase 4	NM_016931	254.56	79.35	-3.21	-2.62	-175.2	*	169.6	103.49	-1.64	-1.4	-66.11	
228235_at	MGC16121: hypothetical protein MGC16121	BE048571	520.04	162.14	-3.21	-2.75	-357.9	*	270.24	247.87	-1.09	-0.98	-22.37	
230682_x_at	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3	BF515888	245.38	76.58	-3.2	-2.67	-168.8	*	68.17	41.89	-1.63	-1.05	-26.28	
235335_at	ABCA9: ATP-binding cassette, sub-family A (ABC1), member 9	AI446543	161.2	50.4	-3.2	-2.76	-110.8	*	81.14	5.87	-13.83	-7.92	-75.27	
240165_at	Hs.271498.0	AI678013	653.76	204.9	-3.19	-2.92	-448.86	*	60.57	71.29	1.18	0.85	10.72	
244597_at	LOC26010: Viral DNA polymerase-transactivated protein 6	AA701247	166.82	52.69	-3.17	-2.26	-114.13	*	25.59	21.67	-1.18	-0.64	-3.92	
210042_s_at	CTSZ: cathepsin Z	AF073890	1256.08	398.46	-3.15	-2.82	-857.61	*	1298.35	1149.47	-1.13	-1.08	-148.87	
238769_at	Hs.257316.0	AW450572	231.36	73.58	-3.14	-2.29	-157.78	*	16.3	22.26	1.37	0.58	5.96	
244530_at	Hs.16135.0	T86276	205.35	65.86	-3.12	-2.29	-139.49	*	76.09	43.03	-1.77	-0.82	-33.06	
1566001_at	Hs2.376189.1	AK096064	291.35	93.44	-3.12	-2.33	-197.92	*	90.06	64.61	-1.39	-0.72	-25.45	
233770_at	Hs.296693.0	AU147115	447.19	143.69	-3.11	-2.7	-303.5	*	30.45	20.65	-1.47	-0.75	-9.8	
236060_at	Hs.158958.0	AA573115	147.81	47.74	-3.1	-2.14	-100.06	*	92.49	104.09	1.13	0.95	11.6	
242922_at	NOMO1 /// NOMO2 /// NOMO3: NODAL modulator 1 /// NODAL modulator 2 /// NODAL modulator 3	AU151198	239.57	77.57	-3.09	-1.98	-162	*	90.49	101.51	1.12	0.71	11.02	
233690_at	Hs.306875.0	AK026743	214.03	69.38	-3.08	-2.5	-144.65	*	21.11	37.49	1.78	0.9	16.38	
213790_at	ADAM12: ADAM metallopeptidase domain 12	W46291	2255.8	734.46	-3.07	-2.93	-1521.34	*	2859.9	2449.34	-1.17	-1.11	-410.56	
1559780_at	Hs2.382178.1	BC036577	354.98	115.6	-3.07	-2.76	-239.38	*	42.3	35.26	-1.2	-0.78	-7.04	
235705_at	Hs.16798.0	BF676361	712.39	232.44	-3.06	-2.77	-479.95	*	47.36	101.23	2.14	1.49	53.87	
202669_s_at	EFNB2: ephrin-B2	U16797	172.53	56.94	-3.03	-2.22	-115.58	*	116.18	31.87	-3.65	-2.4	-84.31	
215828_at	Hs.283850.0	AL359599	281.89	93.16	-3.03	-2.36	-188.73	*	23.93	36.32	1.52	0	12.39	
1561886_a_at	Hs2.301743.1	R00975	182.76	60.99	-3	-2.42	-121.77	*	34.18	31.85	-1.07	-0.67	-2.33	
205128_x_at	PTGS1: prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_000962	167.47	56.55	-2.96	-2.06	-110.91	*	88.58	78.79	-1.12	-0.86	-9.79	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
233276_at	Hs.296674.0	AU146390	917.82	310.11	-2.96	-2.69	-607.71	*	43.01	93.99	2.19	1.34	50.98	
222375_at	Hs.291839.0	AW970944	238.76	81.34	-2.94	-2.16	-157.42	*	29.35	47.43	1.62	0.77	18.08	
215074_at	MYO1B: myosin IB	AK022489	214.64	73.82	-2.91	-2.31	-140.83	*	28.56	31.31	1.1	0.64	2.75	
233036_at	Hs.274273.0	AU146418	393.98	135.66	-2.9	-2.26	-258.32	*	65.2	63.62	-1.02	-0.56	-1.58	
232472_at	Hs.287528.0	AK022461	529.71	183.59	-2.89	-2.45	-346.12	*	12.22	52.85	4.32	2.56	40.63	
205818_at	DBC1: deleted in bladder cancer 1	NM_014618	813.99	286.45	-2.84	-2.53	-527.54	*	474.38	293.91	-1.61	-1.46	-180.46	
236475_at	MICAL2: Microtubule associated monoxygenase, calponin and LIM domain containing 2	W86183	561.77	198.81	-2.83	-2.63	-362.96	*	75.78	44.07	-1.72	-1.26	-31.71	
210230_at	g13177696	BC003629	694.01	245.82	-2.82	-2.35	-448.2	*	105.09	116.95	1.11	0.67	11.86	
209827_s_at	IL16: interleukin 16 (lymphocyte chemoattractant factor)	NM_004513	387.78	138.36	-2.8	-2.36	-249.43	*	221.82	126.68	-1.75	-1.51	-95.14	
232762_at	KIAA1217: KIAA1217	AU146385	162.29	58.04	-2.8	-2.15	-104.24	*	55.24	71.81	1.3	0.96	16.57	
200965_s_at	ABLIM1: actin binding LIM protein 1	NM_006720	1017.1	366.25	-2.78	-2.48	-650.85	*	1133.34	753	-1.51	-1.4	-380.34	
243012_at	Hs.170399.0	BF196252	666.38	241	-2.77	-2.45	-425.38	*	80.96	117.98	1.46	1	37.02	
1552482_at	RAPH1: Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	NM_025252	294.76	106.25	-2.77	-2.24	-188.52	*	19.31	44.29	2.29	1.29	24.99	
241711_at	Hs.270750.0	AI949435	163.49	59.33	-2.76	-2.51	-104.16	*	42.15	50.61	1.2	0.87	8.47	
202952_s_at	ADAM12: ADAM metallopeptidase domain 12	NM_003474	3669.04	1333.87	-2.75	-2.51	-2335.17	*	4567.3	4140.86	-1.1	-1.07	-426.45	
204254_s_at	VDR: vitamin D (1,25- dihydroxyvitamin D3) receptor	NM_000376	3034.82	1105.19	-2.75	-2.59	-1929.64	*	2357.03	1577.14	-1.49	-1.42	-779.9	
232670_at	Hs.306452.0	AL137339	164.63	60.19	-2.74	-2.3	-104.45	*	22.15	37.67	1.7	0.82	15.52	
238449_at	LOC595101: PI-3-kinase-related kinase SMG-1 pseudogene	BG534511	1466.13	538.89	-2.72	-2.46	-927.24	*	428.1	668	1.56	1.14	239.9	
240176_at	Hs.61753.0	AI078180	249.77	91.8	-2.72	-2.33	-157.97	*	21.58	38.46	1.78	1.12	16.88	
1568867_x_at	Hs2.396047.1	R83290	158.72	58.33	-2.72	-2.43	-100.39	*	14.96	13.13	-1.14	-0.56	-1.83	
205529_s_at	RUNX1T1: runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	NM_004349	1431.93	528.71	-2.71	-2.5	-903.22	*	1185.36	739.49	-1.6	-1.48	-445.87	
239557_at	Hs.182258.0	AW474960	241.59	88.99	-2.71	-2.35	-152.6	*	9.78	18.46	1.89	0.81	8.68	
211488_s_at	ITGB8: integrin, beta 8	BC002630	203.57	75.28	-2.7	-2.26	-128.3	*	99.75	91.02	-1.1	-0.93	-8.73	
226676_at	ZNF521: zinc finger protein 521	AK021452	162.93	60.65	-2.69	-2.08	-102.27	*	178.24	162.19	-1.1	-0.96	-16.05	
231403_at	TRIO: Triple functional domain (PTPRF interacting)	N21108	268.06	99.66	-2.69	-2.27	-168.4	*	20.33	36.95	1.82	1.12	16.62	
1568765_at	SERPINE1: serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	BC020765	647.41	242.93	-2.67	-2.27	-404.48	*	143.48	47.13	-3.04	-2	-96.35	
233112_at	Hs.300922.0	AW301393	638.61	240.1	-2.66	-2.42	-398.5	*	42.39	45.49	1.07	0.74	3.11	
227084_at	DTNA: dystrobrevin, alpha	AW339310	414.54	156.37	-2.65	-2.34	-258.18	*	338.44	220.91	-1.53	-1.37	-117.54	
244096_at	Hs.150074.0	BE467068	213.83	80.58	-2.65	-2.37	-133.25	*	176.35	78.98	-2.23	-1.75	-97.37	
1569320_at	GPBP1L1: GC-rich promoter binding protein 1-like 1	CA391618	503.73	190.37	-2.65	-2.15	-313.36	*	40.79	115.74	2.84	2.15	74.95	
232716_at	Hs.121806.0	AU146685	337.37	128.1	-2.63	-2.34	-209.28	*	31.28	40.16	1.28	0.71	8.88	
1557996_at	LOC100132832 /// PMS2L1 /// PMS2L2: postmeiotic segregation increased 2-like 5-like /// postmeiotic segregation increased 2-like 1 pseudogene /// postmeiotic segregation increased 2-like 2 pseudogene	AK091784	601.72	229.1	-2.63	-2.15	-372.62	*	79.32	125.29	1.58	1.13	45.97	
1560031_at	FRMD4A: FERM domain containing 4A	R19413	637.24	242.09	-2.63	-2.27	-395.15	*	96.41	116.89	1.21	0.97	20.48	
206704_at	CLCN5: chloride channel 5	NM_000084	184.09	70.19	-2.62	-1.99	-113.91	*	111.87	105.03	-1.07	-0.86	-6.83	
232861_at	PDP2: pyruvate dehyrogenase phosphatase catalytic subunit 2	AB037769	371	141.6	-2.62	-2.32	-229.41	*	234.12	158.98	-1.47	-1.29	-75.14	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
239879_at	LOC284998: hypothetical protein LOC284998	N63566	162.56	62.08	-2.62	-1.8	-100.48	*	107.39	36.09	-2.98	-2.13	-71.3	
244845_at	Hs.170577.0	BF725383	223.99	85.37	-2.62	-2.1	-138.62	*	12.36	6.31	-1.96	-0.36	-6.05	
235281_x_at	AHNAK: AHNAK nucleoprotein	AA523289	242.39	93.33	-2.6	-2.14	-149.06	*	197.88	122.17	-1.62	-1.29	-75.71	
1554948_at	Hs2.375076.1	BC034024	413.27	159.09	-2.6	-2.32	-254.18	*	30.71	53.05	1.73	1.29	22.34	
1566191_at	SUZ12: Suppressor of zeste 12 homolog (Drosophila)	AI907884	178.57	68.71	-2.6	-1.98	-109.86	*	19.89	33.67	1.69	0.65	13.78	
220918_at	C21orf96: chromosome 21 open reading frame 96	NM_025143	190.28	73.58	-2.59	-2.11	-116.7	*	36.56	33.68	-1.09	-0.64	-2.89	
236114_at	Hs.208726.0	AI798118	194.62	75.31	-2.58	-2.15	-119.31	*	41.84	81.7	1.95	1.37	39.86	
1565743_at	Hs2.379834.1	BG545582	514.5	199.54	-2.58	-2.38	-314.96	*	40.32	61.01	1.51	1.08	20.69	
214257_s_at	Hs.50785.1	AA890010	17976.61	7007.06	-2.57	-1.96	-10969.55	*	6829.71	6864.33	1.01	0.73	34.62	
238957_at	PDXDC2: Pyridoxal-dependent decarboxylase domain containing 2	AL047426	322.29	125.81	-2.56	-2.15	-196.48	*	33.01	21	-1.57	-1.01	-12.01	
235922_at	Hs.194339.0	AW629304	234.19	91.98	-2.55	-1.99	-142.21	*	25.53	60.54	2.37	1.57	35.01	
1569323_at	PTPRG: protein tyrosine phosphatase, receptor type, G	BU853579	300.99	117.91	-2.55	-2	-183.08	*	64.08	73.44	1.15	0.61	9.36	
202876_s_at	PBX2: pre-B-cell leukemia homeobox 2	NM_002586	411.95	162.46	-2.54	-1.97	-249.5	*	466.62	549.46	1.18	1.09	82.84	
243149_at	Hs.173696.0	AI467945	213.31	83.88	-2.54	-2.14	-129.43	*	9.3	17.74	1.91	0.74	8.45	
243233_at	Hs.292669.0	AI701943	208.07	81.86	-2.54	-2.16	-126.21	*	8.24	21.07	2.56	0.86	12.83	
219334_s_at	OBFC2A: oligonucleotide/oligosaccharide-binding fold containing 2A	NM_022837	283.21	111.76	-2.53	-2.11	-171.46	*	106.91	147.1	1.38	1.17	40.19	
227488_at	MGC16121: hypothetical protein MGC16121	AV728999	462.01	182.81	-2.53	-2.13	-279.2	*	205.55	220.89	1.07	0.94	15.34	
233442_at	Hs.287499.0	AU147500	295.3	116.81	-2.53	-2.03	-178.49	*	38.67	40.96	1.06	0.5	2.29	
214111_at	OPCML: opioid binding protein/cell adhesion molecule-like	AF070577	291.91	115.7	-2.52	-2.07	-176.2	*	238.26	170.8	-1.39	-1.18	-67.46	
237290_at	Hs.135288.0	AW138872	553.76	220.3	-2.51	-2.26	-333.45	*	26.89	43.92	1.63	1.08	17.03	
241457_at	Hs.10359.0	AI821935	591.93	236.14	-2.51	-2.29	-355.79	*	25.54	71.23	2.79	1.93	45.69	
1553275_s_at	Hs2.270868.1	NM_173594	1077.16	429.12	-2.51	-2.23	-648.03	*	36.77	89.16	2.42	1.4	52.39	
1556425_a_at	LOC284219: hypothetical protein LOC284219	BF509747	188.84	75.26	-2.51	-2.01	-113.58	*	37.2	42.11	1.13	0.64	4.92	
1557987_at	LOC641298: SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene	BC042832	1642.98	653.76	-2.51	-2.38	-989.21	*	170.93	299.61	1.75	1.29	128.68	
232375_at	Hs.137447.0	AI539443	452.6	180.86	-2.5	-2.24	-271.74	*	42.28	35.87	-1.18	-0.54	-6.41	
236738_at	LOC401097: Similar to LOC166075	AW057589	510.07	203.89	-2.5	-2.3	-306.18	*	256.16	178.04	-1.44	-1.29	-78.12	
1569540_at	Hs2.397505.1	BC035958	274.33	109.71	-2.5	-2.21	-164.62	*	26.68	35.4	1.33	0.7	8.72	
1553407_at	MACF1: microtubule-actin crosslinking factor 1	NM_033044	178.75	71.83	-2.49	-2.11	-106.93	*	16.58	31.97	1.93	0.97	15.39	
201430_s_at	DPYSL3: dihydropyrimidinase-like 3	W72516	3155.85	1273.63	-2.48	-2.24	-1882.22	*	3968.48	2946.74	-1.35	-1.32	-1021.74	
232346_at	LOC388692: hypothetical LOC388692	AW515373	512.42	206.93	-2.48	-2.25	-305.49	*	51.74	70.02	1.35	0.99	18.27	
242113_at	Hs.313839.0	AW468298	172.27	69.5	-2.48	-1.96	-102.77	*	30.85	40.3	1.31	0.35	9.45	
206088_at	LRRC37A /// LRRC37A2 /// LRRC37A3: leucine rich repeat containing 37A /// leucine rich repeat containing 37, member A2 /// leucine rich repeat containing 37, member A3	NM_014834	194.82	78.81	-2.47	-2.16	-116.01	*	31.02	30.81	-1.01	-0.74	-0.21	
209030_s_at	CADM1: cell adhesion molecule 1	NM_014333	956.89	387.92	-2.47	-2.1	-568.97	*	614.97	407.8	-1.51	-1.31	-207.17	
226777_at	Hs.8895.0	AA147933	4068.78	1650.29	-2.47	-2.24	-2418.49	*	5255.52	4559.84	-1.15	-1.08	-695.68	
240450_at	Hs.28653.0	BF061543	619.81	250.96	-2.47	-2.22	-368.85	*	52.33	41.39	-1.26	-0.81	-10.93	
202638_s_at	ICAM1: intercellular adhesion molecule 1	NM_000201	777.55	316.03	-2.46	-2.23	-461.52	*	329.08	313.36	-1.05	-0.96	-15.72	
204439_at	IFI44L: interferon-induced protein 44-like	NM_006820	500.23	204.22	-2.45	-1.93	-296.01	*	842.83	932.54	1.11	1.03	89.71	
205450_at	PHKA1: phosphorylase kinase, alpha 1 (muscle)	NM_002637	190.83	77.87	-2.45	-1.9	-112.96	*	201.75	129.68	-1.56	-1.31	-72.07	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
228919_at	Hs.183418.17	AA601031	1407.27	573.33	-2.45	-2.25	-833.94	*	105.56	156.76	1.49	0.81	51.2	
233609_at	PTPRK: Protein tyrosine phosphatase, receptor type, K	AU145587	243.86	99.46	-2.45	-2.05	-144.39	*	39.52	41.13	1.04	0.56	1.61	
239629_at	CFLAR: CASP8 and FADD-like apoptosis regulator	AI634046	689.6	281.75	-2.45	-2.24	-407.85	*	63.65	105.21	1.65	1.19	41.56	
235486_at	C11orf41: chromosome 11 open reading frame 41	AI879661	579.1	236.85	-2.44	-2.22	-342.25	*	382.3	292.38	-1.31	-1.19	-89.93	
220467_at	g13376557	NM_025032	442.75	182.81	-2.42	-2.23	-259.94	*	69.16	67.87	-1.02	-0.66	-1.29	
1557578_at	PHLDB2: Pleckstrin homology-like domain, family B, member 2	BQ722176	196.76	81.22	-2.42	-2.05	-115.54	*	31.63	22.11	-1.43	-0.54	-9.52	
1563471_at	KIAA1632: KIAA1632	AL833448	192.41	79.63	-2.42	-2.05	-112.77	*	68.44	62.24	-1.1	-0.81	-6.2	
228325_at	KIAA0146: KIAA0146	AI363213	239.84	99.6	-2.41	-2.1	-140.23	*	124.99	53.05	-2.36	-1.82	-71.94	
228866_at	Hs.125063.0	BF514864	287.83	119.51	-2.41	-2.1	-168.32	*	5.11	20	3.91	0.6	14.89	
240552_at	Hs.291911.0	AA811452	365.7	151.53	-2.41	-2.2	-214.18	*	34.45	42.85	1.24	0.73	8.4	
243065_at	Hs.278177.0	AA809449	282.69	117.11	-2.41	-2.11	-165.58	*	257.86	154.86	-1.67	-1.49	-103	
1569864_at	SERAC1: serine active site containing 1	BC028594	212.35	88.56	-2.4	-2.05	-123.78	*	60.17	27.26	-2.21	-1.57	-32.91	
218975_at	COL5A3: collagen, type V, alpha 3	NM_015719	667	279.07	-2.39	-2.02	-387.92	*	2271.13	1571.99	-1.44	-1.4	-699.14	
225496_s_at	SYTL2: synaptotagmin-like 2	N21426	866.91	363.34	-2.39	-2.02	-503.57	*	1710.55	1815.7	1.06	1	105.15	
232030_at	KIAA1632: KIAA1632	AK023817	218.25	91.42	-2.39	-2.03	-126.83	*	41.04	48.33	1.18	0.65	7.29	
239331_at	Hs.184721.0	AW954199	1061.84	444.7	-2.39	-2.27	-617.15	*	27.12	74.5	2.75	1.68	47.38	
216189_at	LOC100289109: hypothetical protein LOC100289109	BC002465	249.94	104.91	-2.38	-2.04	-145.02	*	16.28	14.99	-1.09	-0.46	-1.3	
222783_s_at	SMOC1: SPARC related modular calcium binding 1	BF516292	207.96	87.28	-2.38	-1.54	-120.68	*	424.41	454.14	1.07	1	29.73	
241387_at	Hs.224812.0	AW276701	289.9	121.75	-2.38	-2.05	-168.15	*	24.18	40.19	1.66	1.08	16.01	
1557432_at	RASAL2: RAS protein activator like 2	BQ003426	267.11	112.91	-2.37	-1.95	-154.21	*	16.09	65.26	4.06	2.46	49.18	
204994_at	MX2: myxovirus (influenza virus) resistance 2 (mouse)	NM_002463	245.53	103.86	-2.36	-2.05	-141.67	*	282.52	183.49	-1.54	-1.37	-99.03	
229784_at	MGC16121: hypothetical protein MGC16121	AA234096	988.89	419.66	-2.36	-2.19	-569.23	*	462.99	556.44	1.2	1.13	93.46	
236379_at	Hs.175437.0	AW771958	270.17	114.73	-2.35	-1.97	-155.44	*	27.56	9.62	-2.86	-1.58	-17.94	
240815_at	Hs.269109.0	R62588	532.17	226.73	-2.35	-2.21	-305.44	*	106.51	78.58	-1.36	-1.14	-27.93	
209417_s_at	IFI35: interferon-induced protein 35	BC001356	789.04	337.56	-2.34	-2	-451.47	*	662.11	419.63	-1.58	-1.39	-242.48	
237310_at	Hs.131793.0	AI743607	767.28	328.36	-2.34	-2.17	-438.92	*	29.34	44.77	1.53	0.85	15.43	
239721_at	Hs.119275.0	AI280328	325.35	139.02	-2.34	-2.04	-186.33	*	13.15	49.96	3.8	1.87	36.81	
240600_at	Hs.156501.0	AI342146	176.03	75.26	-2.34	-2.02	-100.77	*	13.39	21.12	1.58	0.51	7.73	
1556352_at	Hs2.421612.1	AI692624	499.67	213.2	-2.34	-2.22	-286.47	*	24.9	36.4	1.46	0.5	11.5	
204592_at	DLG4: discs, large homolog 4 (Drosophila)	NM_001365	228.87	98.15	-2.33	-1.93	-130.72	*	147.23	166.34	1.13	0.99	19.11	
222214_at	Hs.303001.0	AK024988	223.02	95.64	-2.33	-1.95	-127.38	*	33.1	44.1	1.33	0.72	11	
224543_at	SVEP1: sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	AF308289	267.14	114.61	-2.33	-1.82	-152.53	*	281.39	252.39	-1.11	-1.03	-29	
243003_at	Hs.69606.0	AV702197	360.31	154.55	-2.33	-2.12	-205.76	*	121.26	123.77	1.02	0.78	2.51	
1556658_a_at	Hs2.292645.1	AA744622	702.14	301.79	-2.33	-2.11	-400.35	*	43.44	64.47	1.48	1.1	21.03	
216147_at	Hs.306504.0	AL353942	1095.95	473.36	-2.32	-2.16	-622.59	*	81.45	124.96	1.53	1.13	43.52	
223707_at	RPL27A: ribosomal protein L27a	BC004284	540.73	232.67	-2.32	-1.95	-308.05	*	313.06	308.56	-1.01	-0.84	-4.5	
1561167_at	Hs2.384174.1	AF147300	296.49	128.06	-2.32	-1.99	-168.43	*	14.03	49.81	3.55	2.03	35.78	
215318_at	CG012: hypothetical gene CG012	AL049782	340.17	147.46	-2.31	-2.05	-192.71	*	31.55	44.79	1.42	0.66	13.24	
234657_at	Hs.306909.0	AK027174	272.64	117.85	-2.31	-1.98	-154.79	*	18.47	41.97	2.27	1.28	23.5	
238774_at	Hs.222830.0	AW960454	609.69	264.29	-2.31	-2.11	-345.4	*	37.5	59.34	1.58	1.01	21.84	
242068_at	Hs.112592.0	AA608834	290.59	125.56	-2.31	-2.04	-165.03	*	41.07	60.77	1.48	1.1	19.71	
1559037_a_at	Hs2.182210.1	AL041381	761.34	329.74	-2.31	-2.11	-431.61	*	114.82	103.91	-1.1	-0.86	-10.91	
242188_at	Hs.270523.0	AI743332	369.76	160.69	-2.3	-1.73	-209.07	*	19.21	52	2.71	1.58	32.79	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
231292_at	EID3: EP300 interacting inhibitor of differentiation 3	AI964053	248.21	108.38	-2.29	-1.97	-139.83	*	351.31	251.49	-1.4	-1.3	-99.82	
233824_at	Hs.287663.0	AK025081	317.35	138.47	-2.29	-2	-178.88	*	35.16	73.52	2.09	1.37	38.36	
214772_at	C11orf41: chromosome 11 open reading frame 41	H08993	515.2	226.15	-2.28	-2.09	-289.05	*	528.04	363.97	-1.45	-1.36	-164.06	
231979_at	Hs.125232.0	AU155091	279.38	122.43	-2.28	-1.84	-156.95	*	2.05	32.24	15.74	4.63	30.19	
239269_at	Hs.200577.0	AW449577	201.86	88.47	-2.28	-1.71	-113.39	*	88.69	140.54	1.58	1.3	51.86	
1562863_at	Hs2.351804.1	BC017944	201.1	88.28	-2.28	-1.92	-112.82	*	18.34	39.79	2.17	1.47	21.45	
207822_at	FGFR1: fibroblast growth factor receptor 1	NM_023107	262.09	115.51	-2.27	-2.03	-146.57	*	63.62	102.74	1.61	1.32	39.11	
214967_at	Hs.262212.0	AU146983	244.85	107.81	-2.27	-1.88	-137.04	*	28.14	29.91	1.06	0.47	1.77	
1558078_at	Hs2.411589.1	BQ219651	572.5	252.6	-2.27	-2.1	-319.9	*	80.27	109.89	1.37	1.04	29.63	
242320_at	Hs.170651.0	AI435586	273.05	120.66	-2.26	-1.94	-152.4	*	40	53.86	1.35	0.66	13.86	
41660_at	CELSR1: cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	AL031588	379.06	168.49	-2.25	-2.09	-210.57	*	162.94	83.97	-1.94	-1.67	-78.97	
237624_at	Hs.144084.0	BE503711	333.52	148.37	-2.25	-2.01	-185.15	*	66.78	39.48	-1.69	-1.03	-27.3	
238534_at	LRRFIP1: Leucine rich repeat (in FLII) interacting protein 1	AA262583	196.01	87.24	-2.25	-1.92	-108.77	*	28.65	43.24	1.51	0.77	14.59	
238812_at	Hs.128778.0	AA741296	220.61	97.91	-2.25	-1.87	-122.7	*	48.73	68.47	1.41	0.96	19.74	
242244_at	Hs.20526.0	R11654	332.51	148.52	-2.24	-1.99	-183.99	*	13.15	23.2	1.76	0.98	10.05	
1557512_at	Hs2.353079.1	BM664532	391.19	174.4	-2.24	-1.97	-216.79	*	30.12	40.01	1.33	0.62	9.88	
205240_at	GPSM2: G-protein signaling modulator 2 (AGS3-like, C. elegans)	NM_013296	260.49	116.99	-2.23	-1.69	-143.5	*	942.77	643.17	-1.47	-1.4	-299.61	
237600_at	Hs.134053.0	AI023295	207.72	93.24	-2.23	-1.89	-114.49	*	42.84	54.99	1.28	0.81	12.15	
1556657_at	Hs2.292645.1	AA744622	350.83	157.28	-2.23	-1.85	-193.55	*	28.84	41.56	1.44	0.7	12.73	
210701_at	CFDP1: craniofacial development protein 1	D85939	483.75	217.78	-2.22	-2.05	-265.97	*	47.86	101.56	2.12	1.68	53.7	
239597_at	Hs.159983.0	AA993566	360.56	162.25	-2.22	-1.97	-198.31	*	39.19	46.55	1.19	0.67	7.36	
231205_at	Hs.20247.0	BF055351	750.81	340.33	-2.21	-2.04	-410.48	*	63.06	126.33	2	1.27	63.27	
211573_x_at	TGM2: transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	M98478	316.16	143.79	-2.2	-1.89	-172.37	*	111	12.68	-8.75	-5.09	-98.32	
239784_at	Hs.61082.0	AA398740	362.55	165.08	-2.2	-2.01	-197.47	*	38.28	88.14	2.3	1.44	49.86	
239811_at	Hs.129037.0	BF954306	504.27	229.86	-2.19	-2.06	-274.41	*	54.36	109.3	2.01	1.48	54.94	
1552671_a_at	SLC9A7: solute carrier family 9 (sodium/hydrogen exchanger), member 7	NM_032591	245.06	111.85	-2.19	-1.74	-133.2	*	127.62	45.46	-2.81	-2.02	-82.15	
1560342_at	Hs2.382173.1	BC036606	186.04	84.88	-2.19	-1.8	-101.15	*	10.71	15.69	1.46	0.36	4.97	
207635_s_at	KCNH1: potassium voltage-gated channel, subfamily H (eag-related), member 1	NM_002238	230.24	105.51	-2.18	-1.79	-124.72	*	69.8	64.99	-1.07	-0.68	-4.81	
209281_s_at	ATP2B1: ATPase, Ca++ transporting, plasma membrane 1	M95541	3032.85	1391.47	-2.18	-2.05	-1641.38	*	1796.79	1169.84	-1.54	-1.37	-626.95	
211824_x_at	NLRP1: NLR family, pyrin domain containing 1	AF229062	320.48	146.96	-2.18	-1.94	-173.53	*	177.44	150.49	-1.18	-0.99	-26.94	
236007_at	AKAP10: A kinase (PRKA) anchor protein 10	AU147278	710.58	326.57	-2.18	-2.03	-384.01	*	58.01	108.7	1.87	1.3	50.69	
239193_at	FUBP3: far upstream element (FUSE) binding protein 3	BF060981	319.29	146.66	-2.18	-1.88	-172.62	*	91.37	146.69	1.61	1.18	55.32	
1558836_at	Hs2.157344.1	BQ024490	409.68	187.63	-2.18	-1.95	-222.05	*	174.8	149.64	-1.17	-0.86	-25.16	
1562544_at	Hs2.306352.1	AL117560	205.24	94.3	-2.18	-1.86	-110.94	*	25.64	39.35	1.54	0.92	13.72	
236752_at	Hs.152686.0	AA913146	648.81	299.5	-2.17	-1.98	-349.3	*	47.94	66.44	1.39	1.05	18.51	
239614_x_at	Hs.88746.0	AW173003	413.02	190.26	-2.17	-1.97	-222.76	*	38.23	50.98	1.33	0.85	12.75	
239908_at	Hs.36958.0	AA496799	323.09	148.81	-2.17	-1.79	-174.28	*	105.11	110.61	1.05	0.66	5.5	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
201998_at	ST6GAL1: ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	AI743792	483	223.54	-2.16	-1.98	-259.46	*	507.34	363.57	-1.4	-1.28	-143.77	
232264_at	Hs.288719.0	AK022204	226.14	104.94	-2.16	-1.9	-121.2	*	17.65	26.82	1.52	0.45	9.17	
214415_at	PLGLB1 /// PLGLB2: plasminogen-like B1 /// plasminogen-like B2	N58120	431.32	200.52	-2.15	-2.02	-230.8	*	110.18	131.77	1.2	1.03	21.59	
215123_at	LOC100288332 /// LOC100288583 /// NPIPL3: similar to acyl-CoA synthetase medium-chain family member 2 /// hypothetical protein LOC100288583 /// nuclear pore complex interacting protein-like 3	AL049250	752.26	349.86	-2.15	-1.94	-402.4	*	49.6	78.43	1.58	0.92	28.83	
215199_at	CALD1: caldesmon 1	AU147402	1360.28	636.04	-2.14	-2.03	-724.24	*	84.75	152.86	1.8	1.31	68.11	
232914_s_at	SYTL2: synaptotagmin-like 2	AB046817	1089.57	508.29	-2.14	-1.92	-581.28	*	2171.68	2375.82	1.09	1.06	204.14	
235060_at	LOC100190986: hypothetical LOC100190986	AL047052	1578.13	738.62	-2.14	-2	-839.5	*	173.2	249.78	1.44	1.12	76.58	
243646_at	Hs.208675.0	BE349511	199.49	93.2	-2.14	-1.83	-106.29	*	32.16	31.12	-1.03	-0.57	-1.04	
1552867_at	Hs2.334913.1	NM_138474	342.01	159.57	-2.14	-1.85	-182.43	*	60.36	105.43	1.75	1.3	45.07	
234156_at	Hs.306895.0	AK026905	897.07	421.67	-2.13	-1.9	-475.4	*	166.48	145.29	-1.15	-0.79	-21.19	
242856_at	Hs.118101.0	AI291804	318.05	149.3	-2.13	-1.92	-168.75	*	42.15	92.31	2.19	1.63	50.16	
1569041_at	Hs2.373680.1	BC035102	227.73	107.16	-2.13	-1.81	-120.57	*	18.51	48.33	2.61	1.4	29.82	
213089_at	LOC100272216: hypothetical LOC100272216	AU158490	535.81	253.17	-2.12	-1.92	-282.65	*	30.98	87.7	2.83	1.8	56.72	
213486_at	COPG2IT1: COPG2 imprinted transcript 1 (non-protein coding)	BF435376	229.91	108.37	-2.12	-1.65	-121.54	*	63.2	43.51	-1.45	-0.73	-19.69	
214375_at	LOC729222 /// PPFIBP1: similar to PTPRF interacting protein binding protein 1 /// PTPRF interacting protein, binding protein 1 (liprin beta 1)	AI962377	365.14	172.35	-2.12	-1.85	-192.79	*	52.91	59.5	1.12	0.72	6.59	
232952_at	Hs.296676.0	AU146493	228.34	107.56	-2.12	-1.88	-120.78	*	42.26	85.04	2.01	1.27	42.79	
233365_at	Hs.296711.0	AU147809	226.15	106.67	-2.12	-1.72	-119.47	*	107.09	97.24	-1.1	-0.8	-9.85	
235847_at	Hs.136252.0	BF111312	381	179.46	-2.12	-1.88	-201.54	*	31.07	50.71	1.63	0.89	19.63	
204983_s_at	GPC4: glypican 4	AF064826	1062.39	503.84	-2.11	-1.93	-558.54	*	1484.1	1173.92	-1.26	-1.19	-310.17	
215586_at	Hs.288567.0	AK024173	235.95	112.08	-2.11	-1.8	-123.88	*	38.74	36.49	-1.06	-0.68	-2.25	
226576_at	ARHGAP26: Rho GTPase activating protein 26	AI768563	703.06	332.84	-2.11	-1.99	-370.23	*	124.8	152.44	1.22	1.04	27.64	
1559249_at	ATXN1: ataxin 1	BC010948	437.07	206.91	-2.11	-1.87	-230.16	*	20.81	31.47	1.51	0.68	10.66	
202637_s_at	ICAM1: intercellular adhesion molecule 1	AI608725	820.74	390.96	-2.1	-1.94	-429.78	*	356.33	360.97	1.01	0.91	4.63	
215198_s_at	CALD1: caldesmon 1	AU147402	1058.21	503.2	-2.1	-1.95	-555.01	*	96.54	191.02	1.98	1.36	94.48	
221474_at	MYL12B: myosin, light chain 12B, regulatory	U26162	18163.53	8637.39	-2.1	-1.53	-9526.14	*	8223.57	7403.78	-1.11	-0.82	-819.79	
236947_at	Hs.115831.0	AI686664	486.31	231.63	-2.1	-1.84	-254.68	*	194.58	121.35	-1.6	-1.18	-73.23	
238558_at	Hs.282887.0	AI445833	619.44	295.38	-2.1	-1.89	-324.06	*	28.36	63.87	2.25	1.4	35.51	
208851_s_at	THY1: Thy-1 cell surface antigen	AL161958	5081.86	2428.81	-2.09	-1.87	-2653.05	*	9001.72	6598.05	-1.36	-1.31	-2403.68	
218856_at	TNFRSF21: tumor necrosis factor receptor superfamily, member 21	NM_016629	268.69	128.26	-2.09	-1.82	-140.43	*	247.98	355.47	1.43	1.31	107.5	
220512_at	DLC1: deleted in liver cancer 1	NM_024767	513.51	245.12	-2.09	-1.98	-268.4	*	97.21	122.42	1.26	1.03	25.21	
244476_at	Hs.206088.0	R39769	275.35	131.67	-2.09	-1.79	-143.68	*	29.31	64.17	2.19	1.51	34.86	
218501_at	ARHGEF3: Rho guanine nucleotide exchange factor (GEF) 3	NM_019555	899.46	432.68	-2.08	-1.92	-466.79	*	521.52	516.42	-1.01	-0.91	-5.1	
239179_at	Hs.269545.0	AU155612	194.05	93.16	-2.08	-1.71	-100.89	*	32.45	63.89	1.97	1.41	31.44	
230332_at	ZCCHC7: Zinc finger, CCHC domain containing 7	AA872187	384.04	185.09	-2.07	-1.9	-198.94	*	24.04	61.79	2.57	1.26	37.75	
238341_at	Hs.302759.0	BF677084	292.96	141.32	-2.07	-1.79	-151.64	*	39.71	82.87	2.09	1.09	43.16	
243675_at	Hs.248689.0	BF512500	304.97	147.61	-2.07	-1.74	-157.37	*	56.27	69.55	1.24	0.89	13.28	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
1558504_at	Hs2.396849.1	AF086554	420.81	203.19	-2.07	-1.81	-217.61	*	105.23	143.83	1.37	1.05	38.6	
220935_s_at	CDK5RAP2: CDK5 regulatory subunit associated protein 2	NM_018249	2030.29	986.77	-2.06	-1.97	-1043.52	*	832.69	606.94	-1.37	-1.2	-225.75	
236533_at	ASAP1: ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	AW236958	753.41	365.48	-2.06	-1.93	-387.93	*	290.11	395.4	1.36	1.21	105.28	
1569202_x_at	Hs2.318887.1	BF847120	261.52	126.92	-2.06	-1.77	-134.61	*	121.08	107.17	-1.13	-0.89	-13.91	
238619_at	Hs.193767.0	AA417078	615.04	300.66	-2.05	-1.82	-314.38	*	58.89	71.55	1.21	0.55	12.65	
224701_at	PARP14: poly (ADP-ribose) polymerase family, member 14	AA056548	1332.85	652.13	-2.04	-1.95	-680.73	*	779.86	556.44	-1.4	-1.3	-223.42	
229483_at	Hs.101340.0	AA760738	438.75	215.38	-2.04	-1.86	-223.37	*	34.31	74.71	2.18	1.59	40.4	
1555723_at	Hs2.374686.1	AB062480	398.97	195.31	-2.04	-1.84	-203.66	*	12.07	7.77	-1.55	-0.36	-4.29	
1557224_at	Hs2.30893.1	BM682057	247.1	121.04	-2.04	-1.81	-126.06	*	120.02	111.63	-1.08	-0.79	-8.39	
207711_at	C20orf117: chromosome 20 open reading frame 117	NM_015377	230.33	113.2	-2.03	-1.72	-117.13	*	66.6	58.1	-1.15	-0.83	-8.5	
52255_s_at	COL5A3: collagen, type V, alpha 3	AI984221	1362.3	672.09	-2.03	-1.82	-690.21	*	3701.58	2741.47	-1.35	-1.31	-960.12	
233519_at	Hs.302181.0	AF035297	240.14	118.48	-2.03	-1.83	-121.66	*	30.38	53.99	1.78	1.07	23.61	
242029_at	FNDC3B: Fibronectin type III domain containing 3B	N32832	711	350.84	-2.03	-1.78	-360.16	*	111.13	221.73	2	1.18	110.6	
1553534_at	NLRP10: NLR family, pyrin domain containing 10	NM_176821	201.78	99.51	-2.03	-1.79	-102.27	*	109.3	57.73	-1.89	-1.46	-51.58	
213869_x_at	THY1: Thy-1 cell surface antigen	AA218868	4645.39	2297.49	-2.02	-1.74	-2347.89	*	7721.6	5950.31	-1.3	-1.23	-1771.29	
243561_at	Hs.291015.0	AA651631	314.89	155.84	-2.02	-1.77	-159.06	*	15.58	36.17	2.32	0.77	20.59	
227099_s_at	LOC387763: hypothetical protein LOC387763	AW276078	1598.06	794.55	-2.01	-1.69	-803.51	*	6089.01	3962.58	-1.54	-1.43	-2126.43	
234032_at	Hs.283940.0	AF119847	452.66	225.28	-2.01	-1.86	-227.38	*	37.62	37.33	-1.01	-0.56	-0.29	
242052_at	Hs.291997.0	AW979272	621.16	310.74	-2	-1.86	-310.43	*	106.37	144.62	1.36	1.07	38.25	
209754_s_at	TMPO: thymopoietin	AF113682	765.92	383.95	-1.99	-1.92	-381.97	*	425.98	317.07	-1.34	-1.22	-108.92	
213067_at	MYH10: myosin, heavy chain 10, non-muscle	AI382123	422.61	212.64	-1.99	-1.78	-209.97	*	158.23	280.19	1.77	1.49	121.97	
213605_s_at	LOC100272216 /// LOC100292101: hypothetical LOC100272216 /// hypothetical protein LOC100292101	AL049987	1147.41	576.83	-1.99	-1.82	-570.58	*	139.67	233.92	1.67	1.48	94.26	
232541_at	Hs.272227.0	AK000106	317.19	159.08	-1.99	-1.79	-158.12	*	41.65	70.46	1.69	1.23	28.82	
242440_at	Hs.269412.0	N52821	345.68	173.85	-1.99	-1.71	-171.83	*	31.19	55.63	1.78	0.97	24.44	
242862_x_at	Hs.270577.0	AI804210	516.68	260.14	-1.99	-1.84	-256.54	*	77.39	131.86	1.7	1.28	54.47	
239129_at	Hs.187486.0	AA521218	300.05	151.22	-1.98	-1.81	-148.83	*	28.23	12.87	-2.19	-1.05	-15.36	
1557527_at	Hs2.381949.1	BU789637	523.73	264.44	-1.98	-1.84	-259.3	*	129.78	232.02	1.79	1.35	102.24	
215204_at	Hs.288575.0	AU147295	254.79	129.64	-1.97	-1.8	-125.15	*	20.96	36.51	1.74	1.01	15.55	
1557270_at	Hs2.37834.1	AA632049	385.86	196.36	-1.97	-1.79	-189.5	*	101.02	167.48	1.66	1.34	66.47	
232459_at	Hs.221941.0	AI669804	233.74	119.08	-1.96	-1.66	-114.66	*	14.42	30.43	2.11	1.21	16	
1560128_x_at	LOC441108: Hypothetical gene supported by AK128882	AL713721	326.87	166.91	-1.96	-1.76	-159.97	*	61.55	68.97	1.12	0.64	7.42	
1561166_a_at	Hs2.302213.1	T52172	425.04	216.53	-1.96	-1.84	-208.51	*	15.96	45.82	2.87	1.76	29.86	
242693_at	Hs.193002.0	AW664859	419.39	215.06	-1.95	-1.77	-204.32	*	41.99	71.81	1.71	1.22	29.81	
242786_at	Hs.133984.1	AI521166	365.55	187.5	-1.95	-1.63	-178.05	*	272.18	166.17	-1.64	-1.33	-106.01	
1559490_at	LRCH3: leucine-rich repeats and calponin homology (CH) domain containing 3	AL832278	417.15	213.48	-1.95	-1.71	-203.67	*	53.33	82.96	1.56	1.17	29.63	
1561181_at	Hs2.282797.1	AI075770	266.39	136.62	-1.95	-1.6	-129.77	*	11.44	19.28	1.69	0.18	7.84	
202450_s_at	CTSK: cathepsin K	NM_000396	1550.83	801.25	-1.94	-1.58	-749.58	*	6883.99	7608	1.11	1.07	724.01	
202672_s_at	ATF3: activating transcription factor 3	NM_001674	521.67	268.88	-1.94	-1.84	-252.79	*	136.45	46.92	-2.91	-2.04	-89.53	
240728_at	PLCB4: Phospholipase C, beta 4	AI224105	481.33	248.69	-1.94	-1.73	-232.64	*	103.9	80.99	-1.28	-0.86	-22.91	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
227223_at	LOC643167 /// RBM39: similar to RNA binding motif protein 39 /// RNA binding motif protein 39	BE466173	1794.58	931.53	-1.93	-1.79	-863.05	*	278.14	465.63	1.67	1.45	187.49	
229802_at	Hs.9812.0	AA147884	1909.88	991.27	-1.93	-1.73	-918.61	*	3950.86	2989.91	-1.32	-1.28	-960.95	
206796_at	WISP1: WNT1 inducible signaling pathway protein 1	NM_003882	586.92	305.51	-1.92	-1.63	-281.41	*	1805.76	1137.96	-1.59	-1.46	-667.8	
219687_at	HHAT: hedgehog acyltransferase	NM_018194	461.86	240.93	-1.92	-1.73	-220.93	*	336.64	199.39	-1.69	-1.46	-137.25	
235985_at	Hs.136544.0	AI821477	381.36	198.74	-1.92	-1.75	-182.62	*	52.48	81.58	1.55	1.08	29.1	
242778_at	LPXN: leupaxin	AA250935	302.24	157.02	-1.92	-1.72	-145.23	*	70.08	99.81	1.42	1.13	29.73	
206118_at	STAT4: signal transducer and activator of transcription 4	NM_003151	725.49	379.18	-1.91	-1.75	-346.3	*	378.63	213.73	-1.77	-1.46	-164.9	
235236_at	LOC100131897: Uncharacterized protein LOC100131897	AI991459	437.4	228.73	-1.91	-1.79	-208.67	*	143.07	180.49	1.26	1.11	37.42	
242688_at	Hs.188809.0	AI149880	393.79	205.72	-1.91	-1.75	-188.06	*	41.12	83.74	2.04	1.32	42.62	
1570210_x_at	SAPS2: SAPS domain family, member 2	BC022346	407.4	213.62	-1.91	-1.69	-193.78	*	59.25	109.81	1.85	1.42	50.56	
212303_x_at	KHSRP: KH-type splicing regulatory protein	BG026366	285.47	150.57	-1.9	-1.6	-134.9	*	217.9	146.75	-1.48	-1.24	-71.15	
232595_at	Hs.149341.0	AK023294	288.33	152.12	-1.9	-1.63	-136.21	*	27.87	51.67	1.85	0.85	23.8	
239005_at	Hs.193620.0	AW675572	254.5	133.65	-1.9	-1.7	-120.85	*	32.38	32.83	1.01	0.52	0.45	
242945_at	FAM20A: family with sequence similarity 20, member A	AI860568	248.99	131.19	-1.9	-1.69	-117.8	*	183.05	258.63	1.41	1.23	75.59	
1560741_at	SNRPN: small nuclear ribonucleoprotein polypeptide N	AL832250	282.75	148.47	-1.9	-1.73	-134.28	*	45.02	69.31	1.54	1.17	24.29	
215013_s_at	USP34: ubiquitin specific peptidase 34	AK023845	230.54	122.04	-1.89	-1.76	-108.49	*	12.18	42	3.45	2.02	29.82	
230389_at	FNBP1: formin binding protein 1	BE046511	304.07	160.49	-1.89	-1.55	-143.58	*	31.83	42.29	1.33	0.69	10.47	
239740_at	ETV6: ets variant 6	BF436898	635.14	336.8	-1.89	-1.72	-298.34	*	98.35	136.22	1.39	0.8	37.87	
1564424_at	Hs2.385680.1	BC035983	278.4	147.1	-1.89	-1.61	-131.3	*	43.67	62.85	1.44	0.77	19.17	
213546_at	DKFZP586I1420: hypothetical protein DKFZp586I1420	AL050378	327.38	173.91	-1.88	-1.7	-153.47	*	126.12	133.41	1.06	0.88	7.29	
214657_s_at	NEAT1: nuclear paraspeckle assembly transcript 1 (non-protein coding)	AU134977	1332.03	709.6	-1.88	-1.83	-622.43	*	405.02	436.86	1.08	1.03	31.84	
235167_at	LOC100190986: hypothetical LOC100190986	BE972419	531.07	282.22	-1.88	-1.7	-248.85	*	46.05	85.85	1.86	1.25	39.8	
235969_at	FLJ33996: hypothetical protein FLJ33996	R40373	366.51	194.5	-1.88	-1.69	-172.01	*	164.47	117.62	-1.4	-1.09	-46.85	
236561_at	TGFBR1: Transforming growth factor, beta receptor 1	AV700621	911.21	483.61	-1.88	-1.76	-427.6	*	72.4	82.89	1.14	0.62	10.48	
236978_at	Hs.47342.0	N51961	221.83	117.79	-1.88	-1.55	-104.04	*	43.17	64.32	1.49	1.04	21.15	
239605_x_at	Hs.145611.0	AI743727	465.9	247.64	-1.88	-1.7	-218.27	*	45.93	44.57	-1.03	-0.55	-1.36	
208850_s_at	THY1: Thy-1 cell surface antigen	AL558479	7059.86	3781.83	-1.87	-1.76	-3278.03	*	10420.03	8187.35	-1.27	-1.24	-2232.68	
215083_at	Hs.306292.0	AL049263	351.56	187.75	-1.87	-1.73	-163.81	*	34.55	58.66	1.7	1.15	24.11	
233540_s_at	CDK5RAP2: CDK5 regulatory subunit associated protein 2	AK025867	2979.75	1592.52	-1.87	-1.79	-1387.23	*	1454.37	1126.29	-1.29	-1.24	-328.09	
238909_at	S100A10: S100 calcium binding protein A10	BF126155	285.52	152.51	-1.87	-1.66	-133.01	*	121.74	96.41	-1.26	-1.06	-25.33	
205944_s_at	CLTCL1: clathrin, heavy chain-like 1	NM_007098	818.9	439.72	-1.86	-1.72	-379.18	*	206.43	186.3	-1.11	-0.85	-20.14	
208622_s_at	EZR: ezrin	AA670344	1345.91	724.85	-1.86	-1.73	-621.07	*	2111.97	1959.16	-1.08	-1.02	-152.81	
215175_at	PCNX: pecanex homolog (Drosophila)	AB023212	246.91	132.6	-1.86	-1.54	-114.31	*	36.26	61.59	1.7	0.89	25.33	
233003_at	Hs.296676.0	AK022004	327.17	176.37	-1.86	-1.58	-150.8	*	154.4	171.61	1.11	0.82	17.21	
238970_at	Hs.137551.0	BF509781	222.94	119.99	-1.86	-1.6	-102.95	*	52.83	79.43	1.5	0.9	26.6	
244535_at	Hs.116937.0	AI760944	315.26	169.12	-1.86	-1.64	-146.14	*	63	57.11	-1.1	-0.61	-5.89	
230229_at	DLG1: Discs, large homolog 1 (Drosophila)	AI692879	934.21	505.62	-1.85	-1.76	-428.59	*	80.91	141.22	1.75	1.32	60.32	
237239_at	Hs.189079.0	AW183655	298.57	161.68	-1.85	-1.68	-136.89	*	24.83	102.12	4.11	2.94	77.28	
238918_at	Hs.233442.0	AI985021	722.91	390.34	-1.85	-1.73	-332.57	*	74.41	142.05	1.91	1.45	67.63	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
244766_at	LOC100288704 /// LOC595101 /// LOC641298 /// SMG1: similar to hCG1994151 /// PI-3-kinase-related kinase SMG-1 pseudogene /// SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene /// SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	BG180003	484.46	262.09	-1.85	-1.72	-222.37	*	52.8	94.61	1.79	1.36	41.81	
208178_x_at	TRIO: triple functional domain (PTPRF interacting)	NM_007118	1277.1	695.92	-1.84	-1.73	-581.18	*	768.04	557.67	-1.38	-1.28	-210.37	
215521_at	PHC3: polyhomeotic homolog 3 (Drosophila)	AK023029	268.03	145.42	-1.84	-1.56	-122.61	*	83.95	120.4	1.43	1.02	36.45	
216048_s_at	RHOBTB3: Rho-related BTB domain containing 3	AK023621	1729.06	940.05	-1.84	-1.75	-789.01	*	1070.93	729.7	-1.47	-1.37	-341.24	
232179_at	Hs.138411.0	AL110203	302.48	164.52	-1.84	-1.5	-137.96	*	104.4	85.45	-1.22	-0.82	-18.96	
236545_at	Hs.178604.0	AA532718	289.61	157.38	-1.84	-1.63	-132.23	*	30.95	89.05	2.88	2	58.1	
242710_at	Hs.90877.0	AI791820	298.21	162.34	-1.84	-1.6	-135.87	*	31.98	40.29	1.26	0.74	8.31	
243031_at	Hs.163615.0	N90377	800	435.8	-1.84	-1.72	-364.2	*	77.27	145.63	1.88	1.54	68.36	
1558199_at	FN1: fibronectin 1	W73431	4919.4	2674.02	-1.84	-1.76	-2245.38	*	555.05	715.67	1.29	1.14	160.62	
215599_at	LOC653188: glucuronidase, beta pseudogene	X83300	557.09	303.8	-1.83	-1.7	-253.29	*	42.06	84.69	2.01	1.45	42.63	
235421_at	MAP3K8: Mitogen-activated protein kinase kinase kinase 8	AV713062	225.53	123.44	-1.83	-1.63	-102.09	*	39.61	19.46	-2.04	-1.38	-20.15	
243808_at	Hs.205647.0	AW193531	230.41	126.06	-1.83	-1.59	-104.35	*	47.46	44	-1.08	-0.64	-3.46	
243827_at	Hs.119770.0	AL038125	278.52	152.6	-1.83	-1.59	-125.93	*	61.9	73.58	1.19	0.88	11.67	
244414_at	Hs.222120.0	AI148006	549.09	300.62	-1.83	-1.67	-248.47	*	42.01	83.98	2	1.42	41.97	
202388_at	RGS2: regulator of G-protein signaling 2, 24kDa	NM_002923	1021.89	560.72	-1.82	-1.67	-461.16	*	839.22	1196.68	1.43	1.35	357.46	
202947_s_at	GYPC: glycophorin C (Gerbich blood group)	NM_002101	1404.65	773.65	-1.82	-1.69	-631	*	778.35	581.71	-1.34	-1.23	-196.64	
219213_at	JAM2: junctional adhesion molecule 2	NM_021219	322.09	177.1	-1.82	-1.56	-144.99	*	471.46	500.35	1.06	0.99	28.88	
222358_x_at	Hs.293495.0	AI523613	450.98	247.89	-1.82	-1.61	-203.1	*	50.83	67.83	1.33	0.98	17	
238893_at	LOC338758: hypothetical LOC338758	AI377324	736.41	403.78	-1.82	-1.68	-332.63	*	314.43	290.41	-1.08	-0.92	-24.03	
239780_at	Hs.267200.0	AA468422	245.59	134.6	-1.82	-1.66	-110.99	*	37.01	66.18	1.79	1.19	29.17	
242194_at	CUL4A: Cullin 4A	W80462	229.44	126.37	-1.82	-1.59	-103.07	*	68.65	107.48	1.57	1.27	38.83	
1564378_a_at	Hs2.306766.1	AK025101	797.75	437.5	-1.82	-1.73	-360.24	*	22.32	66.38	2.97	1.82	44.07	
209982_s_at	NRXN2: neurexin 2	AA608820	248.61	137.13	-1.81	-1.52	-111.48	*	170.81	146.84	-1.16	-0.99	-23.97	
226930_at	FNDC1: fibronectin type III domain containing 1	AI345957	4828.67	2661.52	-1.81	-1.66	-2167.15	*	6394.61	10121.11	1.58	1.46	3726.5	
236355_s_at	Hs.36190.0	AI076172	364.31	201.23	-1.81	-1.63	-163.08	*	60.6	72.64	1.2	0.84	12.04	
236404_at	Hs.170527.0	AW197320	329.1	182.21	-1.81	-1.59	-146.89	*	26.82	58.84	2.19	1.57	32.03	
243524_at	Hs.153800.0	AI571719	318.27	175.54	-1.81	-1.62	-142.73	*	27.95	54.29	1.94	1.11	26.34	
1557238_s_at	Hs2.403859.1	BQ446762	412.44	228.24	-1.81	-1.67	-184.2	*	32.43	43.08	1.33	0.83	10.65	
1557813_at	Hs2.302216.1	BF724621	262.35	144.89	-1.81	-1.6	-117.47	*	53.04	53.32	1.01	0.63	0.28	
218893_at	ISOC2: isochorismatase domain containing 2	NM_024710	1089.35	604.81	-1.8	-1.6	-484.54	*	1734.58	1558.17	-1.11	-1.03	-176.41	
228613_at	RAB11FIP3: RAB11 family interacting protein 3 (class II)	BF183535	404.68	225.42	-1.8	-1.63	-179.26	*	69.06	155.71	2.25	1.75	86.65	
238736_at	REV3L: REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	AA805939	433.07	240.92	-1.8	-1.59	-192.15	*	63.1	79.58	1.26	0.72	16.48	
244165_at	C10orf18: chromosome 10 open reading frame 18	AI809511	275.36	153.38	-1.8	-1.65	-121.98	*	27.01	42.69	1.58	0.77	15.69	
209278_s_at	TFPI2: tissue factor pathway inhibitor 2	L27624	1717.9	958.01	-1.79	-1.67	-759.89	*	520.01	849.24	1.63	1.43	329.23	
216769_x_at	Hs.306779.0	AK025180	580.75	324.51	-1.79	-1.66	-256.24	*	47.91	116.71	2.44	1.68	68.79	
237884_x_at	TRPM7: transient receptor potential cation channel, subfamily M, member 7	BF939551	393.39	219.67	-1.79	-1.66	-173.72	*	95.23	146.71	1.54	1.35	51.48	
242691_at	Hs.293493.0	AA829017	1205.99	675.43	-1.79	-1.64	-530.57	*	422.35	472.39	1.12	1.02	50.04	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
1562062_at	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF12 /// NBPF20 /// NBPF3 /// NBPF8 /// RP11-94I2.2: KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 12 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 11-like	BM041211	721.98	403.35	-1.79	-1.65	-318.63	*	128.8	231.45	1.8	1.35	102.66	
207177_at	PTGFR: prostaglandin F receptor (FP)	NM_000959	319.08	179.5	-1.78	-1.53	-139.58	*	835.94	690	-1.21	-1.14	-145.93	
210598_at	g11493408	AF130051	296.34	166.24	-1.78	-1.56	-130.1	*	160.65	146.14	-1.1	-0.92	-14.51	
237180_at	PSME4: Proteasome (prosome, macropain) activator subunit 4	T97717	241.01	135.46	-1.78	-1.65	-105.54	*	44.39	61.91	1.39	1.02	17.52	
241595_at	Hs.282929.0	BF223007	263.3	147.82	-1.78	-1.57	-115.48	*	81.02	79.17	-1.02	-0.6	-1.86	
241777_x_at	Hs.270669.0	AA404501	358.02	201.01	-1.78	-1.61	-157.01	*	28.53	58.57	2.05	1.31	30.05	
1556339_a_at	Hs2.231711.1	BM353142	387.92	218.51	-1.78	-1.53	-169.4	*	62.76	93.27	1.49	1.09	30.51	
1558569_at	UNQ6228: Hypothetical LOC100131541	AL832308	374	210.46	-1.78	-1.64	-163.55	*	24.74	73.66	2.98	1.96	48.92	
215067_x_at	PRDX2: peroxiredoxin 2	AU147942	299.7	169.79	-1.77	-1.6	-129.91	*	64.61	64.93	1.01	0.78	0.33	
217523_at	CD44: CD44 molecule (Indian blood group)	AV700298	292.9	165.07	-1.77	-1.64	-127.84	*	50.6	56.9	1.12	0.73	6.31	
218920_at	FLJ10404: hypothetical protein FLJ10404	NM_019057	1075.43	607.8	-1.77	-1.68	-467.63	*	577	476.16	-1.21	-1.07	-100.84	
239227_at	Hs.187820.0	AW182675	407.53	230.86	-1.77	-1.55	-176.66	*	21.3	25.74	1.21	0.38	4.45	
1552621_at	POLR2J2: polymerase (RNA) II (DNA directed) polypeptide J2	BQ613856	1217.92	687.02	-1.77	-1.63	-530.9	*	272.59	491.01	1.8	1.47	218.42	
1559038_at	SEPT2: septin 2	BC043180	369.68	208.44	-1.77	-1.6	-161.24	*	88.04	137.33	1.56	1.08	49.3	
202328_s_at	PKD1: polycystic kidney disease 1 (autosomal dominant)	NM_000296	1487.27	843.82	-1.76	-1.68	-643.44	*	803.73	647.39	-1.24	-1.16	-156.33	
205068_s_at	ARHGAP26: Rho GTPase activating protein 26	BE671084	472.91	268.69	-1.76	-1.61	-204.22	*	101.94	127.32	1.25	0.93	25.38	
205871_at	PLGLA /// PLGLB1 /// PLGLB2: plasminogen-like A /// plasminogen-like B1 /// plasminogen-like B2	BC005379	296.82	169.09	-1.76	-1.56	-127.72	*	130.34	125.19	-1.04	-0.91	-5.15	
211368_s_at	CASP1: caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	U13700	631.75	358.36	-1.76	-1.6	-273.39	*	348.97	311.9	-1.12	-0.99	-37.07	
230415_at	Hs.17602.0	AU148090	280.64	159.14	-1.76	-1.59	-121.5	*	15.25	52.37	3.44	1.6	37.12	
241681_at	Hs.24605.0	AW296451	809.09	460.42	-1.76	-1.54	-348.67	*	64.77	90.98	1.4	0.96	26.21	
244022_at	Hs.269804.0	AA703239	246.95	140.42	-1.76	-1.55	-106.52	*	28.42	55.21	1.94	1.09	26.79	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
1562063_x_at	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF12 /// NBPF20 /// NBPF3 /// NBPF8 /// RP11-94I2.2: KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 12 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 11-like	BM041211	814.18	462.15	-1.76	-1.64	-352.03	*	108.65	199.37	1.84	1.05	90.72	
215268_at	KIAA0754: KIAA0754	AW663712	328.18	187.36	-1.75	-1.57	-140.82	*	23.57	38.54	1.64	1.01	14.97	
228119_at	LRCH3: leucine-rich repeats and calponin homology (CH) domain containing 3	AI598213	325.12	185.91	-1.75	-1.59	-139.21	*	56.85	118.34	2.08	1.45	61.49	
232168_x_at	MACF1: microtubule-actin crosslinking factor 1	AK023821	1685.42	963.23	-1.75	-1.65	-722.18	*	355.7	422.75	1.19	1.03	67.05	
240399_at	Hs.194600.0	AA668261	270.25	154.52	-1.75	-1.58	-115.72	*	53.49	53.87	1.01	0.6	0.38	
240452_at	GSPT1: G1 to S phase transition 1	AA580082	234.48	133.92	-1.75	-1.53	-100.55	*	61.67	91.08	1.48	1.2	29.4	
242448_at	Hs.131929.0	AI800895	582.71	332.78	-1.75	-1.64	-249.92	*	41.97	125.84	3	2.09	83.86	
208109_s_at	C15orf5: chromosome 15 open reading frame 5	NM_030944	361.81	209.72	-1.73	-1.54	-152.09	*	30.96	36.2	1.17	0.7	5.24	
238589_s_at	Hs.202234.0	AW601184	434.95	252.04	-1.73	-1.56	-182.91	*	21.21	89.73	4.23	3.06	68.52	
242143_at	Hs.190065.0	BE674964	405.96	234.35	-1.73	-1.54	-171.6	*	41.88	81.38	1.94	1.39	39.5	
242471_at	Hs.28170.0	AI916641	819.86	473.34	-1.73	-1.63	-346.51	*	33.24	130.09	3.91	2.72	96.85	
1566482_at	Hs2.376912.1	AL833114	797	462	-1.73	-1.62	-335.01	*	46.46	124.69	2.68	1.94	78.23	
201929_s_at	PKP4: plakophilin 4	NM_003628	1029.36	600.13	-1.72	-1.56	-429.23	*	813.75	568.62	-1.43	-1.26	-245.13	
219892_at	TM6SF1: transmembrane 6 superfamily member 1	NM_023003	582.75	338.58	-1.72	-1.57	-244.17	*	143.35	124.93	-1.15	-0.7	-18.42	
241435_at	Hs.189679.0	AA702930	242.83	141.52	-1.72	-1.53	-101.31	*	37.01	100.11	2.7	1.92	63.09	
242362_at	Hs.159577.0	AI797788	306.47	178.54	-1.72	-1.54	-127.93	*	76.3	104.04	1.36	0.91	27.74	
216867_s_at	PDGFA: platelet-derived growth factor alpha polypeptide	X03795	561.77	328.89	-1.71	-1.64	-232.88	*	165.74	123.1	-1.35	-1.15	-42.64	
228950_s_at	GPR177: G protein-coupled receptor 177	AL534095	1769.65	1036.95	-1.71	-1.56	-732.7	*	2373.28	2548.65	1.07	1.03	175.38	
201983_s_at	EGFR: epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	AW157070	1144.38	671.94	-1.7	-1.61	-472.44	*	524.41	440.59	-1.19	-1.08	-83.82	
215462_at	PLK3: polo-like kinase 3 (Drosophila)	AI978990	1068.77	629.91	-1.7	-1.56	-438.87	*	215.03	255.21	1.19	0.96	40.17	
230099_at	Hs.293560.0	AI139993	876.15	514.82	-1.7	-1.56	-361.33	*	115.97	125.2	1.08	0.77	9.23	
235299_at	SLC41A2: solute carrier family 41, member 2	AI769269	640.51	377.61	-1.7	-1.58	-262.9	*	1252.37	1022.25	-1.23	-1.17	-230.12	
211965_at	ZFP36L1: zinc finger protein 36, C3H type-like 1	BE620915	592.82	350.4	-1.69	-1.55	-242.42	*	381.3	247.86	-1.54	-1.28	-133.44	
214492_at	SGCD: sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	NM_000337	1137.92	673.54	-1.69	-1.54	-464.37	*	1337.34	1943.7	1.45	1.37	606.36	
214860_at	SLC9A7: solute carrier family 9 (sodium/hydrogen exchanger), member 7	AL022165	291.7	172.24	-1.69	-1.55	-119.46	*	138.38	68.88	-2.01	-1.7	-69.49	
216115_at	NF1: neurofibromin 1	AK024873	521.93	309.48	-1.69	-1.58	-212.45	*	86.11	131.48	1.53	1.16	45.37	
232174_at	Hs.188536.0	AA480392	1639.92	970.58	-1.69	-1.61	-669.35	*	79.67	174.76	2.19	1.51	95.09	
232355_at	SNORD114-3: small nucleolar RNA, C/D box 114-3	AU146318	383.51	227.37	-1.69	-1.52	-156.14	*	44.72	121.99	2.73	1.99	77.27	
238049_at	GRAMD3: GRAM domain containing 3	AW971198	417.35	246.74	-1.69	-1.54	-170.61	*	50.58	77.04	1.52	1.06	26.46	
238678_at	tcag7.907: hypothetical LOC402483	AI094787	912.68	539.66	-1.69	-1.54	-373.01	*	326.3	379.77	1.16	0.95	53.47	

probe set	gene	Accession	GFP 4 day	GFP 4 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered
240868_at	LOC100129406: hypothetical protein LOC100129406	AI021983	332.21	196.01	-1.69	-1.54	-136.21	*	43.45	60.02	1.38	1.02	16.57	
244659_at	LOC100131015: hypothetical LOC100131015	AL120025	363.63	214.97	-1.69	-1.5	-148.66	*	66.01	109.35	1.66	1.09	43.33	
1558515_at	NCRNA00182: non-protein coding RNA 182	AK057701	902.7	533.74	-1.69	-1.55	-368.96	*	74.38	123.97	1.67	1.14	49.59	
227014_at	ASPHD2: aspartate beta-hydroxylase domain containing 2	BE550881	1194.34	709.16	-1.68	-1.6	-485.18	*	781.62	482.13	-1.62	-1.43	-299.49	
235879_at	MBNL1: Muscleblind-like (Drosophila)	AI697540	1530.54	912.46	-1.68	-1.58	-618.09	*	127.94	198.95	1.55	1.31	71	
244503_at	Hs.224793.0	BF674612	535.86	319.14	-1.68	-1.58	-216.72	*	32.56	27.18	-1.2	-0.55	-5.37	
1554703_at	ARHGEF10: Rho guanine nucleotide exchange factor (GEF) 10	BC040474	574.92	343.23	-1.68	-1.57	-231.69	*	158.65	208.61	1.31	1.11	49.96	
214964_at	Hs.269421.0	AA554430	344.34	205.81	-1.67	-1.51	-138.53	*	45.7	107.75	2.36	1.68	62.05	
240499_at	Hs.191364.0	AA482221	371.06	221.81	-1.67	-1.52	-149.25	*	31.12	61.82	1.99	1.35	30.69	
243963_at	SDCCAG8: Serologically defined colon cancer antigen 8	AI473707	267.28	160.31	-1.67	-1.52	-106.97	*	40.34	50.28	1.25	0.89	9.94	
244708_at	FLJ33996: hypothetical protein FLJ33996	R49644	427.04	255.78	-1.67	-1.53	-171.26	*	147.61	120.49	-1.23	-0.99	-27.13	
1558111_at	MBNL1: muscleblind-like (Drosophila)	AL562860	647.74	388.32	-1.67	-1.5	-259.43	*	96.44	127.07	1.32	0.98	30.63	
209277_at	TFPI2: tissue factor pathway inhibitor 2	AL574096	738.09	445.61	-1.66	-1.51	-292.48	*	261.81	388.45	1.48	1.26	126.64	
214682_at	LOC399491: GPS, PLAT and transmembrane domain-containing protein	AK023376	1205.69	727.46	-1.66	-1.54	-478.23	*	283.69	294.06	1.04	0.88	10.37	
219158_s_at	NARG1: NMDA receptor regulated 1	NM_025085	1240.65	748.7	-1.66	-1.56	-491.96	*	655.53	609.54	-1.08	-0.99	-45.99	
1556820_a_at	DLEU2: deleted in lymphocytic leukemia 2 (non-protein coding)	H48516	465.09	279.35	-1.66	-1.57	-185.74	*	12.67	55.78	4.4	1.72	43.11	
1558075_at	LOC339047: Hypothetical protein LOC339047	BM989131	262.62	157.75	-1.66	-1.51	-104.87	*	50.38	59.55	1.18	0.94	9.17	
1561079_at	ANKRD28: ankyrin repeat domain 28	BC035170	384.28	231.77	-1.66	-1.52	-152.51	*	103.84	86.23	-1.2	-1.05	-17.61	
238299_at	Hs.193969.0	AW005866	510.08	309.42	-1.65	-1.54	-200.66	*	105.73	173.24	1.64	1.34	67.51	
239228_at	Hs.292385.0	AI298887	323.03	195.88	-1.65	-1.52	-127.15	*	43.38	91.23	2.1	1.38	47.84	
241865_at	Hs.133538.0	AI056689	361.34	219.49	-1.65	-1.51	-141.85	*	49.94	115.66	2.32	1.76	65.72	
215222_x_at	MACF1: microtubule-actin crosslinking factor 1	AK023406	3285.07	2002.25	-1.64	-1.54	-1282.81	*	1511.53	1496.53	-1.01	-0.92	-15.01	
208893_s_at	DUSP6: dual specificity phosphatase 6	BC005047	1412.51	867.39	-1.63	-1.55	-545.12	*	635.7	605.69	-1.05	-0.98	-30.01	
209013_x_at	TRIO: triple functional domain (PTPRF interacting)	AF091395	1157.29	710.93	-1.63	-1.56	-446.36	*	673.88	543.39	-1.24	-1.19	-130.5	
207563_s_at	OGT: O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	U77413	2196.04	1355.01	-1.62	-1.53	-841.04	*	552.02	525.7	-1.05	-0.95	-26.32	
241775_at	Hs.202536.0	AW298119	637.02	392.74	-1.62	-1.55	-244.28	*	60.95	145.13	2.38	1.92	84.18	
242646_at	Hs.191202.0	AA702946	386.44	238.93	-1.62	-1.5	-147.51	*	50.52	83.47	1.65	1.32	32.95	
227383_at	LOC727820: hypothetical protein LOC727820	AW340595	749.4	464.83	-1.61	-1.53	-284.57	*	76.26	148.55	1.95	1.35	72.29	
243318_at	DCAF8: DDB1 and CUL4 associated factor 8	AI208342	402.07	249.51	-1.61	-1.51	-152.56	*	59.3	115.55	1.95	1.63	56.25	
200784_s_at	LRP1: low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	BF304759	2035.7	1270.25	-1.6	-1.51	-765.45	*	1209.75	1133.15	-1.07	-0.99	-76.6	
208476_s_at	FRMD4A: FERM domain containing 4A	NM_018027	530.42	331.26	-1.6	-1.51	-199.15	*	279.41	167.67	-1.67	-1.43	-111.74	
1563467_at	Hs2.407118.1	AL833266	574.93	361.64	-1.59	-1.51	-213.29	*	44.6	108.42	2.43	1.77	63.81	
215206_at	Hs.288700.0	AK025143	796.43	505.95	-1.57	-1.51	-290.48	*	61.48	70.39	1.14	0.75	8.91	

Down-Regulated Genes at Day 10 in Response to 20nM BMP6

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
209395_at	CHI3L1: chitinase 3-like 1 (cartilage glycoprotein-39)	M80927	81.83	7.48	-10.94	-6.27	-74.35		343.85	2.17	-158.61	-91.58	-341.68	*
244745_at	RERG: RAS-like, estrogen-regulated, growth inhibitor	BG484193	29.43	15.72	-1.87	-0.88	-13.71		324.53	15.34	-21.16	-12.39	-309.2	*
226028_at	ROBO4: roundabout homolog 4, magic roundabout (Drosophila)	AA156022	79.11	1.57	-50.4	-11.69	-77.54		121.05	6.55	-18.47	-8.77	-114.49	*
227758_at	RERG: RAS-like, estrogen-regulated, growth inhibitor	AW294092	88.72	11.47	-7.74	-4.98	-77.25		808.28	53.1	-15.22	-12.32	-755.18	*
206336_at	CXCL6: chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993	191.7	143.77	-1.33	-1.14	-47.92		1412.53	107.3	-13.16	-11.86	-1305.24	*
230565_at	ATP6V1G3: ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G3	BF509031	107.63	26.21	-4.11	-2.39	-81.42		753.95	67.62	-11.15	-8.24	-686.33	*
209981_at	CSDC2: cold shock domain containing C2, RNA binding	AL023553	200.26	200.37	1	0.84	0.11		196.3	18.7	-10.5	-4.96	-177.6	*
209800_at	KRT16: keratin 16	AF061812	55.23	27.49	-2.01	-1.1	-27.74		181.49	18.98	-9.56	-5.48	-162.51	*
214038_at	CCL8: chemokine (C-C motif) ligand 8	AI984980	29.6	18.5	-1.6	-0.94	-11.1		148.69	17.5	-8.49	-5.86	-131.18	*
238451_at	MPP7: membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	BF693302	112.51	23.93	-4.7	-2.57	-88.58		172.68	21.75	-7.94	-5.96	-150.93	*
205619_s_at	MEOX1: mesenchyme homeobox 1	NM_004527	11.64	22.54	1.94	0.34	10.89		209.08	26.38	-7.93	-5.19	-182.7	*
205207_at	IL6: interleukin 6 (interferon, beta 2)	NM_000600	6635.74	4977.95	-1.33	-1.28	-1657.79		4453.35	573.52	-7.76	-7.12	-3879.83	*
213782_s_at	MYOZ2: myozenin 2	BF939176	229.46	132.87	-1.73	-1.48	-96.59		146.7	18.91	-7.76	-4.49	-127.78	*
204470_at	CXCL1: chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	NM_001511	708.69	598.1	-1.18	-1.02	-110.59		2982.27	385.34	-7.74	-7.21	-2596.93	*
227058_at	C13orf33: chromosome 13 open reading frame 33	AW084730	982	685.71	-1.43	-1.31	-296.3		2052.49	272.57	-7.53	-6.13	-1779.92	*
204052_s_at	SFRP4: secreted frizzled-related protein 4	NM_003014	259.27	224.87	-1.15	-1.03	-34.4		385.02	52.65	-7.31	-5.01	-332.37	*
209016_s_at	KRT7: keratin 7	BC002700	1482.51	1629.28	1.1	1.04	146.76		1150.71	159.31	-7.22	-5.38	-991.41	*
209351_at	KRT14: keratin 14	BC002690	74.06	35.11	-2.11	-1.09	-38.95		2054.13	301.3	-6.82	-6.22	-1752.83	*
219064_at	ITIH5: inter-alpha (globulin) inhibitor H5	NM_030569	96.43	60.18	-1.6	-1.13	-36.25		564.58	83.91	-6.73	-4.62	-480.67	*
1558972_s_at	THEMIS: thymocyte selection associated	BC043608	88.08	44.5	-1.98	-1.55	-43.57		144.39	21.87	-6.6	-4.43	-122.52	*
204051_s_at	SFRP4: secreted frizzled-related protein 4	AW089415	2098.72	1345.91	-1.56	-1.48	-752.81		2559.33	389.63	-6.57	-5.06	-2169.69	*
222020_s_at	NTM: neurotrimin	AW117456	5196.8	3178.23	-1.64	-1.49	-2018.57		3321.31	521.57	-6.37	-4.97	-2799.74	*
220351_at	CCRL1: chemokine (C-C motif) receptor-like 1	NM_016557	37.3	31.42	-1.19	-0.68	-5.87		161.03	25.76	-6.25	-4.73	-135.28	*
1558501_at	DNM3: dynamin 3	AI631915	33.91	91.86	2.71	1.14	57.95		202.34	33.15	-6.1	-3.18	-169.19	*
227566_at	NTM: neurotrimin	AW085558	8774.09	6081.03	-1.44	-1.38	-2693.06		6716.69	1125.76	-5.97	-5.42	-5590.92	*
239272_at	MMP28: matrix metallopeptidase 28	AI927208	271.72	206.79	-1.31	-1.18	-64.93		243.27	41.69	-5.83	-4.16	-201.57	*
223620_at	GPR34: G protein-coupled receptor 34	AF039686	116.02	37.43	-3.1	-2.22	-78.59		188.79	33.08	-5.71	-3.82	-155.71	*
200795_at	SPARCL1: SPARC-like 1 (hevin)	NM_004684	19.65	28.33	1.44	0.29	8.68		212.68	37.65	-5.65	-3.82	-175.03	*
202987_at	TRAF3IP2: TRAF3 interacting protein 2	AW296296	134.03	161.49	1.2	1.09	27.45		154.6	27.64	-5.59	-3.57	-126.96	*
221829_s_at	TNPO1: transportin 1	AI307759	4785.7	4377.99	-1.09	-0.52	-407.71		19593.51	3520.26	-5.57	-3.61	-16073.25	*
231781_s_at	LRRC2: leucine rich repeat containing 2	AK021919	143.94	82.53	-1.74	-1.34	-61.42		169.55	31.73	-5.34	-3.51	-137.82	*
213060_s_at	CHI3L2: chitinase 3-like 2	U58515	78.78	80.12	1.02	0.83	1.33		377.29	71.11	-5.31	-4.29	-306.18	*
204338_s_at	RGS4: regulator of G-protein signaling 4	NM_005613	4263.82	3979.38	-1.07	-1.01	-284.44		4533.27	867.76	-5.22	-4.73	-3665.5	*
210130_s_at	TM7SF2: transmembrane 7 superfamily member 2	AF096304	227.09	135.96	-1.67	-1.32	-91.13		323.22	63.61	-5.08	-3.91	-259.62	*
205117_at	FGF1: fibroblast growth factor 1 (acidic)	X59065	426.82	292.55	-1.46	-1.3	-134.27		601.03	118.94	-5.05	-4.1	-482.1	*
1558971_at	THEMIS: thymocyte selection associated	BC043608	94.55	39.18	-2.41	-1.77	-55.38		172.66	34.34	-5.03	-3.66	-138.32	*
219970_at	GIPC2: GIPC PDZ domain containing family, member 2	NM_017655	113.85	45.46	-2.5	-1.97	-68.4		189.99	40.93	-4.64	-3.96	-149.06	*
226522_at	PODN: podocan	AW015571	222.92	145.23	-1.53	-1.18	-77.69		715.14	154.66	-4.62	-3.73	-560.48	*
239273_s_at	MMP28: matrix metallopeptidase 28	AI927208	146.21	111.41	-1.31	-0.96	-34.8		156.25	34.09	-4.58	-3.52	-122.16	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
202628_s_at	SERPINE1: serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_000602	12631.8	7671.67	-1.65	-1.48	-4960.14		10827.64	2371.12	-4.57	-3.49	-8456.52	*
233533_at	KRTAP1-5: keratin associated protein 1-5	AJ406928	983.51	1258.34	1.28	1.21	274.83		482.93	106.17	-4.55	-3.64	-376.76	*
241986_at	BMPER: BMP binding endothelial regulator	AI423201	480.37	361.27	-1.33	-1.24	-119.1		1205.86	268.75	-4.49	-4.12	-937.11	*
1552721_a_at	FGF1: fibroblast growth factor 1 (acidic)	NM_033136	323.85	235.83	-1.37	-1.23	-88.02		501.62	111.83	-4.49	-3.62	-389.8	*
212592_at	IGJ: immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	AV733266	54.62	39.98	-1.37	-0.99	-14.63		181.45	41.7	-4.35	-3.6	-139.75	*
204339_s_at	RGS4: regulator of G-protein signaling 4	BC000737	4416.59	4160.21	-1.06	-1.02	-256.38		4291.62	996.68	-4.31	-3.6	-3294.95	*
235736_at	Hs.178144.0	BF000047	81.27	59.31	-1.37	-0.95	-21.96		233.62	55.05	-4.24	-3.02	-178.57	*
1555673_at	hCG_1749898: KRTAP2-4 protein	BC012486	319.41	238.09	-1.34	-1.2	-81.32		338.76	81.96	-4.13	-3.22	-256.8	*
202267_at	LAMC2: laminin, gamma 2	NM_005562	247.69	182.89	-1.35	-1.22	-64.8		305.78	76.54	-3.99	-3.38	-229.23	*
203881_s_at	DMD: dystrophin	NM_004010	688.87	617.48	-1.12	-1.07	-71.39		621.33	156.73	-3.96	-3.6	-464.6	*
205924_at	RAB3B: RAB3B, member RAS oncogene family	BC005035	1403.32	883.36	-1.59	-1.47	-519.96		932.37	236.1	-3.95	-2.88	-696.26	*
239202_at	Hs.65646.0	BE552383	884.01	741.6	-1.19	-1.08	-142.41		545	140.9	-3.87	-3.23	-404.1	*
233234_at	KCTD16: potassium channel tetramerisation domain containing 16	AB037738	594.35	542.62	-1.1	-1.03	-51.73		175.47	45.68	-3.84	-2.66	-129.79	*
229105_at	GPR39: G protein-coupled receptor 39	AV717094	125.05	55.44	-2.26	-1.83	-69.6		163.59	42.75	-3.83	-2.78	-120.84	*
204508_s_at	CA12: carbonic anhydrase XII	BC001012	581.26	430.34	-1.35	-1.25	-150.92		680.91	181.05	-3.76	-3.26	-499.86	*
223657_at	FAM167B: family with sequence similarity 167, member B	BC004269	95.23	39.68	-2.4	-1.75	-55.55		192.95	51.38	-3.76	-3.09	-141.57	*
239787_at	KCTD4: potassium channel tetramerisation domain containing 4	N52767	219.08	129.96	-1.69	-1.48	-89.12		289.48	77.99	-3.71	-2.49	-211.49	*
213332_at	PAPPA2: pappalysin 2	AL031290	1681.42	1184.07	-1.42	-1.33	-497.35		345.94	93.94	-3.68	-2.26	-252	*
206029_at	ANKRD1: ankyrin repeat domain 1 (cardiac muscle)	NM_014391	702.74	900.18	1.28	1.18	197.44		464.74	126.72	-3.67	-3.17	-338.02	*
223640_at	HCST: hematopoietic cell signal transducer	AF285447	104.2	161.84	1.55	1.02	57.65		187.68	51.07	-3.67	-2.2	-136.61	*
211467_s_at	NFIB: nuclear factor I/B	U70862	189.93	111.84	-1.7	-1.45	-78.09		170.26	47.59	-3.58	-2.41	-122.67	*
228640_at	PCDH7: protocadherin 7	BE644809	113.72	59.22	-1.92	-1.59	-54.5		195.99	55.6	-3.53	-2.68	-140.4	*
205193_at	MAFF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	NM_012323	1745.04	1320.84	-1.32	-1.23	-424.2		1394.82	396.74	-3.52	-2.81	-998.08	*
206814_at	NGF: nerve growth factor (beta polypeptide)	NM_002506	1830.98	1574.52	-1.16	-1.1	-256.46		2057.63	599.83	-3.43	-3.17	-1457.8	*
221765_at	UGCG: UDP-glucose ceramide glucosyltransferase	AI378044	2969.92	2000.09	-1.48	-1.41	-969.83		1797.19	526.94	-3.41	-3.09	-1270.25	*
239358_at	Hs.94151.0	BE645256	332.74	366.28	1.1	0.97	33.54		183.32	53.78	-3.41	-1.79	-129.54	*
205715_at	BST1: bone marrow stromal cell antigen 1	NM_004334	1466.13	1386.5	-1.06	-0.98	-79.63		2726.67	803.62	-3.39	-3.05	-1923.05	*
214285_at	FABP3: fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	AI041520	97.71	65.73	-1.49	-1.15	-31.97		895.28	265.05	-3.38	-3.11	-630.23	*
207148_x_at	MYOZ2: myozenin 2	NM_016599	213.98	123.01	-1.74	-1.49	-90.97		155.45	46.1	-3.37	-2.42	-109.36	*
36711_at	MAFF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	AL021977	4246.82	3218.27	-1.32	-1.28	-1028.55		3093.69	935.38	-3.31	-3.11	-2158.31	*
228399_at	OSR1: odd-skipped related 1 (Drosophila)	AI569974	245.48	201.68	-1.22	-1.08	-43.8		250.16	75.78	-3.3	-2.73	-174.38	*
218309_at	CAMK2N1: calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_018584	1325.73	843.68	-1.57	-1.46	-482.05		1455.23	444.02	-3.28	-3.04	-1011.22	*
221087_s_at	APOL3: apolipoprotein L, 3	NM_014349	713.23	561.11	-1.27	-1.19	-152.12		641.94	196.2	-3.27	-2.95	-445.74	*
205738_s_at	FABP3: fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	NM_004102	149.66	109.56	-1.37	-0.89	-40.1		1239.41	380.4	-3.26	-2.99	-859	*
212912_at	RPS6KA2: ribosomal protein S6 kinase, 90kDa, polypeptide 2	AI992251	3577.04	3049.38	-1.17	-1.09	-527.66		1673.19	513.58	-3.26	-2.99	-1159.61	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
233148_at	PODN: podocan	AW292400	65.2	58.1	-1.12	-0.71	-7.11		206.21	63.75	-3.23	-2.49	-142.46	*
204971_at	CSTA: cystatin A (stefin A)	NM_005213	947.06	997.77	1.05	1.01	50.72		464.73	144.73	-3.21	-2.95	-319.99	*
208240_s_at	FGF1: fibroblast growth factor 1 (acidic)	NM_013394	170.56	147.11	-1.16	-0.96	-23.45		292.46	90.98	-3.21	-2.63	-201.49	*
202627_s_at	SERPINE1: serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	AL574210	10960.34	8412.99	-1.3	-1.21	-2547.34		9451.3	2954.24	-3.2	-2.63	-6497.06	*
206074_s_at	HMGA1: high mobility group AT-hook 1	NM_002131	1019.28	629.41	-1.62	-1.36	-389.87		626.67	199.84	-3.14	-2.14	-426.84	*
209621_s_at	PDLIM3: PDZ and LIM domain 3	AF002280	957.16	990.21	1.03	0.95	33.05		656.6	211.76	-3.1	-2.45	-444.84	*
205518_s_at	CMAH: cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	NM_003570	3690.11	2464.5	-1.5	-1.39	-1225.61		2014.16	652.07	-3.09	-2.66	-1362.09	*
210133_at	CCL11: chemokine (C-C motif) ligand 11	D49372	134.7	71.31	-1.89	-1.53	-63.39		236.01	76.84	-3.07	-2.54	-159.17	*
1553243_at	ITIH5: inter-alpha (globulin) inhibitor H5	NM_032817	97.16	45.41	-2.14	-1.74	-51.75		179.92	58.97	-3.05	-2.39	-120.95	*
208394_x_at	ESM1: endothelial cell-specific molecule 1	NM_007036	207.84	301.48	1.45	1.3	93.64		191.91	63.5	-3.02	-2.48	-128.41	*
1554008_at	OSMR: oncostatin M receptor	BC010943	310.06	214.61	-1.44	-1.32	-95.44		394.97	131.91	-2.99	-2.62	-263.07	*
210002_at	GATA6: GATA binding protein 6	D87811	2223.32	2036.51	-1.09	-1.04	-186.8		978.72	335.33	-2.92	-2.64	-643.38	*
218876_at	TPPP3: tubulin polymerization-promoting protein family member 3	NM_016140	744.78	481.43	-1.55	-1.34	-263.35		1670.11	572.59	-2.92	-2.65	-1097.52	*
235496_at	HRCT1: histidine rich carboxyl terminus 1	AI521254	799.04	787.92	-1.01	-0.92	-11.12		1100.3	380.25	-2.89	-2.67	-720.04	*
220976_s_at	KRTAP1-1: keratin associated protein 1-1	NM_030967	504.72	482.62	-1.05	-0.92	-22.1		184.96	64.22	-2.88	-2.05	-120.74	*
213274_s_at	CTSB: cathepsin B	AA020826	2824.98	1854.46	-1.52	-1.43	-970.52		4722.12	1655.5	-2.85	-2.7	-3066.62	*
222549_at	CLDN1: claudin 1	AF101051	3114.61	2924.1	-1.07	-1.02	-190.51		1799.54	641.37	-2.81	-2.55	-1158.17	*
224967_at	UGCG: UDP-glucose ceramide glucosyltransferase	W72338	4661.68	3544.52	-1.32	-1.26	-1117.16		3718.8	1341.72	-2.77	-2.51	-2377.08	*
230523_at	Hs.28456.0	AA603472	249.95	198.09	-1.26	-1.15	-51.86		190.46	69.28	-2.75	-2.1	-121.19	*
202718_at	IGFBP2: insulin-like growth factor binding protein 2, 36kDa	NM_000597	2632.75	1744.57	-1.51	-1.44	-888.18		2610.28	953.84	-2.74	-2.48	-1656.44	*
218182_s_at	CLDN1: claudin 1	NM_021101	1160.43	1001.43	-1.16	-1.03	-159		873.61	319.69	-2.73	-2.31	-553.92	*
212822_at	HEG1: HEG homolog 1 (zebrafish)	AA121502	4097.03	2764.32	-1.48	-1.43	-1332.71		2423.44	891.13	-2.72	-2.41	-1532.31	*
223690_at	LTBP2: latent transforming growth factor beta binding protein 2	AF113211	6557	6213.6	-1.06	-1.01	-343.4		4269.05	1606.98	-2.66	-2.47	-2662.07	*
237016_at	TMEM217: transmembrane protein 217	AI125204	180.26	101.11	-1.78	-1.54	-79.15		224.1	84.14	-2.66	-2.1	-139.96	*
242545_at	TTLL11: tubulin tyrosine ligase-like family, member 11	AA007347	299.7	182.07	-1.65	-1.34	-117.64		434.18	164.74	-2.64	-2.07	-269.43	*
217590_s_at	TRPA1: transient receptor potential cation channel, subfamily A, member 1	AA502609	40.39	41.25	1.02	0.53	0.87		516.19	196.16	-2.63	-2.39	-320.04	*
206907_at	TNFSF9: tumor necrosis factor (ligand) superfamily, member 9	NM_003811	277.46	258.89	-1.07	-0.9	-18.56		1345.31	516.36	-2.61	-2.35	-828.95	*
229760_at	VEPH1: ventricular zone expressed PH domain homolog 1 (zebrafish)	AA988323	489.5	365.84	-1.34	-1.24	-123.65		220.35	84.6	-2.6	-1.96	-135.75	*
236640_at	LOC399959: Hypothetical gene supported by BX647608	AI638169	1087.13	1198.95	1.1	1.04	111.82		881.32	340	-2.59	-2.29	-541.32	*
205925_s_at	RAB3B: RAB3B, member RAS oncogene family	NM_002867	873.52	665.08	-1.31	-1.24	-208.44		680.85	264.8	-2.57	-2.31	-416.05	*
224942_at	PAPPA: pregnancy-associated plasma protein A, pappalysin 1	BG434272	2700.82	2598.21	-1.04	-0.99	-102.62		1765.95	690.65	-2.56	-2.25	-1075.3	*
220407_s_at	TGFB2: transforming growth factor, beta 2	NM_003238	2034.07	2006.15	-1.01	-0.95	-27.91		1038.26	407.97	-2.54	-2.26	-630.29	*
200803_s_at	TMBIM6: transmembrane BAX inhibitor motif containing 6	AF033095	7670.69	7361.48	-1.04	-0.71	-309.21		19179.82	7588.36	-2.53	-1.81	-11591.45	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
224941_at	PAPPA: pregnancy-associated plasma protein A, pappalysin 1	BF107618	2939.84	2652.56	-1.11	-1.05	-287.29		1997.03	790.29	-2.53	-2.27	-1206.75	*
229151_at	SLC14A1: solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	BE673587	496.21	804.8	1.62	1.49	308.59		217.68	86.4	-2.52	-1.95	-131.28	*
204908_s_at	BCL3: B-cell CLL/lymphoma 3	NM_005178	1543.98	974.88	-1.58	-1.49	-569.1		1112.33	443.13	-2.51	-2.33	-669.2	*
209908_s_at	TGFB2: transforming growth factor, beta 2	BF061658	1442.53	1708.17	1.18	1.12	265.64		568.47	227.07	-2.5	-2.22	-341.4	*
201349_at	SLC9A3R1: solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	NM_004252	358.61	209.32	-1.71	-1.47	-149.28		897.04	361.63	-2.48	-2.3	-535.41	*
225283_at	ARRDC4: arrestin domain containing 4	AV701177	3954.13	3133.8	-1.26	-1.22	-820.32		2241.8	902.29	-2.48	-2.31	-1339.51	*
204702_s_at	NFE2L3: nuclear factor (erythroid-derived 2)-like 3	NM_004289	719.26	530.54	-1.36	-1.24	-188.72		437.11	178.16	-2.45	-1.91	-258.96	*
222817_at	HSD3B7: hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	BC004929	526.5	292.58	-1.8	-1.32	-233.93		1392.14	570.86	-2.44	-2.19	-821.29	*
227371_at	BAIAP2L1: BAI1-associated protein 2-like 1	AA496034	515.04	382.2	-1.35	-1.26	-132.84		268.6	110.9	-2.42	-2	-157.71	*
224940_s_at	PAPPA: pregnancy-associated plasma protein A, pappalysin 1	BF107618	3622.46	3445.74	-1.05	-1.01	-176.73		2742.34	1149.39	-2.39	-2.28	-1592.95	*
239370_at	Hs.59507.0	AW081982	2270.65	2149.88	-1.06	-1.01	-120.77		1726.81	728.74	-2.37	-2.18	-998.07	*
243690_at	TRIOBP: TRIO and F-actin binding protein	AW444985	595.02	453.36	-1.31	-1.22	-141.66		287.27	121.35	-2.37	-2.01	-165.92	*
217744_s_at	PERP: PERP, TP53 apoptosis effector	NM_022121	1583.22	1171.48	-1.35	-1.27	-411.74		1910.15	812.67	-2.35	-2.19	-1097.48	*
204420_at	FOSL1: FOS-like antigen 1	BG251266	237.16	243.25	1.03	0.86	6.1		320.17	136.85	-2.34	-1.88	-183.33	*
201981_at	PAPPA: pregnancy-associated plasma protein A, pappalysin 1	AA148534	2589.02	1974.47	-1.31	-1.25	-614.54		1605.12	690.31	-2.33	-1.99	-914.81	*
203812_at	Hs.57929.0	AB011538	1032.84	1269.33	1.23	1.13	236.48		1867.69	806.64	-2.32	-2.1	-1061.05	*
209640_at	PML: promyelocytic leukemia	M79462	406.54	243.45	-1.67	-1.49	-163.09		446.66	193.23	-2.31	-1.99	-253.42	*
210310_s_at	FGF5: fibroblast growth factor 5	AB016517	396.54	275.65	-1.44	-1.23	-120.88		586.73	253.86	-2.31	-2.05	-332.86	*
57588_at	SLC24A3: solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	R62432	380.39	462.92	1.22	1.13	82.53		328.58	142.07	-2.31	-1.95	-186.51	*
229731_at	FOXS1: forkhead box S1	AL160175	296.06	204.99	-1.44	-1.3	-91.08		414.11	178.94	-2.31	-2.07	-235.17	*
212713_at	MFAP4: microfibrillar-associated protein 4	R72286	1568.38	1276.66	-1.23	-1.12	-291.72		3783.74	1654.56	-2.29	-2.2	-2129.18	*
221760_at	MAN1A1: Mannosidase, alpha, class 1A, member 1	BG287153	2509.56	1683.93	-1.49	-1.33	-825.63		5178.27	2264.87	-2.29	-2.13	-2913.4	*
209980_s_at	SHMT1: serine hydroxymethyltransferase 1 (soluble)	L23928	72.28	26.54	-2.72	-1.47	-45.75		232.32	102.06	-2.28	-2.02	-130.26	*
226973_at	VSTM2L: V-set and transmembrane domain containing 2 like	AA206763	209.72	122.76	-1.71	-1.4	-86.96		375.72	165.85	-2.27	-2.03	-209.87	*
201015_s_at	JUP: junction plakoglobin	NM_021991	384.72	224.49	-1.71	-1.49	-160.23		407.04	180.42	-2.26	-1.93	-226.62	*
206090_s_at	DISC1: disrupted in schizophrenia 1	NM_018662	285.11	173.15	-1.65	-1.46	-111.95		321.95	142.54	-2.26	-2	-179.41	*
215034_s_at	TM4SF1: transmembrane 4 L six family member 1	AI189753	1943.69	1274.86	-1.52	-1.42	-668.82		2982.64	1327.64	-2.25	-2.12	-1654.99	*
213032_at	NFIB: nuclear factor I/B	AI186739	752.18	478.6	-1.57	-1.46	-273.58		546.04	243.52	-2.24	-2.01	-302.52	*
241455_at	Hs.135744.0	AW135306	117.62	150.26	1.28	1.07	32.63		199.52	88.91	-2.24	-1.79	-110.61	*
203666_at	CXCL12: chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	NM_000609	2015.68	1933.66	-1.04	-1	-82.02		1232.81	555.96	-2.22	-1.98	-676.85	*
206027_at	S100A3: S100 calcium binding protein A3	NM_002960	104.3	134	1.28	0.92	29.7		880.41	397.21	-2.22	-2.08	-483.2	*
231882_at	FLJ39632: hypothetical LOC642477	AL530703	1912.07	1468.42	-1.3	-1.18	-443.65		1160.11	522.24	-2.22	-1.82	-637.87	*
209909_s_at	TGFB2: transforming growth factor, beta 2	M19154	2873.99	3151.42	1.1	1.04	277.43		1349.47	610.95	-2.21	-2.05	-738.52	*
221583_s_at	KCNMA1: potassium large conductance calcium-activated channel, subfamily M, alpha member 1	AI129381	794.07	578.26	-1.37	-1.26	-215.81		412.84	186.81	-2.21	-1.81	-226.03	*
1554378_a_at	PDE1C: phosphodiesterase 1C, calmodulin-dependent 70kDa	BC022479	751.71	512.65	-1.47	-1.36	-239.07		319.09	144.54	-2.21	-1.83	-174.55	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
204347_at	AK3L1: adenylate kinase 3-like 1	AI653169	1142.55	905.44	-1.26	-1.21	-237.11		691.16	315.51	-2.19	-1.98	-375.64	*
1554960_at	C1orf110: chromosome 1 open reading frame 110	BC040018	93.62	81.63	-1.15	-0.89	-11.99		209.1	95.65	-2.19	-1.86	-113.45	*
206382_s_at	BDNF: brain-derived neurotrophic factor	NM_001709	4034.48	3755.82	-1.07	-1.01	-278.65		1813.36	830.9	-2.18	-1.74	-982.47	*
207923_x_at	PAX8: paired box 8	NM_013953	112.5	99.08	-1.14	-0.9	-13.42		230.7	106.25	-2.17	-1.81	-124.45	*
241470_x_at	Hs.34950.0	R97781	265.63	290.48	1.09	1.01	24.85		401.63	185.77	-2.16	-2.01	-215.85	*
203683_s_at	VEGFB: vascular endothelial growth factor B	NM_003377	900.75	589.24	-1.53	-1.37	-311.51		1209.73	561.8	-2.15	-1.99	-647.93	*
230820_at	Hs.194477.1	BF111169	1247.05	1239.66	-1.01	-0.92	-7.39		1016.91	472.05	-2.15	-1.94	-544.85	*
243010_at	MSI2: musashi homolog 2 (Drosophila)	BE000929	131.72	185.08	1.41	1.27	53.36		202.09	94.19	-2.15	-1.77	-107.9	*
1569807_at	Hs2.382123.1	BC031234	179.66	141.25	-1.27	-1.12	-38.41		209.52	97.39	-2.15	-1.82	-112.13	*
219047_s_at	ZNF668: zinc finger protein 668	NM_024706	780.84	510.23	-1.53	-1.39	-270.6		1335.17	624.95	-2.14	-2.03	-710.22	*
232020_at	SMURF2: SMAD specific E3 ubiquitin protein ligase 2	AU157259	1258	1162.19	-1.08	-1.04	-95.81		1035.34	483.44	-2.14	-2.02	-551.9	*
1560208_at	Hs2.334419.1	AK097618	191.88	185.42	-1.03	-0.88	-6.46		375.26	175.27	-2.14	-1.86	-199.98	*
202997_s_at	LOXL2: lysyl oxidase-like 2	BE251211	2923.51	3027.89	1.04	1	104.38		2487.2	1168.01	-2.13	-1.95	-1319.2	*
204475_at	MMP1: matrix metallopeptidase 1 (interstitial collagenase)	NM_002421	203.44	176.47	-1.15	-0.88	-26.97		490.94	230.37	-2.13	-1.6	-260.58	*
227015_at	ASPHD2: aspartate beta-hydroxylase domain containing 2	Z99714	614.57	385.58	-1.59	-1.42	-228.99		371.22	174.58	-2.13	-1.73	-196.64	*
201850_at	CAPG: capping protein (actin filament), gelsolin-like	NM_001747	615.73	419.56	-1.47	-1.3	-196.17		1149.69	543.24	-2.12	-1.96	-606.45	*
1555434_a_at	SLC39A14: solute carrier family 39 (zinc transporter), member 14	BC015770	1181.95	788.12	-1.5	-1.37	-393.83		1819.65	859.97	-2.12	-1.95	-959.68	*
202896_s_at	SIRPA: signal-regulatory protein alpha	NM_004648	353.14	322.87	-1.09	-0.95	-30.28		422.04	200	-2.11	-1.86	-222.05	*
216869_at	PDE1C: phosphodiesterase 1C, calmodulin-dependent 70kDa	U40372	1140.15	882.89	-1.29	-1.18	-257.26		353.05	167.57	-2.11	-1.51	-185.48	*
236277_at	Hs.30974.0	H23551	356.31	297.31	-1.2	-1.08	-59		670.29	319.72	-2.1	-1.95	-350.57	*
201982_s_at	PAPPA: pregnancy-associated plasma protein A, pappalysin 1	NM_002581	596.46	444.4	-1.34	-1.18	-152.05		463.03	221.56	-2.09	-1.61	-241.47	*
230163_at	GFRA1: GDNF family receptor alpha 1	AW263087	119.69	67.95	-1.76	-1.27	-51.75		223.15	107.47	-2.08	-1.83	-115.68	*
1560826_at	Hs2.339831.1	BC010527	298.05	191.55	-1.56	-1.37	-106.5		308.45	148.48	-2.08	-1.69	-159.97	*
209506_s_at	NR2F1: nuclear receptor subfamily 2, group F, member 1	BC004154	412.72	310.1	-1.33	-1.21	-102.62		420.91	203.54	-2.07	-1.89	-217.37	*
204906_at	RPS6KA2: ribosomal protein S6 kinase, 90kDa, polypeptide 2	BC002363	1725.97	1445.26	-1.19	-1.11	-280.71		725.38	354.07	-2.05	-1.7	-371.31	*
209387_s_at	TM4SF1: transmembrane 4 L six family member 1	M90657	2239.08	1457.32	-1.54	-1.41	-781.76		3332.42	1628.87	-2.05	-1.95	-1703.54	*
213506_at	F2RL1: coagulation factor II (thrombin) receptor-like 1	BE965369	432.43	274.98	-1.57	-1.41	-157.46		386.33	188.27	-2.05	-1.79	-198.06	*
235512_at	CDKL1: cyclin-dependent kinase-like 1 (CDC2-related kinase)	AW976363	126.97	110.85	-1.15	-0.99	-16.12		232.84	113.67	-2.05	-1.78	-119.17	*
226506_at	THSD4: thrombospondin, type I, domain containing 4	AI742570	673.92	474.53	-1.42	-1.32	-199.4		544.95	267.78	-2.04	-1.8	-277.17	*
213343_s_at	GDPD5: glycerophosphodiester phosphodiesterase domain containing 5	AL041124	415.43	295.24	-1.41	-1.27	-120.19		263.98	129.72	-2.03	-1.76	-134.25	*
214012_at	ERAP1: endoplasmic reticulum aminopeptidase 1	BE551138	831.04	789.68	-1.05	-1.01	-41.36		560.92	277.1	-2.02	-1.83	-283.81	*
229507_at	C3orf54: chromosome 3 open reading frame 54	AI857629	184.52	137.72	-1.34	-1	-46.8		335.68	166.77	-2.01	-1.72	-168.91	*
211663_x_at	PTGDS: prostaglandin D2 synthase 21kDa (brain)	M61900	1690.49	1526.48	-1.11	-1.02	-164.01		3445.99	1722.83	-2	-1.9	-1723.16	*
203813_s_at	SLIT3: slit homolog 3 (Drosophila)	NM_003062	1912.93	2552.92	1.33	1.2	640		4686.67	2355.63	-1.99	-1.88	-2331.04	*
227487_s_at	SERPINE2: Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	AI359165	648.36	527.72	-1.23	-1.14	-120.64		561.13	285.48	-1.97	-1.75	-275.65	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
229604_at	CMAH: cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	AW205659	375.1	237.38	-1.58	-1.42	-137.73		224.52	114.2	-1.97	-1.54	-110.33	*
1558540_s_at	MIF /// SLC2A11: macrophage migration inhibitory factor (glycosylation-inhibiting factor) /// solute carrier family 2 (facilitated glucose transporter), member 11	AK055523	528.78	321.77	-1.64	-1.45	-207.01		342.87	174.74	-1.96	-1.62	-168.13	*
201009_s_at	TXNIP: thioredoxin interacting protein	AI439556	8751.36	8030.14	-1.09	-1.05	-721.22		4297.71	2208.33	-1.95	-1.72	-2089.38	*
205696_s_at	GFRA1: GDNF family receptor alpha 1	NM_005264	141.68	43.5	-3.26	-2.25	-98.18		229.91	118.39	-1.94	-1.78	-111.52	*
219270_at	CHAC1: ChaC, cation transport regulator homolog 1 (E. coli)	NM_024111	4032.27	3794.31	-1.06	-1.02	-237.96		521.1	268.5	-1.94	-1.64	-252.6	*
201008_s_at	TXNIP: thioredoxin interacting protein	AA812232	8568.77	8549.55	-1	-0.96	-19.22		4627.92	2408.41	-1.92	-1.7	-2219.52	*
203382_s_at	APOE: apolipoprotein E	NM_000041	77.13	60.65	-1.27	-0.69	-16.48		1129.56	590.46	-1.91	-1.84	-539.11	*
212613_at	BTN3A2: butyrophilin, subfamily 3, member A2	AI991252	454.58	295.71	-1.54	-1.4	-158.87		784.24	410.39	-1.91	-1.66	-373.85	*
219716_at	APOL6: apolipoprotein L, 6	NM_030641	677.8	583.04	-1.16	-1.09	-94.76		436.84	228.92	-1.91	-1.7	-207.92	*
205200_at	CLEC3B: C-type lectin domain family 3, member B	NM_003278	1105.82	744.15	-1.49	-1.17	-361.67		9792.28	5204.33	-1.88	-1.77	-4587.95	*
227341_at	BEND7: BEN domain containing 7	AW195407	565.49	381.08	-1.48	-1.38	-184.4		332.61	177.35	-1.88	-1.66	-155.27	*
230630_at	Hs.292805.0	AI566130	869.66	738.38	-1.18	-1.11	-131.29		442.32	234.98	-1.88	-1.58	-207.34	*
203348_s_at	ETV5: ets variant 5	BF060791	1670.23	1699.65	1.02	0.96	29.42		697.09	372.9	-1.87	-1.61	-324.2	*
203381_s_at	APOE: apolipoprotein E	N33009	81.94	60.66	-1.35	-0.87	-21.27		1133.64	607.47	-1.87	-1.78	-526.18	*
206510_at	SIX2: SIX homeobox 2	AF332197	2088.92	1355.34	-1.54	-1.46	-733.58		3619.2	1933.34	-1.87	-1.78	-1685.86	*
210612_s_at	SYNJ2: synaptojanin 2	AF318616	1209.54	1322.31	1.09	1.05	112.77		964.39	517.21	-1.86	-1.72	-447.18	*
223586_at	ARNTL2: aryl hydrocarbon receptor nuclear translocator-like 2	AF256215	520.5	338.84	-1.54	-1.38	-181.66		759.83	408.04	-1.86	-1.72	-351.79	*
203349_s_at	ETV5: ets variant 5	NM_004454	2272.03	1946.73	-1.17	-1.09	-325.29		1404.38	760.78	-1.85	-1.7	-643.6	*
211312_s_at	WISP1: WNT1 inducible signaling pathway protein 1	AB034725	191.73	147.61	-1.3	-1.02	-44.12		863.24	466.83	-1.85	-1.75	-396.41	*
223062_s_at	PSAT1: phosphoserine aminotransferase 1	BC004863	10180.5	10561.2	1.04	0.99	380.7		4825.94	2604.87	-1.85	-1.51	-2221.07	*
221753_at	SSH1: slingshot homolog 1 (Drosophila)	AI651213	1332.73	1164.88	-1.14	-1.06	-167.85		815.61	442.33	-1.84	-1.58	-373.28	*
239218_at	Hs.12024.0	AI800515	2405.06	2056.87	-1.17	-1.09	-348.19		1276.2	693.98	-1.84	-1.73	-582.22	*
227862_at	TRNP1: TMF1-regulated nuclear protein 1	AA037766	818.14	874.73	1.07	0.96	56.58		2001.91	1093.47	-1.83	-1.71	-908.44	*
200808_s_at	ZYX: zyxin	NM_003461	2592.21	1810.32	-1.43	-1.32	-781.9		2866.96	1578.93	-1.82	-1.57	-1288.03	*
209552_at	PAX8: paired box 8	BC001060	221	148.3	-1.49	-1.21	-72.7		380.49	208.49	-1.82	-1.67	-172	*
211756_at	PTHLH: parathyroid hormone-like hormone	BC005961	133.58	148.61	1.11	0.92	15.03		358.93	197.26	-1.82	-1.69	-161.67	*
227372_s_at	BAIAP2L1: BAI1-associated protein 2-like 1	AA496034	1997.68	1639.99	-1.22	-1.17	-357.69		1197.87	656.78	-1.82	-1.74	-541.09	*
239367_at	BDNF: brain-derived neurotrophic factor	AI127530	865.11	761.7	-1.14	-1.04	-103.41		315.52	173.32	-1.82	-1.59	-142.2	*
212816_s_at	CBS: cystathionine-beta-synthase	BE613178	2504.84	1978.94	-1.27	-1.21	-525.9		724.9	401.77	-1.8	-1.54	-323.13	*
220892_s_at	PSAT1: phosphoserine aminotransferase 1	NM_021154	9404.88	8830.13	-1.07	-1.04	-574.75		3031.42	1695.33	-1.79	-1.54	-1336.09	*
207788_s_at	SORBS3: sorbin and SH3 domain containing 3	NM_005775	474.04	395.89	-1.2	-1.11	-78.15		629.2	353.45	-1.78	-1.61	-275.74	*
209426_s_at	AMACR: alpha-methylacyl-CoA racemase	AF047020	511.13	426.39	-1.2	-1.05	-84.75		2056.93	1158.22	-1.78	-1.7	-898.71	*
228748_at	CD59: CD59 molecule, complement regulatory protein	AI653117	292.22	197.27	-1.48	-1.34	-94.95		531.16	299.18	-1.78	-1.63	-231.98	*
206511_s_at	SIX2: SIX homeobox 2	NM_016932	478.17	357.42	-1.34	-1.23	-120.75		929.58	525.55	-1.77	-1.66	-404.03	*
235046_at	Hs.176376.0	AA456099	326.96	233.22	-1.4	-1.32	-93.74		483.75	273.91	-1.77	-1.61	-209.83	*
243564_at	Hs.148334.0	BE784669	1611.31	1091.32	-1.48	-1.43	-519.99		490.37	276.36	-1.77	-1.61	-214.01	*
236344_at	PDE1C: phosphodiesterase 1C, calmodulin-dependent 70kDa	AW299452	2713.27	2098.92	-1.29	-1.23	-614.35		1362.62	776.35	-1.76	-1.58	-586.27	*

probe set	gene	Accession	GFP 4 day	GFP 4 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered	GFP 10 day	GFP 10 day 2 nM BMP6	fold change	lower bound of FC	difference of means	filtered
200671_s_at	SPTBN1: spectrin, beta, non-erythrocytic 1	N92501	1703.69	1221.3	-1.39	-1.32	-482.39		1363.63	781.35	-1.75	-1.59	-582.27	*
207836_s_at	RBPMS: RNA binding protein with multiple splicing	NM_006867	880.19	766.21	-1.15	-1.08	-113.98		646.41	370.07	-1.75	-1.62	-276.34	*
229669_at	LOC440416: hypothetical gene supported by BC072410	AA166965	320.42	464.31	1.45	1.33	143.89		1167.03	665.1	-1.75	-1.66	-501.93	*
237465_at	USP53: ubiquitin specific peptidase 53	BF196943	612.06	595.24	-1.03	-0.96	-16.82		291.25	166.77	-1.75	-1.53	-124.48	*
225590_at	SH3RF1: SH3 domain containing ring finger 1	AI686957	1528.07	1395.04	-1.1	-1.03	-133.03		737.42	423.02	-1.74	-1.51	-314.4	*
201625_s_at	INSIG1: insulin induced gene 1	BE300521	1555.14	1016.76	-1.53	-1.37	-538.38		3627.1	2100.48	-1.73	-1.64	-1526.62	*
209424_s_at	AMACR: alpha-methylacyl-CoA racemase	AI796120	573.41	476.79	-1.2	-1.07	-96.61		1957.59	1129.63	-1.73	-1.61	-827.95	*
221218_s_at	TPK1: thiamin pyrophosphokinase 1	NM_022445	176.84	108.09	-1.64	-1.39	-68.74		287.35	165.7	-1.73	-1.57	-121.65	*
226668_at	WDSUB1: WD repeat, sterile alpha motif and U-box domain containing 1	W80623	1879.94	1610.56	-1.17	-1.11	-269.39		963.96	557.4	-1.73	-1.67	-406.56	*
226789_at	EMB: embigin homolog (mouse)	W84421	947.78	582.25	-1.63	-1.49	-365.54		1408.05	816.06	-1.73	-1.62	-591.99	*
201675_at	AKAP1: A kinase (PRKA) anchor protein 1	NM_003488	626.24	566.56	-1.11	-0.97	-59.68		438.49	255.29	-1.72	-1.53	-183.21	*
202847_at	PCK2: phosphoenolpyruvate carboxykinase 2 (mitochondrial)	NM_004563	5854.48	5079.17	-1.15	-1.12	-775.3		1193.38	695.78	-1.72	-1.5	-497.59	*
204899_s_at	SAP30: Sin3A-associated protein, 30kDa	BF247098	295.57	341.92	1.16	1.04	46.35		513.3	300.66	-1.71	-1.61	-212.65	*
215495_s_at	SAMD4A: sterile alpha motif domain containing 4A	AL117523	128.15	128.9	1.01	0.75	0.75		289.97	169.68	-1.71	-1.52	-120.3	*
206201_s_at	MEOX2: mesenchyme homeobox 2	NM_005924	90.19	112.77	1.25	1.03	22.58		508.67	299.57	-1.7	-1.52	-209.1	*
209286_at	CDC42EP3: CDC42 effector protein (Rho GTPase binding) 3	AI754416	3834.76	4183.94	1.09	1.05	349.18		1794.54	1052.88	-1.7	-1.56	-741.66	*
209425_at	AMACR: alpha-methylacyl-CoA racemase	AA888589	327.85	295.99	-1.11	-0.99	-31.87		917.99	541.36	-1.7	-1.62	-376.63	*
209610_s_at	SLC1A4: solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	BF340083	3387.59	2793.88	-1.21	-1.17	-593.71		1942.44	1145.61	-1.7	-1.55	-796.83	*
205499_at	SRPX2: sushi-repeat-containing protein, X-linked 2	NM_014467	778.53	504.71	-1.54	-1.42	-273.82		1738.14	1026.51	-1.69	-1.63	-711.64	*
212811_x_at	SLC1A4: solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	AI889380	2990.05	2300.85	-1.3	-1.23	-689.2		1770.77	1046.59	-1.69	-1.55	-724.18	*
223276_at	MST150: MSTP150	AF313413	1990.65	1930.91	-1.03	-0.99	-59.74		1274.39	758.88	-1.68	-1.56	-515.51	*
225685_at	Hs.6774.0	AI801777	5633.91	5564.71	-1.01	-0.94	-69.21		2885.62	1722.72	-1.68	-1.51	-1162.9	*
229055_at	GPR68: G protein-coupled receptor 68	AI805006	494.88	378	-1.31	-1.18	-116.88		785.1	467.45	-1.68	-1.57	-317.65	*
230002_at	GPSM2: G-protein signaling modulator 2 (AGS3-like, C. elegans)	AA406603	174.07	102.84	-1.69	-1.39	-71.22		421.52	251.69	-1.67	-1.5	-169.83	*
243813_at	Hs.98284.0	AA418028	1668.18	1117.58	-1.49	-1.38	-550.6		1718.08	1032.24	-1.66	-1.58	-685.83	*
1554885_a_at	PRIM2: primase, DNA, polypeptide 2 (58kDa)	BC017833	279.35	262.37	-1.06	-0.9	-16.98		820.37	504.2	-1.63	-1.55	-316.17	*
211162_x_at	SCD: stearoyl-CoA desaturase (delta-9-desaturase)	AF116616	485.67	391.05	-1.24	-1.15	-94.62		1198.96	739.13	-1.62	-1.55	-459.83	*
220955_x_at	RAB23: RAB23, member RAS oncogene family	NM_016277	2517.92	2307.24	-1.09	-0.99	-210.69		5628.65	3586.65	-1.57	-1.5	-2042	*

Appendix 1.5 Enriched Biological Process (Genes) Up-Regulated by 2nM BMP6

GO:0001501 - Skeletal System Development (25/319, P=7.14E-10)	
ID	Gene Name
1568598_at, 221000_s_at, 217511_at	Kazal-type serine peptidase inhibitor domain 1
207692_s_at, 205679_x_at	aggrecan
205713_s_at	cartilage oligomeric matrix protein
233109_at, 234951_s_at	collagen, type XII, alpha 1
242138_at	distal-less homeobox 1
207147_at	distal-less homeobox 2
213707_s_at	distal-less homeobox 5
239309_at	distal-less homeobox 6
218995_s_at	endothelin 1
1487_at	estrogen-related receptor alpha
204379_s_at	fibroblast growth factor receptor 3
214520_at	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
201654_s_at	heparan sulfate proteoglycan 2
221350_at	homeobox C8
204926_at	inhibin, beta A
210881_s_at, 202409_at, 202410_x_at	insulin-like growth factor 2 (somatomedin A); insulin; INS-IGF2 readthrough transcript
211958_at, 203426_s_at	insulin-like growth factor binding protein 5
231688_at	matrix metallopeptidase 8 (neutrophil collagenase)
231798_at	noggin
219729_at	paired related homeobox 2
228481_at	periostin, osteoblast specific factor
209465_x_at, 209466_x_at, 211737_x_at	pleiotrophin
203793_x_at	polycomb group ring finger 2
216949_s_at	polycystic kidney disease 1 (autosomal dominant)
37022_at, 204223_at, 228224_at	proline/arginine-rich end leucine-rich repeat protein

GO:0010721 - Negative regulation of Cell Development (9/48, P=1.14E-06)	
ID	Gene Name
266_s_at, 209772_s_at, 209771_x_at, 208651_x_at, 208650_s_at, 216379_x_at	CD24 molecule; CD24 molecule-like 4
213606_s_at	Rho GDP dissociation inhibitor (GDI) alpha
204790_at	SMAD family member 7
204999_s_at	activating transcription factor 5
242138_at	distal-less homeobox 1
207147_at	distal-less homeobox 2
209291_at, 209292_at, 226933_s_at, 209293_x_at	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
227933_at	leucine rich repeat and Ig domain containing 1
231798_at	noggin

GO:0031327 - Negative Regulation of Cellular Biosynthetic Process (26/561, P=7.63E-06)	
ID	Gene Name
1559583_at, 1552914_a_at	CD276 molecule
204790_at	SMAD family member 7
208871_at	atrophin 1
206724_at	chromobox homolog 4 (Pc class homolog, Drosophila)
242138_at	distal-less homeobox 1
207147_at	distal-less homeobox 2
218995_s_at	endothelin 1
204452_s_at	frizzled homolog 1 (Drosophila)
202046_s_at	glucocorticoid receptor DNA binding factor 1
241355_at	hairless homolog (mouse)
203395_s_at, 203394_s_at	hairy and enhancer of split 1, (Drosophila)
221350_at	homeobox C8
222921_s_at, 219743_at	hypothetical LOC100129733; hairy/enhancer-of-split related with YRPW motif 2
204926_at	inhibin, beta A
208937_s_at	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
201566_x_at, 213931_at, 201565_s_at	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
207826_s_at	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
209291_at, 209292_at, 226933_s_at	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
210881_s_at, 202409_at, 202410_x_at	insulin-like growth factor 2 (somatomedin A); insulin; INS-IGF2 readthrough transcript
211958_at, 203426_s_at	insulin-like growth factor binding protein 5
203793_x_at	polycomb group ring finger 2
214794_at	proliferation-associated 2G4, 38kDa; proliferation-associated 2G4 pseudogene 4
203448_s_at	similar to telomeric repeat binding factor (NIMA-interacting) 1; telomeric repeat binding factor (NIMA-interacting) 1; telomeric repeat binding factor (NIMA-interacting) 1 pseudogene
203222_s_at	similar to transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila); transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
207788_s_at	sorbin and SH3 domain containing 3
208033_s_at	zinc finger homeobox 3; hypothetical LOC100132068

GO:0045596 - Negative Regulation of Cell Differentiation (14/216, P=6.97E-05)	
ID	Gene Name
266_s_at, 209772_s_at, 209771_x_at, 208651_x_at, 208650_s_at, 216379_x_at	CD24 molecule; CD24 molecule-like 4
213606_s_at	Rho GDP dissociation inhibitor (GDI) alpha
204790_at	SMAD family member 7
204999_s_at	activating transcription factor 5
242138_at	distal-less homeobox 1
207147_at	distal-less homeobox 2
203395_s_at, 203394_s_at	hairy and enhancer of split 1, (Drosophila)
217937_s_at	histone deacetylase 7
204926_at	inhibin, beta A
209291_at, 209292_at, 226933_s_at, 209293_x_at	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
231183_s_at, 209098_s_at	jagged 1 (Alagille syndrome)
227933_at	leucine rich repeat and Ig domain containing 1
231798_at	noggin
208033_s_at	zinc finger homeobox 3; hypothetical LOC100132068

GO:0001568 - Blood Vessel Development (12/245, P=2.77E-03)	
ID	Gene Name
204790_at	SMAD family member 7
204657_s_at	Src homology 2 domain containing adaptor protein B
200879_s_at	endothelial PAS domain protein 1
218995_s_at	endothelin 1
214520_at	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
222921_s_at, 219743_at	hypothetical LOC100129733; hairy/enhancer-of-split related with YRPW motif 2
208937_s_at	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
231183_s_at, 209098_s_at	jagged 1 (Alagille syndrome)
211356_x_at, 211355_x_at	leptin receptor
219729_at	paired related homeobox 2
209652_s_at	placental growth factor
216949_s_at	polycystic kidney disease 1 (autosomal dominant)

Appendix 1.6 Enriched Biological Process (Genes) Down-Regulated by 2nM BMP6

GO:0010941 - Regulation of Cell Death (28/815, P=2.04E-05)	
ID	Gene Name
204908_s_at	B-cell CLL/lymphoma 3
228780_at	POU class 3 homeobox 3
218501_at	Rho guanine nucleotide exchange factor (GEF) 3
202986_at	aryl-hydrocarbon receptor nuclear translocator 2
210538_s_at	baculoviral IAP repeat-containing 3
211518_s_at	bone morphogenetic protein 4
211368_s_at	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
209031_at	cell adhesion molecule 1
216598_s_at	chemokine (C-C motif) ligand 2
206914_at	cytotoxic and regulatory T cell molecule
234986_at, 236140_at	glutamate-cysteine ligase, modifier subunit
206614_at	growth differentiation factor 5
203382_s_at	hypothetical LOC100129500; apolipoprotein E
209541_at	insulin-like growth factor 1 (somatomedin C)
201596_x_at	keratin 18; keratin 18 pseudogene 26; keratin 18 pseudogene 19
240148_at	mutS homolog 6 (E. coli)
202086_at	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
209193_at	pim-1 oncogene
225842_at, 217996_at, 217997_at, 217999_s_at, 217998_at	pleckstrin homology-like domain, family A, member 1
227751_at	programmed cell death 5
209640_at, 239582_at	promyelocytic leukemia; similar to promyelocytic leukemia protein isoform 1
1566342_at	superoxide dismutase 2, mitochondrial
201042_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
200803_s_at	transmembrane BAX inhibitor motif containing 6
202688_at, 202687_s_at	tumor necrosis factor (ligand) superfamily, member 10
221371_at	tumor necrosis factor (ligand)
223827_at, 227812_at	tumor necrosis factor receptor superfamily, member 19
204255_s_at, 204254_s_at	vitamin D (1,25- dihydroxyvitamin D3) receptor

GO:0006955 - Immune Response (25/690, P=2.83E-05)	
204972_at	2'-5'-oligoadenylate synthetase 2, 69/71kDa
204908_s_at	B-cell CLL/lymphoma 3
227749_at	POU class 2 homeobox 2
201998_at	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1
209546_s_at	apolipoprotein L, 1
209031_at	cell adhesion molecule 1
210133_at	chemokine (C-C motif) ligand 11
216598_s_at	chemokine (C-C motif) ligand 2
208075_s_at	chemokine (C-C motif) ligand 7
204470_at	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
206336_at	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
210659_at, 229121_at, 207652_s_at	chemokine-like receptor 1
221019_s_at	collectin sub-family member 12
206417_at	cyclic nucleotide gated channel alpha 1
206914_at	cytotoxic and regulatory T cell molecule
210848_at	glucose phosphate isomerase
209417_s_at	interferon-induced protein 35
204439_at	interferon-induced protein 44-like
209827_s_at	interleukin 16 (lymphocyte chemoattractant factor)
203828_s_at	interleukin 32
205266_at	leukemia inhibitory factor (cholinergic differentiation factor)
240148_at	mutS homolog 6 (E. coli)
217767_at	similar to Complement C3 precursor; complement component 3; hypothetical protein LOC100133511
202688_at, 202687_s_at	tumor necrosis factor (ligand) superfamily, member 10
221371_at	tumor necrosis factor (ligand) superfamily, member 18

GO:0007155 - Cell Adhesion (23/700, 2.68E-04)	
ID	Gene Name
213790_at	ADAM metallopeptidase domain 12
236029_at	FAT tumor suppressor homolog 3 (Drosophila)
41660_at	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
209031_at	cell adhesion molecule 1
210133_at	chemokine (C-C motif) ligand 11
216598_s_at	chemokine (C-C motif) ligand 2
207571_x_at, 210785_s_at	chromosome 1 open reading frame 38
228335_at	claudin 11
218975_at, 52255_s_at	collagen, type V, alpha 3
204136_at	collagen, type VII, alpha 1
203917_at	coxsackie virus and adenovirus receptor pseudogene 2; coxsackie virus and adenovirus receptor
207977_s_at, 213068_at, 213071_at	dermatopontin
240259_at, 204359_at	fibronectin leucine rich transmembrane protein 2
207370_at, 236028_at	integrin-binding sialoprotein
203828_s_at	interleukin 32
201015_s_at	junction plakoglobin
229127_at, 219213_at	junctional adhesion molecule 2
212843_at, 227394_at	neural cell adhesion molecule 1
204105_s_at	neuronal cell adhesion molecule
214111_at	opioid binding protein/cell adhesion molecule-like
204879_at, 221898_at	podoplanin
228635_at	protocadherin 10
213247_at	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1

GO:0031099 - Regeneration (7/69, P=3.75E-04)	
ID	Gene Name
202912_at	adrenomedullin
216598_s_at	chemokine (C-C motif) ligand 2
209541_at	insulin-like growth factor 1 (somatomedin C)
205302_at	insulin-like growth factor binding protein 1
205266_at	leukemia inhibitory factor (cholinergic differentiation factor)
223925_s_at	myotrophin; leucine zipper protein 6
205479_s_at	plasminogen activator, urokinase

GO:0001568 - Blood Vessel Development (10/245, P=7.04E-03)	
ID	Gene Name
209212_s_at, 209211_at	Kruppel-like factor 5 (intestinal)
206298_at, 1560821_at	Rho GTPase activating protein 22
211518_s_at	bone morphogenetic protein 4
205767_at	epiregulin
210848_at	glucose phosphate isomerase
203382_s_at	hypothetical LOC100129500; apolipoprotein E
215073_s_at	nuclear receptor subfamily 2, group F, member 2
205479_s_at	plasminogen activator, urokinase
219700_at	plexin domain containing 1
201042_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)

Appendix 1.7 Enriched Biological Process (Genes) Up-Regulated by 20nM BMP6

GO:0001501 Skeletal System Development (57/319, P=1.66E-16)	
ID	Gene Name
203685_at	B-cell CLL/lymphoma 2
228173_at	GNAS complex locus
221000_s_at, 217511_at, 1568598_at	Kazal-type serine peptidase inhibitor domain 1
1569150_x_at	PDZ and LIM domain 7 (enigma)
213435_at	SATB homeobox 2
228214_at	SRY (sex determining region Y)-box 6
202935_s_at	SRY (sex determining region Y)-box 9
1552340_at	Sp7 transcription factor
219682_s_at, 225544_at	T-box 3
217161_x_at, 207692_s_at	aggrecan
215783_s_at, 1557924_s_at	alkaline phosphatase, liver/bone/kidney
205290_s_at, 205289_at	bone morphogenetic protein 2
205713_s_at	cartilage oligomeric matrix protein
242558_at, 1554411_at, 223679_at	catenin (cadherin-associated protein), beta 1, 88kDa
232458_at	collagen, type III, alpha 1
213622_at	collagen, type IX, alpha 2
229271_x_at	collagen, type XI, alpha 1
213870_at	collagen, type XI, alpha 2
234951_s_at, 233109_at	collagen, type XII, alpha 1
206788_s_at	core-binding factor, beta subunit
242138_at	distal-less homeobox 1
207147_at	distal-less homeobox 2
213707_s_at	distal-less homeobox 5
221289_at, 239309_at	distal-less homeobox 6
218995_s_at, 222802_at	endothelin 1
204380_s_at, 204379_s_at	fibroblast growth factor receptor 3
213260_at	forkhead box C1
214520_at	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
203697_at, 203698_s_at	frizzled-related protein
203146_s_at	gamma-aminobutyric acid (GABA) B receptor,
232889_at	glucuronidase, beta pseudogene; glucuronidase, beta pseudogene 1
216860_s_at	growth differentiation factor 11
205498_at	growth hormone receptor
208557_at	homeobox A6
229667_s_at	homeobox B8
231936_at	homeobox C9
205522_at	homeobox D4
204926_at	inhibin, beta A

GO:0001501 Skeletal System Development (Continued) (57/319, P=1.66E-16)	
209540_at, 211577_s_at, 209542_x_at, 209541_at	insulin-like growth factor 1 (somatomedin C)
202409_at, 202410_x_at, 210881_s_at	insulin-like growth factor 2 (somatomedin A); insulin; INS-IGF2 readthrough transcript
211958_at, 203426_s_at, 1555997_s_at, 203425_s_at	insulin-like growth factor binding protein 5
236028_at, 207370_at	integrin-binding sialoprotein
205959_at	matrix metallopeptidase 13 (collagenase 3)
207329_at, 231688_at	matrix metallopeptidase 8 (neutrophil collagenase)
205932_s_at	msh homeobox 1
231798_at	noggin
226695_at, 238852_at, 205991_s_at	paired related homeobox 1
219729_at	paired related homeobox 2
205911_at	parathyroid hormone 1 receptor
228481_at	periostin, osteoblast specific factor
209466_x_at, 211737_x_at, 209465_x_at	pleiotrophin
212151_at, 212148_at	pre-B-cell leukemia homeobox 1
204223_at, 37022_at, 228224_at	proline/arginine-rich end leucine-rich repeat protein
204748_at	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
216994_s_at, 232231_at, 236859_at	runt-related transcription factor 2
209875_s_at	secreted phosphoprotein 1
230746_s_at,	stanniocalcin 1

GO:0043062 - Extracellular Structure Organization (34/163, 6.75E-12)	
ID	Gene Name
214535_s_at, 236901_at, 214454_at	ADAM metallopeptidase with thrombospondin type 1 motif, 2
221000_s_at, 217511_at, 1568598_at	Kazal-type serine peptidase inhibitor domain 1
207692_s_at	aggrecan
209462_at	amyloid beta (A4) precursor-like protein 1
206385_s_at	ankyrin 3, node of Ranvier (ankyrin G)
242558_at, 1554411_at, 223679_at	catenin (cadherin-associated protein), beta 1, 88kDa
219747_at, 230319_at, 215059_at	chromosome 4 open reading frame 31
203989_x_at	coagulation factor II (thrombin) receptor
232458_at	collagen, type III, alpha 1
229271_x_at	collagen, type XI, alpha 1
213870_at	collagen, type XI, alpha 2
234951_s_at, 233109_at	collagen, type XII, alpha 1
212865_s_at	collagen, type XIV, alpha 1
209082_s_at	collagen, type XVIII, alpha 1
221541_at	cysteine-rich secretory protein LCCL domain containing 2
216269_s_at, 212670_at	elastin
1568779_a_at	extracellular matrix protein 2, female organ and adipocyte specific
213260_at	forkhead box C1
214520_at	forkhead box C2
206377_at	forkhead box F2
235666_at, 214265_at	integrin, alpha 8
236028_at, 207370_at	integrin-binding sialoprotein
229554_at	lumican
201496_x_at, 201497_x_at	myosin, heavy chain 11, smooth muscle
229422_at	nardilysin (N-arginine dibasic convertase)
228481_at	periostin, osteoblast specific factor
223854_at	protocadherin beta 10; protocadherin beta 9
231726_at	protocadherin beta 14
232099_at	protocadherin beta 16
223629_at	protocadherin beta 5
239443_at	protocadherin beta 6
216005_at, 237169_at	tenascin C
201506_at	transforming growth factor, beta-induced, 68kDa
218731_s_at	von Willebrand factor A domain containing 1

GO:0001568 - Blood Vessel Development (38/245, P=2.51E-09)	
ID	Gene Name
1557383_a_at	ATPase inhibitory factor 1
204249_s_at	LIM domain only 2 (rhombotin-like 1)
204790_at	SMAD family member 7
219682_s_at, 225544_at	T-box 3
205609_at, 205608_s_at	angiopoietin 1
205572_at, 211148_s_at, 236034_at	angiopoietin 2
242558_at, 1554411_at, 223679_at	catenin (cadherin-associated protein), beta 1, 88kDa
232458_at	collagen, type III, alpha 1
209082_s_at	collagen, type XVIII, alpha 1
231778_at	distal-less homeobox 3
242868_at, 200879_s_at	endothelial PAS domain protein 1
218995_s_at, 222802_at	endothelin 1
216235_s_at, 243555_at, 244832_at, 204464_s_at, 204463_s_at	endothelin receptor type A
213260_at	forkhead box C1
214520_at	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
204845_s_at, 204844_at	glutamyl aminopeptidase (aminopeptidase A)
44783_s_at, 218839_at	hairy/enhancer-of-split related with YRPW motif 1
225263_at	heparan sulfate 6-O-sulfotransferase 1
219743_at, 222921_s_at	hypothetical LOC100129733; hairy/enhancer-of-split related with YRPW motif 2
208937_s_at	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
205884_at	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
232797_at, 236251_at,	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
211506_s_at	interleukin 8
232406_at, 231183_s_at, 209098_s_at	jagged 1 (Alagille syndrome)
210089_s_at, 210990_s_at, 202202_s_at	laminin, alpha 4
211354_s_at	leptin receptor
221796_at	neurotrophic tyrosine kinase, receptor, type 2

GO:0001568 - Blood Vessel Development (Continued) (38/245, P=2.51E-09)	
226695_at, 238852_at, 205991_s_at	paired related homeobox 1
219729_at	paired related homeobox 2
209355_s_at	phosphatidic acid phosphatase type 2B
209652_s_at	placental growth factor
201860_s_at	plasminogen activator, tissue
241938_at	quaking homolog, KH domain RNA binding (mouse)
239251_at	reticulon 4
228850_s_at, 209897_s_at	slit homolog 2 (Drosophila)
204642_at	sphingosine-1-phosphate receptor 1
205016_at	transforming growth factor, alpha
219778_at	zinc finger protein, multitype 2

GO:0016055 - Wnt Receptor Signaling Pathway (22/133, P=3.49E-06)	
ID	Gene Name
216379_x_at, 209772_s_at, 208650_s_at, 208651_x_at, 209771_x_at, 266_s_at	CD24 molecule; CD24 molecule-like 4
206022_at	Norrie disease (pseudoglioma)
201416_at, 213668_s_at, 201418_s_at	SRY (sex determining region Y)-box 4
211062_s_at	carboxypeptidase Z
1556007_s_at, 240221_at, 243338_at	casein kinase 1, alpha 1
242558_at, 1554411_at, 223679_at	catenin (cadherin-associated protein), beta 1, 88kDa
204602_at	dickkopf homolog 1 (Xenopus laevis)
224199_at	dickkopf homolog 2 (Xenopus laevis)
219889_at	frequently rearranged in advanced T-cell lymphomas
204451_at, 204452_s_at	frizzled homolog 1 (Drosophila)
219683_at	frizzled homolog 3 (Drosophila)
218665_at	frizzled homolog 4 (Drosophila)
221245_s_at, 206136_at	frizzled homolog 5 (Drosophila)
227405_s_at, 216587_s_at, 224325_at	frizzled homolog 8 (Drosophila)
203697_at, 203698_s_at	frizzled-related protein
227250_at	kringle containing transmembrane protein 1
221558_s_at, 210948_s_at	lymphoid enhancer-binding factor 1
202036_s_at	secreted frizzled-related protein 1
228284_at, 203222_s_at	similar to transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila); transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
201869_s_at, 201867_s_at	transducin (beta)-like 1X-linked
224022_x_at	wingless-type MMTV integration site family, member 16
214631_at	zinc finger and BTB domain containing 33

GO:0001649 - Osteoblast Differentiation (12/42, P=5.55E-06)	
ID	Gene Name
213435_at	SATB homeobox 2
1552340_at	Sp7 transcription factor
205290_s_at, 205289_at	bone morphogenetic protein 2
206788_s_at	core-binding factor, beta subunit
203146_s_at	gamma-aminobutyric acid (GABA) B receptor, 1
209540_at, 211577_s_at, 209542_x_at, 209541_at	insulin-like growth factor 1 (somatomedin C)
202409_at, 202410_x_at, 210881_s_at	insulin-like growth factor 2 (somatomedin A); insulin; INS-IGF2 readthrough transcript
211958_at, 203426_s_at, 1555997_s_at, 203425_s_at	insulin-like growth factor binding protein 5
231798_at	noggin
205911_at	parathyroid hormone 1 receptor
216994_s_at, 232231_at, 236859_at	runt-related transcription factor 2
209875_s_at	secreted phosphoprotein 1

Appendix 1.8 Enriched Biological Process (Genes) Down-Regulated by 20nM BMP6

GO:0007155 - Cell Adhesion (59/700, P=2.40E-08)	
ID	Gene Name
202952_s_at, 213790_at, 226777_at	ADAM metallopeptidase domain 12
217523_at	CD44 molecule (Indian blood group)
217744_s_at	PERP, TP53 apoptosis effector
226989_at, 227340_s_at, 227339_at	RGM domain family, member B
243012_at, 1552482_at	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
206702_at	TEK tyrosine kinase, endothelial
208850_s_at, 213869_x_at, 208851_s_at	Thy-1 cell surface antigen
211312_s_at, 229802_at, 235821_at, 206796_at	WNT1 inducible signaling pathway protein 1
214953_s_at	amyloid beta (A4) precursor protein
41660_at	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
209030_s_at, 209032_s_at, 209031_at	cell adhesion molecule 1
210133_at	chemokine (C-C motif) ligand 11
216598_s_at	chemokine (C-C motif) ligand 2
203666_at	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
210785_s_at, 207571_x_at	chromosome 1 open reading frame 38
218182_s_at, 222549_at	claudin 1
228335_at	claudin 11
52255_s_at, 218975_at	collagen, type V, alpha 3
212940_at, 212091_s_at, 212937_s_at, 212938_at	collagen, type VI, alpha 1
221900_at, 52651_at	collagen, type VIII, alpha 2
203477_at	collagen, type XV, alpha 1
210701_at	craniofacial development protein 1
220512_at	deleted in liver cancer 1
207977_s_at, 213068_at, 213071_at	dermatopontin
230229_at	discs, large homolog 1 (Drosophila)
232098_at	dystonin
201983_s_at, 232541_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
1558199_at	fibronectin 1
204359_at, 240259_at	fibronectin leucine rich transmembrane protein 2

GO:0007155 - Cell Adhesion (Continued) (59/700, P=2.40E-08)	
208622_s_at	hypothetical protein LOC100129652; ezrin
201474_s_at	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
209663_s_at	integrin, alpha 7
211488_s_at	integrin, beta 8
202637_s_at, 202638_s_at	intercellular adhesion molecule 1
203828_s_at	interleukin 32
201650_at, 201015_s_at	junction plakoglobin
219213_at	junctional adhesion molecule 2
202267_at	laminin, gamma 2
242778_at	leupaxin
202997_s_at	lysyl oxidase-like 2
203037_s_at	metastasis suppressor 1
212713_at	microfibrillar-associated protein 4
227394_at, 212843_at	neural cell adhesion molecule 1
209982_s_at	neurexin 2
215020_at, 229649_at, 215021_s_at, 205795_at	neurexin 3
204105_s_at	neuronal cell adhesion molecule
227566_at, 222020_s_at	neurotrimin
214111_at	opioid binding protein/cell adhesion molecule-like
236752_at, 201929_s_at	plakophilin 4
221898_at, 204879_at	podoplanin
202328_s_at	polycystic kidney disease 1 (autosomal dominant)
233609_at, 233770_at	protein tyrosine phosphatase, receptor type, K
228635_at	protocadherin 10
228640_at	protocadherin 7
202896_s_at	signal-regulatory protein alpha
207788_s_at	sorbin and SH3 domain containing 3
213247_at, 219552_at, 224543_at	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
237884_x_at	transient receptor potential cation channel, subfamily M, member 7
200808_s_at	zyxin

GO:0001568 - Blood Vessel Development (29/245, 2.50E-7)	
ID	Gene Name
217523_at	CD44 molecule (Indian blood group)
209211_at, 209212_s_at	Kruppel-like factor 5 (intestinal)
219158_s_at	NMDA receptor regulated 1
241387_at	PTK2 protein tyrosine kinase 2
1560821_at, 206298_at	Rho GTPase activating protein 22
208850_s_at, 213869_x_at, 208851_s_at	Thy-1 cell surface antigen
211518_s_at	bone morphogenetic protein 4
203666_at	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
203477_at	collagen, type XV, alpha 1
214012_at	endoplasmic reticulum aminopeptidase 1
205767_at	epiregulin
1552721_a_at, 208240_s_at, 205117_at	fibroblast growth factor 1 (acidic)
203382_s_at, 203381_s_at	hypothetical LOC100129500; apolipoprotein E
209663_s_at	integrin, alpha 7
211506_s_at	interleukin 8
201465_s_at	jun oncogene
202827_s_at, 217279_x_at	matrix metallopeptidase 14 (membrane-inserted)
206201_s_at	mesenchyme homeobox 2
216115_at	neurofibromin 1
211668_s_at, 205479_s_at	plasminogen activator, urokinase
216867_s_at	platelet-derived growth factor alpha polypeptide
202328_s_at	polycystic kidney disease 1 (autosomal dominant)
243031_at, 239251_at	reticulon 4
226028_at	roundabout homolog 4, magic roundabout (Drosophila)
236947_at, 240815_at, 203788_s_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
209909_s_at, 220407_s_at, 209908_s_at	transforming growth factor, beta 2
239129_at, 239605_x_at, 236561_at	transforming growth factor, beta receptor 1
201042_at, 211573_x_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
211965_at	zinc finger protein 36, C3H type-like 1

GO:0042127 - Regulation of Cell Proliferation (60/787, P=5.65E-07)	
ID	Gene Name
204420_at	FOS-like antigen 1
209211_at, 209212_s_at	Kruppel-like factor 5 (intestinal)
237891_at	Mdm2 p53 binding protein homolog (mouse)
219773_at	NADPH oxidase 4
1557543_at	Notch homolog 2 (Drosophila)
244745_at, 227758_at	RAS-like, estrogen-regulated, growth inhibitor
239448_at, 205397_x_at	SMAD family member 3
206702_at	TEK tyrosine kinase, endothelial
202672_s_at	activating transcription factor 3
202912_at	adrenomedullin
202986_at	aryl-hydrocarbon receptor nuclear translocator 2
242068_at	baculoviral IAP repeat-containing 6
211518_s_at	bone morphogenetic protein 4
244503_at, 239367_at, 206382_s_at	brain-derived neurotrophic factor
242693_at	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
216598_s_at	chemokine (C-C motif) ligand 2
204470_at	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
210701_at	craniofacial development protein 1
242362_at	cullin 3
242194_at	cullin 4A
243808_at	cyclin-dependent kinase 6
220512_at	deleted in liver cancer 1
207977_s_at, 213068_at, 213071_at	dermatopontin
201983_s_at, 232541_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
205767_at	epiregulin
205738_s_at, 214285_at	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)
1552721_a_at, 208240_s_at, 205117_at	fibroblast growth factor 1 (acidic)
207822_at	fibroblast growth factor receptor 1
230415_at, 1561166_a_at, 244535_at, 244845_at	forkhead box P1
203382_s_at, 203381_s_at	hypothetical LOC100129500; apolipoprotein E
209184_s_at, 209185_s_at	insulin receptor substrate 2
205207_at	interleukin 6 (interferon, beta 2)
211506_s_at	interleukin 8

GO:0042127 - Regulation of Cell Proliferation (Continued) (60/787, P=5.65E-07)	
201465_s_at	jun oncogene
205266_at	leukemia inhibitory factor (cholinergic differentiation factor)
206814_at	nerve growth factor (beta polypeptide)
208241_at	neuregulin 1
216115_at	neurofibromin 1
213032_at, 213029_at, 209290_s_at, 211467_s_at	nuclear factor I/B
1554008_at	oncostatin M receptor
211756_at	parathyroid hormone-like hormone
211668_s_at, 205479_s_at	plasminogen activator, urokinase
1563467_at	platelet derived growth factor C
216867_s_at	platelet-derived growth factor alpha polypeptide
220049_s_at, 224399_at	programmed cell death 1 ligand 2
239582_at, 209640_at	promyelocytic leukemia; similar to promyelocytic leukemia protein isoform 1
205128_x_at, 215813_s_at	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
233609_at, 233770_at	protein tyrosine phosphatase, receptor type, K
1568765_at, 202627_s_at, 202628_s_at	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
209969_s_at, 232375_at	signal transducer and activator of transcription 1, 91kDa
221477_s_at, 216841_s_at, 215223_s_at	superoxide dismutase 2, mitochondrial
1566191_at	suppressor of zeste 12 homolog (Drosophila)
201008_s_at, 201009_s_at	thioredoxin interacting protein
209909_s_at, 220407_s_at, 209908_s_at	transforming growth factor, beta 2
239129_at, 239605_x_at, 236561_at	transforming growth factor, beta receptor 1
201042_at, 211573_x_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
241435_at	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
203683_s_at	vascular endothelial growth factor B
204254_s_at, 204255_s_at	vitamin D (1,25- dihydroxyvitamin D3) receptor
212758_s_at, 210875_s_at	zinc finger E-box binding homeobox 1

GO:0010941 - Regulation of Cell Death (60/815, P=1.78E-06)	
ID	Gene Name
204908_s_at	B-cell CLL/lymphoma 3
239629_at	CASP8 and FADD-like apoptosis regulator
217523_at	CD44 molecule (Indian blood group)
204420_at	FOS-like antigen 1
240452_at	G1 to S phase transition 1
204224_s_at	GTP cyclohydrolase 1
211824_x_at	NLR family, pyrin domain containing 1
1557543_at	Notch homolog 2 (Drosophila)
217744_s_at	PERP, TP53 apoptosis effector
228780_at	POU class 3 homeobox 3
218501_at	Rho guanine nucleotide exchange factor (GEF) 3
1555723_at, 225590_at	SH3 domain containing ring finger 1
239448_at, 205397_x_at	SMAD family member 3
214953_s_at	amyloid beta (A4) precursor protein
202986_at	aryl-hydrocarbon receptor nuclear translocator 2
210538_s_at	baculoviral IAP repeat-containing 3
242068_at	baculoviral IAP repeat-containing 6
211518_s_at	bone morphogenetic protein 4
244503_at, 239367_at, 206382_s_at	brain-derived neurotrophic factor
211368_s_at	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
213274_s_at	cathepsin B
209030_s_at, 209032_s_at, 209031_at	cell adhesion molecule 1
216598_s_at	chemokine (C-C motif) ligand 2
210701_at	craniofacial development protein 1
242362_at	cullin 3
242194_at	cullin 4A
206914_at	cytotoxic and regulatory T cell molecule
220512_at	deleted in liver cancer 1
201983_s_at, 232541_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
242320_at	forkhead box O3; forkhead box O3B pseudogene
230090_at	glial cell derived neurotrophic factor
236140_at, 234986_at	glutamate-cysteine ligase, modifier subunit
206614_at	growth differentiation factor 5
203382_s_at, 203381_s_at	hypothetical LOC100129500; apolipoprotein E
205207_at	interleukin 6 (interferon, beta 2)
201465_s_at	jun oncogene
201596_x_at	keratin 18; keratin 18 pseudogene 26; keratin 18 pseudogene 19

GO:0010941 - Regulation of Cell Death (Continued) (60/815, P=1.78E-06)	
202086_at	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
206814_at	nerve growth factor (beta polypeptide)
208241_at	neuregulin 1
216115_at	neurofibromin 1
215067_x_at	peroxiredoxin 2
209193_at	pim-1 oncogene
219566_at	pleckstrin homology domain containing, family F (with FYVE domain) member 1
217999_s_at, 218000_s_at, 217996_at, 217998_at, 225842_at, 217997_at	pleckstrin homology-like domain, family A, member 1
221583_s_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1
239582_at, 209640_at	promyelocytic leukemia; similar to promyelocytic leukemia protein isoform 1
243031_at, 239251_at	reticulon 4
209969_s_at, 232375_at	signal transducer and activator of transcription 1, 91kDa
221477_s_at, 216841_s_at, 215223_s_at	superoxide dismutase 2, mitochondrial
201008_s_at, 201009_s_at	thioredoxin interacting protein
209909_s_at, 220407_s_at, 209908_s_at	transforming growth factor, beta 2
239129_at, 239605_x_at, 236561_at	transforming growth factor, beta receptor 1
201042_at, 211573_x_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
200803_s_at	transmembrane BAX inhibitor motif containing 6
240399_at, 208178_x_at, 209013_x_at, 235705_at, 231403_at	triple functional domain (PTPRF interacting)
202688_at, 202687_s_at	tumor necrosis factor (ligand) superfamily, member 10
221371_at	tumor necrosis factor (ligand) superfamily, member 18
241435_at	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
204254_s_at, 204255_s_at	vitamin D (1,25- dihydroxyvitamin D3) receptor

GO:0007626 - Locomotory Behavior (26/274, P=5.55E-06)	
ID	Gene Name
204420_at	FOS-like antigen 1
214953_s_at	amyloid beta (A4) precursor protein
236404_at, 1559249_at	ataxin 1
210133_at	chemokine (C-C motif) ligand 11
216598_s_at	chemokine (C-C motif) ligand 2
208075_s_at	chemokine (C-C motif) ligand 7
214038_at	chemokine (C-C motif) ligand 8
220351_at	chemokine (C-C motif) receptor-like 1
204470_at	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
203666_at	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
209774_x_at	chemokine (C-X-C motif) ligand 2
206336_at	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
207652_s_at, 210659_at, 229121_at	chemokine-like receptor 1
230090_at	glial cell derived neurotrophic factor
209827_s_at	interleukin 16 (lymphocyte chemoattractant factor)
205207_at	interleukin 6 (interferon, beta 2)
211506_s_at	interleukin 8
206814_at	nerve growth factor (beta polypeptide)
211668_s_at, 205479_s_at	plasminogen activator, urokinase
216867_s_at	platelet-derived growth factor alpha polypeptide
221583_s_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1
211663_x_at	prostaglandin D2 synthase, hematopoietic; prostaglandin D2 synthase 21kDa (brain)
201136_at	proteolipid protein 2 (colonic epithelium-enriched)
218974_at	sine oculis binding protein homolog (Drosophila)
221477_s_at, 216841_s_at, 215223_s_at	superoxide dismutase 2, mitochondrial
209909_s_at, 220407_s_at, 209908_s_at	transforming growth factor, beta 2

Appendix 2.1 Differentially Expressed Genes in OSX Null hMSCs from All Three Donors

BMP6 Responsive Genes Differentially Expressed in OSX Null hMSCs from All Three Donors

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7975613	ACOT6	NM_001037162	21.68	56.37	2.6	0.3	34.69	*	56.37	27.78	-2.03	-0.23	-28.59	*
8088560	ADAMTS9	NM_182920	26.03	206.92	7.95	2.86	180.89	*	206.92	96.98	-2.13	-0.78	-109.94	*
7985522	ADAMTSL3	NM_207517	52.96	81.06	1.53	0.87	28.1	*	81.06	151.53	1.87	1.09	70.48	*
8170364	AFF2	NM_002025	85.56	278.47	3.25	1.6	192.91	*	278.47	181.62	-1.53	-0.86	-96.85	*
8096116	AGPAT9	NM_032717	90.93	162.95	1.79	1.1	72.01	*	162.95	94.14	-1.73	-1.01	-68.81	*
8122045	AKAP7	NM_016377	48.45	137.23	2.83	1.47	88.78	*	137.23	85.83	-1.6	-0.84	-51.4	*
8023528	ALPK2	NM_052947	85.73	146.29	1.71	1.18	60.57	*	146.29	84.11	-1.74	-1.23	-62.18	*
7898693	ALPL	NM_000478	62.73	251	4	0	188.27	*	251	48.63	-5.16	0	-202.36	*
8149071	ANGPT2	NM_001147	36.22	119.57	3.3	0.8	83.35	*	119.57	73.75	-1.62	-0.36	-45.81	*
7933772	ANK3	NM_020987	64.79	203.37	3.14	2.38	138.58	*	203.37	126.86	-1.6	-1.24	-76.51	*
8162394	ASPN	NM_017680	100.35	527.56	5.26	2.77	427.22	*	527.56	338.65	-1.56	-0.7	-188.91	*
7986068	BLM	NM_000057	53.59	98.5	1.84	0.85	44.91	*	98.5	63.22	-1.56	-0.71	-35.28	*
8060850	BMP2	NM_001200	225.71	340.23	1.51	0.66	114.53	*	340.23	106.14	-3.21	-1.94	-234.1	*
7958352	BTBD11	NM_001018072	33.26	108.07	3.25	2.19	74.81	*	108.07	70.24	-1.54	-1.08	-37.83	*
8104825	BXDC2	NM_018321	394.69	837.33	2.12	1.58	442.64	*	837.33	1350.31	1.61	1.23	512.98	*
7964687	C12orf56	NM_001099676	18.08	69.55	3.85	2.83	51.47	*	69.55	29.62	-2.35	-1.54	-39.92	*
8022310	C18orf58	AK092226	76.41	38.81	-1.97	-0.95	-37.6	*	38.81	71.29	1.84	0.72	32.48	*
8111552	C5orf33	NM_001085411	597.83	374	-1.6	-1.2	-223.83	*	374	655.63	1.75	1.3	281.63	*
8023401	CCDC68	NM_025214	53.17	483.03	9.09	4.94	429.86	*	483.03	236.53	-2.04	-1.07	-246.49	*
8006433	CCL2	NM_002982	906.27	131.12	-6.91	-5.14	-775.15	*	131.12	249	1.9	0.93	117.89	*
8137468	CCT8L1	ENST00000021776	97.37	60.42	-1.61	-1.07	-36.95	*	60.42	119.97	1.99	0.45	59.55	*
8112376	CENPK	NM_022145	56.17	93.85	1.67	1.04	37.68	*	93.85	61.8	-1.52	-0.85	-32.06	*
8077270	CHL1	NM_006614	23.55	72.85	3.09	0.77	49.3	*	72.85	39.84	-1.83	-0.44	-33.01	*
8088866	CNTN3	NM_020872	43.74	104.23	2.38	0.57	60.49	*	104.23	64.31	-1.62	-0.39	-39.93	*
7918064	COL11A1	NM_001854	273.86	134.99	-2.03	-0.73	-138.87	*	134.99	252.03	1.87	0.36	117.04	*
8148070	COL14A1	NM_021110	995.11	229.85	-4.33	-2.53	-765.26	*	229.85	424.93	1.85	0.85	195.07	*
8092621	CRYGS	NM_017541	60.84	519.38	8.54	3.81	458.53	*	519.38	282.39	-1.84	-0.79	-236.99	*
7916853	DIRAS3	NM_004675	47.02	144.48	3.07	1.28	97.45	*	144.48	92.91	-1.55	-0.71	-51.56	*
8016609	DLX3	NM_005220	28.95	162.52	5.61	1.73	133.56	*	162.52	107.56	-1.51	-0.47	-54.96	*
8056222	DPP4	NM_001935	822.42	193.02	-4.26	-3.29	-629.4	*	193.02	322.51	1.67	0.96	129.48	*
7965335	DUSP6	NM_001946	117.34	62.83	-1.87	-1.22	-54.52	*	62.83	103.51	1.65	0.98	40.68	*
8014066	EVI2A	NM_001003927	128.55	42.07	-3.06	-1.55	-86.48	*	42.07	77.73	1.85	0.03	35.66	*
8022283	FAM38B	NM_022068	150.58	61.23	-2.46	-0.64	-89.35	*	61.23	99.58	1.63	0.4	38.35	*
8022295	FAM38B2	AK127627	141.95	56.7	-2.5	-0.8	-85.25	*	56.7	109.82	1.94	0.49	53.12	*
8113800	FBN2	NM_001999	47.93	80.85	1.69	1.01	32.92	*	80.85	193.95	2.4	1.36	113.1	*
8170119	FHL1	NM_001449	236.34	137.7	-1.72	-0.79	-98.64	*	137.7	210.42	1.53	0.9	72.72	*
8056323	FIGN	NM_018086	81.06	140.48	1.73	1.06	59.42	*	140.48	80.64	-1.74	-1.11	-59.84	*
8054344	FLJ42986	AK298610	91.41	51	-1.79	-1.19	-40.41	*	51	77.08	1.51	0.64	26.09	*
7917954	FRRS1	NM_001013660	141.34	285.79	2.02	1.61	144.45	*	285.79	171.38	-1.67	-1.46	-114.41	*
7974341	GNG2	NM_053064	59.27	498.64	8.41	5.35	439.37	*	498.64	195.32	-2.55	-1.8	-303.31	*
8045336	GPR39	NM_001508	120.67	775.84	6.43	4.76	655.17	*	775.84	298.98	-2.59	-2.01	-476.85	*
7954065	GPRC5A	NM_003979	94.83	49.09	-1.93	-0.62	-45.74	*	49.09	92.31	1.88	0.25	43.22	*
8081758	GRAMD1C	NM_017577	27.19	53.32	1.96	0.93	26.13	*	53.32	25.99	-2.05	-0.96	-27.32	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8162908	GRIN3A	NM_133445	32.91	79.06	2.4	1.63	46.15	*	79.06	35.27	-2.24	-1.5	-43.79	*
8046906	GULP1	NM_016315	71.67	333.76	4.66	3.26	262.1	*	333.76	154.82	-2.16	-1.44	-178.95	*
8083690	IL12A	NM_000882	36.95	79.73	2.16	0.78	42.78	*	79.73	232.8	2.92	0.85	153.06	*
8104901	IL7R	NM_002185	22.95	270.45	11.78	7.11	247.5	*	270.45	47.05	-5.75	-3.43	-223.4	*
8061013	ISM1	NM_080826	27.66	60.61	2.19	1.2	32.95	*	60.61	34.98	-1.73	-0.92	-25.63	*
8143341	JHDM1D	NM_030647	74.03	117.34	1.58	1.13	43.31	*	117.34	75.96	-1.54	-1.15	-41.38	*
8009502	KCNJ2	NM_000891	97.74	41.34	-2.36	-1.49	-56.41	*	41.34	91.69	2.22	1.11	50.36	*
8095110	KIT	NM_000222	10.02	130.08	12.98	5.46	120.06	*	130.08	238.2	1.83	0.94	108.12	*
7961182	KLRC2	NM_002260	15.72	121.54	7.73	0	105.81	*	121.54	63.04	-1.93	0	-58.5	*
7955637	KRT18	NM_199187	305.85	161.72	-1.89	-0.4	-144.14	*	161.72	99.4	-1.63	-0.41	-62.31	*
7989937	LCTL	NM_207338	73	148.19	2.03	0.97	75.18	*	148.19	65.02	-2.28	-1.16	-83.17	*
7963024	LMBR1L	NM_018113	43.65	102.85	2.36	1.65	59.2	*	102.85	160.76	1.56	0.89	57.91	*
8160431	LOC554202	AK124391	63.74	124.25	1.95	1.49	60.51	*	124.25	81.29	-1.53	-1.12	-42.96	*
7984771	LOXL1	NM_005576	219.56	125.77	-1.75	-1.12	-93.8	*	125.77	210.61	1.67	1.21	84.85	*
8077366	LRRN1	NM_020873	91.28	181.66	1.99	0.58	90.38	*	181.66	91.67	-1.98	-0.55	-89.98	*
8089714	LSAMP	NM_002338	127.34	64.95	-1.96	-1.4	-62.39	*	64.95	100.68	1.55	1.03	35.73	*
8055314	LYPD1	NM_144586	105.13	375.88	3.58	2.59	270.75	*	375.88	158.91	-2.37	-1.93	-216.97	*
7987385	MEIS2	NM_172316	221.02	363.53	1.64	0.89	142.51	*	363.53	228.65	-1.59	-0.87	-134.88	*
8175256	MGC16121	BC007360	89.16	276.39	3.1	0.99	187.22	*	276.39	76.25	-3.62	-1.15	-200.13	*
8063634	MGC4294	BC002831	155.86	235.82	1.51	0.87	79.96	*	235.82	140.53	-1.68	-1.27	-95.3	*
8083494	MME	NM_007288	336.21	104.55	-3.22	-1.51	-231.66	*	104.55	184.78	1.77	0.91	80.23	*
8059852	MSL3L2	NR_024322	46.85	72.02	1.54	0.77	25.17	*	72.02	115.36	1.6	0.72	43.34	*
8021376	NEDD4L	NM_015277	110.56	181.57	1.64	1.16	71.01	*	181.57	98.43	-1.84	-1.33	-83.15	*
8145361	NEFM	NM_005382	138.45	1717.9	12.41	9.07	1579.45	*	1717.9	267.82	-6.41	-3.98	-1450.08	*
7908543	NEK7	NM_133494	391.36	231.11	-1.69	-0.86	-160.25	*	231.11	581.63	2.52	1.5	350.52	*
8162388	OMD	NM_005014	21.93	638.78	29.13	17.14	616.85	*	638.78	143.55	-4.45	-2.42	-495.24	*
7948322	OR5B17	NM_001005489	96.4	323.52	3.36	0	227.12	*	323.52	55.78	-5.8	0	-267.74	*
7903227	PALMD	NM_017734	103.57	370.64	3.58	1.39	267.07	*	370.64	236.14	-1.57	-0.6	-134.5	*
8105495	PART1	AF163475	29.14	100.66	3.45	1.96	71.52	*	100.66	27.1	-3.71	-2.07	-73.55	*
8122222	PDE7B	NM_018945	201.1	115.58	-1.74	-1.24	-85.52	*	115.58	224.21	1.94	1.02	108.63	*
8142981	PODXL	NM_001018111	47.17	238.69	5.06	2.49	191.52	*	238.69	127.21	-1.88	-0.9	-111.49	*
7930980	PPAPDC1A	NM_001030059	234.62	453.84	1.93	1.61	219.22	*	453.84	300.67	-1.51	-1.19	-153.17	*
8102468	PRSS12	NM_003619	202.04	119.82	-1.69	-0.58	-82.22	*	119.82	193.24	1.61	0.67	73.42	*
7902527	PTGFR	NM_001039585	179.01	63.88	-2.8	-0.18	-115.13	*	63.88	150.94	2.36	0.36	87.07	*
7918657	PTPN22	NM_015967	58.07	21.4	-2.71	-1.61	-36.67	*	21.4	47.3	2.21	0.67	25.89	*
8111569	RANBP3L	NM_145000	274.6	34.21	-8.03	-3.37	-240.39	*	34.21	88.17	2.58	0.51	53.96	*
7940775	RARRES3	NM_004585	246.43	106.96	-2.3	-1.4	-139.47	*	106.96	51.71	-2.07	-0.66	-55.25	*
8157324	RGS3	NM_144488	75.71	117.22	1.55	0.93	41.51	*	117.22	77.32	-1.52	-0.89	-39.9	*
7919269	RNU1A	NR_004421	195.88	499.29	2.55	0.21	303.41	*	499.29	229.33	-2.18	-0.18	-269.96	*
7919349	RNU1A	NR_004421	195.88	499.29	2.55	0.21	303.41	*	499.29	229.33	-2.18	-0.18	-269.96	*
7898375	RNU1A	NR_004421	176.91	426.66	2.41	0.25	249.75	*	426.66	208.95	-2.04	-0.21	-217.71	*
7898411	RNU1A	NR_004421	176.91	426.66	2.41	0.25	249.75	*	426.66	208.95	-2.04	-0.21	-217.71	*
7912800	RNU1A	NR_004421	176.91	426.66	2.41	0.25	249.75	*	426.66	208.95	-2.04	-0.21	-217.71	*
7912850	RNU1A	NR_004421	176.91	426.66	2.41	0.25	249.75	*	426.66	208.95	-2.04	-0.21	-217.71	*
7919576	RNU1A	NR_004421	176.91	426.66	2.41	0.25	249.75	*	426.66	208.95	-2.04	-0.21	-217.71	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7973896	RNU1A	NR_004421	178.6	426.62	2.39	0.25	248.03	*	426.62	210.84	-2.02	-0.21	-215.78	*
7978568	RNU1A	NR_004421	178.6	426.62	2.39	0.25	248.03	*	426.62	210.84	-2.02	-0.21	-215.78	*
7967030	RNU4-1	NR_003925	58.36	176.25	3.02	0.22	117.89	*	176.25	80.2	-2.2	-0.16	-96.05	*
8171762	RPS6KA3	NM_004586	374.1	568.37	1.52	1.19	194.27	*	568.37	270.35	-2.1	-1.55	-298.02	*
8011214	RTN4RL1	NM_178568	38.08	68.66	1.8	0.54	30.58	*	68.66	42.79	-1.6	-0.46	-25.87	*
8140668	SEMA3A	NM_006080	90.58	175.86	1.94	1.2	85.28	*	175.86	99.36	-1.77	-1.18	-76.5	*
7951077	SESN3	NM_144665	133.82	333.56	2.49	1.47	199.74	*	333.56	570.94	1.71	1.01	237.38	*
8021081	SLC14A1	NM_001128588	808.21	369.89	-2.18	-1.01	-438.32	*	369.89	683.87	1.85	0.65	313.98	*
8104930	SLC1A3	NM_004172	196.12	63.39	-3.09	-0.89	-132.73	*	63.39	130.39	2.06	0.59	67	*
7940717	SLC3A2	NM_001012661	127.34	213.53	1.68	0.77	86.19	*	213.53	140.56	-1.52	-0.69	-72.97	*
7977933	SLC7A8	NM_012244	218.57	491.6	2.25	1.28	273.03	*	491.6	273.63	-1.8	-1.02	-217.96	*
7972239	SLITRK6	NM_032229	23.45	144.72	6.17	3.9	121.27	*	144.72	44.64	-3.24	-1.76	-100.08	*
7975390	SMOC1	NM_001034852	90	135.7	1.51	1.19	45.71	*	135.7	246.5	1.82	1.4	110.79	*
8121319	SOBP	NM_018013	122.23	74.83	-1.63	-1.03	-47.4	*	74.83	116.65	1.56	1.08	41.82	*
7963664	SP7	NM_152860	25.38	404.46	15.94	5.9	379.08	*	404.46	64.01	-6.32	-2.66	-340.45	*
8096301	SPP1	NM_001040058	392.8	716.05	1.82	1.24	323.25	*	716.05	463.99	-1.54	-1.06	-252.06	*
8149825	STC1	NM_003155	47.43	114.61	2.42	1.65	67.19	*	114.61	72.95	-1.57	-1.15	-41.66	*
8115851	STC2	NM_003714	108.37	360.72	3.33	1.33	252.35	*	360.72	239.56	-1.51	-0.62	-121.15	*
8155707	TJP2	NM_004817	132.19	310.55	2.35	1.54	178.36	*	310.55	181.72	-1.71	-1.17	-128.83	*
8016841	TMEM100	NM_001099640	19.35	156.03	8.07	5.26	136.69	*	156.03	50.39	-3.1	-2.34	-105.64	*
8157092	TMEM38B	NM_018112	140.22	262.52	1.87	1.44	122.3	*	262.52	173.43	-1.51	-1.19	-89.09	*
7957417	TMTC2	NM_152588	48.29	231.57	4.8	2.53	183.28	*	231.57	116.94	-1.98	-1.01	-114.63	*
7903358	VCAM1	NM_001078	640.47	198.38	-3.23	-2.46	-442.08	*	198.38	586.67	2.96	2.2	388.28	*
8088979	VGLL3	NM_016206	392.85	185.12	-2.12	-1.6	-207.72	*	185.12	280.91	1.52	1.23	95.78	*

BMP6 Responsive Genes Differentially Expressed in hMSCs from All Three Donors

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8083409	AADACL2	NM_207365	51.25	25.31	-2.02	-1.58	-25.94	*	25.31	31.01	1.23	0.7	5.7	
8008454	ABCC3	NM_003786	80.46	51.7	-1.56	-1.2	-28.76	*	51.7	43.15	-1.2	-0.87	-8.55	
7961710	ABCC9	NM_005691	41.53	79.42	1.91	0.71	37.89	*	79.42	80.14	1.01	0.56	0.72	
7936463	ABLIM1	NM_002313	93.19	45.05	-2.07	-1.18	-48.14	*	45.05	46.52	1.03	0.86	1.47	
7985786	ACAN	NM_013227	49.47	225.86	4.57	0	176.39	*	225.86	212.49	-1.06	0	-13.37	
7987315	ACTC1	NM_005159	68.81	1242.84	18.06	5.84	1174.03	*	1242.84	1352.14	1.09	0.51	109.3	
8145293	ADAM28	NM_014265	38.27	152.84	3.99	0.37	114.56	*	152.84	151.35	-1.01	-0.09	-1.49	
8111387	ADAMTS12	NM_030955	121.8	75.07	-1.62	-0.98	-46.73	*	75.07	102.13	1.36	0.86	27.06	
8069689	ADAMTS5	NM_007038	151.12	344.88	2.28	1.78	193.76	*	344.88	400.25	1.16	0.96	55.37	
7905233	ADAMTSL4	NM_019032	101.99	44.08	-2.31	-1.06	-57.91	*	44.08	57.7	1.31	0.77	13.62	
8049448	AGAP1	NM_001037131	299.61	196.06	-1.53	-0.79	-103.55	*	196.06	192.8	-1.02	-0.57	-3.26	
7981514	AHNAK2	NM_138420	543.45	195.53	-2.78	-1.08	-347.92	*	195.53	231.53	1.18	0.54	36	
8121277	AIM1	NM_001624	255.87	68.34	-3.74	-0.99	-187.53	*	68.34	92.02	1.35	0.16	23.68	
7902452	AK5	NM_174858	376.22	227.56	-1.65	-1.12	-148.66	*	227.56	296.48	1.3	0.28	68.92	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7960427	AKAP3	NM_006422	60.71	35.29	-1.72	-1.14	-25.43	*	35.29	30.83	-1.14	-0.96	-4.46	
8136336	AKR1B10	NM_020299	560.37	298.79	-1.88	-1.08	-261.58	*	298.79	296.1	-1.01	-0.48	-2.69	
7986446	ALDH1A3	NM_000693	108.91	65.62	-1.66	-0.74	-43.29	*	65.62	69.63	1.06	0.57	4.01	
8121489	AMD1	NM_001634	301.51	537.17	1.78	1.19	235.66	*	537.17	474.71	-1.13	-0.71	-62.47	
7962579	AMIGO2	NM_181847	112.67	575.35	5.11	1.68	462.68	*	575.35	521.53	-1.1	-0.36	-53.82	
8164200	ANGPTL2	NM_012098	221.51	597.88	2.7	1.89	376.38	*	597.88	677.9	1.13	0.72	80.01	
8022559	ANKRD29	NM_173505	59.22	31.39	-1.89	-1.21	-27.83	*	31.39	48.39	1.54	0.86	17.01	
8132318	ANLN	NM_018685	45.93	80.17	1.75	0.31	34.23	*	80.17	88.07	1.1	0	7.91	
7939024	ANO3	NM_031418	20.2	108.8	5.39	2.77	88.61	*	108.8	141.75	1.3	0.32	32.95	
8047300	AOX1	NM_001159	90.24	44.46	-2.03	-1.6	-45.79	*	44.46	42.95	-1.04	-0.72	-1.51	
7926786	APBB1IP	NM_019043	325.83	215.77	-1.51	-1.07	-110.06	*	215.77	237.25	1.1	0.57	21.48	
8072735	APOL1	NM_145343	275.72	134.08	-2.06	-1.46	-141.64	*	134.08	89.48	-1.5	-0.8	-44.6	
8072710	APOL6	NM_030641	170.6	87.53	-1.95	-1.1	-83.07	*	87.53	63.69	-1.37	-0.39	-23.83	
7955297	AQP5	NM_001651	224.22	104.23	-2.15	-1.68	-119.99	*	104.23	119.73	1.15	0.96	15.5	
7933469	ARHGAP22	NM_021226	434.05	124.56	-3.48	-2.62	-309.49	*	124.56	184.54	1.48	1.09	59.98	
8019964	ARHGAP28	NM_001010000	71.7	45.64	-1.57	-0.96	-26.06	*	45.64	37.04	-1.23	-0.49	-8.6	
7917850	ARHGAP29	NM_004815	140.71	64.75	-2.17	-0.85	-75.96	*	64.75	73.48	1.13	0.76	8.74	
8088247	ARHGEF3	NM_001128615	124.04	75.63	-1.64	-1.05	-48.42	*	75.63	83.95	1.11	0.78	8.33	
7986350	ARRDC4	NM_183376	267.4	140.54	-1.9	-1.23	-126.87	*	140.54	193.41	1.38	0.89	52.87	
8094911	ATP10D	NM_020453	630.46	380.16	-1.66	-1.03	-250.3	*	380.16	362.23	-1.05	-0.64	-17.93	
7907160	ATP1B1	NM_001677	858.22	2083.4	2.43	1.91	1225.18	*	2083.4	1497.9	-1.39	-1.16	-585.5	
8023497	ATP8B1	NM_005603	403.91	155.08	-2.6	-1.69	-248.83	*	155.08	146.94	-1.06	-0.74	-8.14	
7903676	ATXN7L2	NM_153340	151.93	94.34	-1.61	-1.02	-57.59	*	94.34	81.78	-1.15	-0.85	-12.56	
7926875	BAMBI	NM_012342	332.44	1435.38	4.32	2.87	1102.95	*	1435.38	975.95	-1.47	-1.06	-459.44	
8065569	BCL2L1	NM_138578	330.04	160.65	-2.05	-1.54	-169.39	*	160.65	179.09	1.11	0.9	18.44	
8092691	BCL6	NM_001706	314.76	191.29	-1.65	-1.03	-123.47	*	191.29	188.42	-1.02	-0.81	-2.87	
7976567	BDKRB1	NM_000710	66.94	108.76	1.62	1.09	41.82	*	108.76	126.98	1.17	0.65	18.21	
7981309	BEGAIN	NM_020836	79.18	48.59	-1.63	-0.83	-30.59	*	48.59	53.72	1.11	0.9	5.13	
8065124	BFSP1	NM_001195	106.19	163	1.53	0.65	56.81	*	163	201.27	1.23	0.76	38.27	
7963289	BIN2	NM_016293	80.55	40.55	-1.99	-1.31	-40	*	40.55	54.3	1.34	0.94	13.75	
7943413	BIRC3	NM_001165	80.09	30.61	-2.62	-1.7	-49.48	*	30.61	38.53	1.26	0.98	7.92	
8132250	BMPER	NM_133468	197.52	49.24	-4.01	-2.42	-148.28	*	49.24	60.22	1.22	0.67	10.98	
8160260	BNC2	NM_017637	181.89	96.53	-1.88	-1.51	-85.35	*	96.53	112.86	1.17	0.94	16.32	
8041031	BRE	NM_199193	383.44	230.05	-1.67	-1.2	-153.4	*	230.05	251.05	1.09	0.76	21.01	
8094228	BST1	NM_004334	238.04	118.02	-2.02	-0.74	-120.02	*	118.02	134.74	1.14	0.55	16.72	
7930299	C10orf78	NM_145247	21.06	71.63	3.4	2.63	50.58	*	71.63	63.37	-1.13	-0.97	-8.27	
7940315	C11orf64	BC029583	70.67	38.21	-1.85	-1.29	-32.46	*	38.21	45.43	1.19	0.82	7.22	
7957092	C12orf28	AK057785	68.46	42.91	-1.6	-0.97	-25.55	*	42.91	42.77	-1	-0.74	-0.15	
7968789	C13orf15	NM_014059	200.8	127.11	-1.58	-1.04	-73.69	*	127.11	93.83	-1.35	-0.81	-33.29	
7968351	C13orf33	NM_032849	82.9	42.61	-1.95	-1.42	-40.29	*	42.61	39.15	-1.09	-0.75	-3.46	
7993889	C16orf52	BC027604	184.65	109.61	-1.68	-1.04	-75.04	*	109.61	108.12	-1.01	-0.9	-1.48	
7921909	C1orf110	NM_178550	61.11	29.82	-2.05	-1.09	-31.3	*	29.82	30.74	1.03	0.74	0.92	
7919743	C1orf138	BC132992	94.38	44.45	-2.12	-0.76	-49.93	*	44.45	48.67	1.09	0.6	4.22	
7924996	C1orf198	NM_032800	288.43	191.25	-1.51	-0.59	-97.18	*	191.25	194.36	1.02	0.63	3.1	
7960744	C1R	NM_001733	309.01	163.63	-1.89	-1.53	-145.38	*	163.63	167.95	1.03	0.72	4.32	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8068083	C21orf7	NM_020152	174.54	37.38	-4.67	-1.7	-137.15	*	37.38	41.72	1.12	0.65	4.34	
8048272	C2orf62	BC052750	116.42	74.36	-1.57	-0.96	-42.06	*	74.36	79.66	1.07	0.71	5.3	
8057954	C2orf66	AY358249	82	52.29	-1.57	-0.98	-29.71	*	52.29	50.11	-1.04	-0.76	-2.18	
8042769	C2orf78	NM_001080474	76.36	38.31	-1.99	-0.83	-38.05	*	38.31	42.94	1.12	0.88	4.63	
8033257	C3	NM_000064	259.23	40.7	-6.37	-1.11	-218.52	*	40.7	53.85	1.32	0.4	13.15	
8102587	C4orf31	NM_024574	145.47	508.17	3.49	2.25	362.7	*	508.17	693.06	1.36	0.31	184.89	
8102831	C4orf49	NM_032623	141.56	49.9	-2.84	-1.12	-91.66	*	49.9	71.74	1.44	1.11	21.84	
8121911	C6orf173	NM_001012507	185.37	301.2	1.62	0.95	115.82	*	301.2	277.17	-1.09	-0.62	-24.03	
8148955	C8orf33	NM_023080	186.39	359.56	1.93	1.29	173.17	*	359.56	326.97	-1.1	-0.7	-32.59	
8147132	CA2	NM_000067	69.24	41.28	-1.68	-1.32	-27.96	*	41.28	50.98	1.24	0.92	9.71	
8031084	CACNG8	NM_031895	376.4	198.18	-1.9	-1.39	-178.22	*	198.18	213.89	1.08	0.97	15.71	
7951807	CADM1	NM_014333	172.45	73.03	-2.36	-1.02	-99.42	*	73.03	74.38	1.02	0.54	1.34	
8142585	CADPS2	NM_017954	59.83	34.46	-1.74	-1.27	-25.37	*	34.46	27.81	-1.24	-0.86	-6.64	
8085206	CAMK1	NM_003656	302.26	159.2	-1.9	-1.37	-143.06	*	159.2	173.47	1.09	0.94	14.27	
7913237	CAMK2N1	NM_018584	349.78	161.89	-2.16	-1.21	-187.89	*	161.89	219.07	1.35	0.65	57.18	
8135594	CAV1	NM_001753	1204.94	520.69	-2.31	-1.67	-684.25	*	520.69	779.11	1.5	0.31	258.42	
7996393	CBFB	NM_001755	791.99	1582.5	2	1.65	790.51	*	1582.5	1236.26	-1.28	-1.02	-346.24	
8051197	CCDC121	NM_024584	124.27	69.66	-1.78	-1.09	-54.61	*	69.66	87.44	1.26	0.82	17.77	
8073513	CCDC134	NM_024821	138.46	77.59	-1.78	-0.97	-60.87	*	77.59	81.3	1.05	0.8	3.71	
8099746	CCKAR	NM_000730	27.27	405.45	14.87	9.04	378.18	*	405.45	309.41	-1.31	-0.74	-96.04	
8102643	CCNA2	NM_001237	55.67	112.63	2.02	1.54	56.96	*	112.63	126.1	1.12	0.91	13.47	
8105828	CCNB1	NM_031966	94.46	163.83	1.73	0.74	69.37	*	163.83	152.63	-1.07	-0.38	-11.2	
7983969	CCNB2	NM_004701	41.82	85.54	2.05	0.75	43.71	*	85.54	80.59	-1.06	-0.36	-4.95	
8079401	CCR5	NM_000579	101.9	49.52	-2.06	-0.93	-52.39	*	49.52	58.81	1.19	0.97	9.29	
8093298	CCR5	NM_000579	101.9	49.52	-2.06	-0.93	-52.39	*	49.52	58.81	1.19	0.97	9.29	
8081657	CD200	NM_001004196	39.01	83.29	2.14	1.02	44.28	*	83.29	99.58	1.2	0.43	16.29	
8177222	CD24	NM_013230	11.88	133.55	11.24	5.39	121.67	*	133.55	119.47	-1.12	-0.54	-14.08	
7949588	CD248	NM_020404	814.65	419.75	-1.94	-1.32	-394.89	*	419.75	438.16	1.04	0.7	18.41	
8115147	CD74	NM_001025159	188.57	92.45	-2.04	-1.1	-96.13	*	92.45	84.65	-1.09	-0.55	-7.8	
7953291	CD9	NM_001769	556.74	366.52	-1.52	-0.87	-190.22	*	366.52	474.06	1.29	0.83	107.54	
7903334	CDC14A	NM_003672	80.3	144.62	1.8	1.24	64.32	*	144.62	111.51	-1.3	-0.86	-33.11	
8046488	CDCA7	NM_031942	88.58	49.92	-1.77	-1.55	-38.66	*	49.92	65.17	1.31	0.76	15.25	
8086517	CDCP1	NM_022842	355.23	131.53	-2.7	-1.24	-223.7	*	131.53	161.75	1.23	0.22	30.22	
7997504	CDH13	NM_001257	436.36	288.93	-1.51	-0.75	-147.43	*	288.93	277.5	-1.04	-0.6	-11.43	
8104663	CDH6	NM_004932	331.31	624.89	1.89	0.76	293.58	*	624.89	580.92	-1.08	-0.47	-43.97	
8160441	CDKN2A	NM_058197	109.58	165.23	1.51	0.87	55.65	*	165.23	123.13	-1.34	-0.77	-42.1	
8113641	CDO1	NM_001801	101.23	65.96	-1.53	-0.7	-35.26	*	65.96	77.74	1.18	0.71	11.77	
7909708	CENPF	NM_016343	80.2	130.24	1.62	0.48	50.04	*	130.24	114.54	-1.14	-0.3	-15.7	
8156341	CENPP	NM_001012267	95.6	189.15	1.98	1.55	93.55	*	189.15	145.26	-1.3	-1.01	-43.89	
8097058	CEP170L	ENST00000336415	46.03	93.61	2.03	1.14	47.59	*	93.61	90.38	-1.04	-0.59	-3.24	
8118345	CFB	NM_001710	425.36	152.57	-2.79	-1.9	-272.79	*	152.57	139.22	-1.1	-0.55	-13.35	
8178115	CFB	NM_001710	433.58	155.51	-2.79	-1.9	-278.07	*	155.51	141.82	-1.1	-0.55	-13.69	
8135661	CFTR	NM_000492	63.1	36.14	-1.75	-0.94	-26.97	*	36.14	40.87	1.13	0.77	4.73	
7934916	CH25H	NM_003956	131.4	49.51	-2.65	0	-81.9	*	49.51	45.31	-1.09	-0.43	-4.19	
7923547	CHI3L1	NM_001276	1525.38	396.53	-3.85	-0.75	-1128.85	*	396.53	501.6	1.26	0	105.07	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8107850	CHSY3	NM_175856	185.72	434.87	2.34	1.74	249.15	*	434.87	335.05	-1.3	-1.04	-99.82	
7981427	CKB	NM_001823	101.63	158.67	1.56	0.58	57.04	*	158.67	128.21	-1.24	-0.46	-30.46	
7902702	CLCA2	NM_006536	185.01	27.49	-6.73	-4.03	-157.53	*	27.49	20.97	-1.31	-0.71	-6.51	
8083887	CLDN11	NM_005602	125.85	76.46	-1.65	-0.99	-49.39	*	76.46	93.74	1.23	0.75	17.28	
7961083	CLEC2B	NM_005127	181.66	116.93	-1.55	-0.68	-64.73	*	116.93	104.35	-1.12	-0.25	-12.58	
8102877	CLGN	NM_004362	67.6	41.27	-1.64	-1	-26.32	*	41.27	41.67	1.01	0.46	0.4	
7914851	CLSPN	NM_022111	53.48	88.54	1.66	0.34	35.06	*	88.54	75.55	-1.17	-0.24	-12.99	
8124307	CMAH	NR_002174	299.92	69.92	-4.29	-1.31	-230.01	*	69.92	85.06	1.22	0.61	15.15	
7966089	CMKLR1	NM_004072	275.26	81.6	-3.37	-0.66	-193.67	*	81.6	87.6	1.07	0.24	6	
8056343	COBLL1	NM_014900	76.74	153.28	2	0.65	76.55	*	153.28	139.42	-1.1	-0.36	-13.87	
8069269	COL6A1	NM_001848	862.09	380.32	-2.27	-1.72	-481.77	*	380.32	416.33	1.09	0.79	36.01	
8035517	COMP	NM_000095	222.82	444.39	1.99	0.82	221.57	*	444.39	473.99	1.07	0.41	29.6	
7921099	CRABP2	NM_001878	392.44	121.75	-3.22	-1.37	-270.69	*	121.75	174.47	1.43	0.66	52.72	
8157731	CRB2	NM_173689	169.15	106.27	-1.59	-1.01	-62.88	*	106.27	110.28	1.04	0.82	4.01	
7997642	CRISPLD2	NM_031476	52.78	94.83	1.8	1.23	42.05	*	94.83	79.65	-1.19	-0.87	-15.18	
8065412	CST1	NM_001898	295.59	178.31	-1.66	-1.06	-117.28	*	178.31	193.24	1.08	0.77	14.93	
8065400	CST9	NM_001008693	75.22	45.16	-1.67	-1.01	-30.06	*	45.16	55.86	1.24	0.89	10.7	
8110990	CTNND2	NM_001332	192.19	96.7	-1.99	-1.22	-95.5	*	96.7	104.63	1.08	0.83	7.93	
7900510	CTPS	NM_001905	189.69	330.98	1.74	1	141.3	*	330.98	261.27	-1.27	-0.73	-69.72	
7919815	CTSK	NM_000396	701.22	412.22	-1.7	-0.58	-289	*	412.22	479.96	1.16	0.08	67.74	
8011713	CXCL16	NM_022059	173.66	68.67	-2.53	-1.77	-104.99	*	68.67	84.29	1.23	1.07	15.62	
8049471	CXCR7	NM_020311	76.83	38.55	-1.99	-1.15	-38.28	*	38.55	43.92	1.14	0.5	5.37	
7929478	CYP2C19	NM_000769	60.4	35.06	-1.72	-1.07	-25.34	*	35.06	37.71	1.08	0.67	2.65	
8099132	CYTL1	NM_018659	235.56	133.07	-1.77	-0.26	-102.49	*	133.07	115.23	-1.15	-0.31	-17.84	
8163716	DBC1	NM_014618	172.89	96.64	-1.79	-0.88	-76.25	*	96.64	104.84	1.08	0.38	8.21	
8121685	DCBLD1	NM_173674	282.8	546.26	1.93	1.43	263.46	*	546.26	670.49	1.23	0.86	124.22	
7970954	DCLK1	NM_004734	96.98	49.46	-1.96	-1.19	-47.53	*	49.46	45.87	-1.08	-0.8	-3.58	
8097753	DCLK2	NM_001040260	66	157.33	2.38	0.9	91.33	*	157.33	157.76	1	0.37	0.43	
8101952	DDIT4L	NM_145244	100.62	41.35	-2.43	-1.02	-59.27	*	41.35	45.66	1.1	0.76	4.32	
7968800	DGKH	NM_178009	48.67	89.44	1.84	1.22	40.76	*	89.44	66.5	-1.34	-0.9	-22.94	
7939657	DGKZ	NM_001105540	166.34	96.66	-1.72	-0.88	-69.67	*	96.66	111.52	1.15	0.98	14.86	
7980485	DIO2	NM_013989	10.54	597.67	56.72	14.93	587.13	*	597.67	479.43	-1.25	-0.35	-118.24	
8132840	DKFZp564N2472	NM_182595	110.11	56.07	-1.96	-1.34	-54.04	*	56.07	64.7	1.15	0.91	8.63	
7927631	DKK1	NM_012242	143.44	1521.59	10.61	6.08	1378.14	*	1521.59	1026.64	-1.48	-0.82	-494.95	
7979307	DLGAP5	NM_014750	30.4	60.66	2	0.17	30.26	*	60.66	71.64	1.18	0	10.98	
8056784	DLX2	NM_004405	79.98	628.73	7.86	5.03	548.75	*	628.73	578.09	-1.09	-0.79	-50.65	
8141140	DLX5	NM_005221	170.32	919.56	5.4	3.86	749.24	*	919.56	690.81	-1.33	-0.96	-228.74	
8171921	DMD	NM_000109	102.09	59.6	-1.71	-0.59	-42.49	*	59.6	73.69	1.24	0.52	14.09	
8021695	DOK6	NM_152721	36.68	62.49	1.7	1.19	25.81	*	62.49	57.95	-1.08	-0.71	-4.54	
7958019	DRAM	NM_018370	470.83	183.35	-2.57	-1.92	-287.48	*	183.35	237.36	1.29	0.95	54.01	
8115831	DUSP1	NM_004417	214.02	353.57	1.65	1.33	139.55	*	353.57	346.22	-1.02	-0.86	-7.35	
7905220	ECM1	NM_004425	237.67	144.75	-1.64	-1.01	-92.93	*	144.75	160.89	1.11	0.76	16.14	
8097692	EDNRA	NM_001957	162.99	516.25	3.17	1.72	353.26	*	516.25	421.39	-1.23	-0.77	-94.86	
8052355	EFEMP1	NM_004105	1538.39	857.17	-1.79	-0.69	-681.22	*	857.17	1007.05	1.17	0.37	149.88	
7975760	EIF2B2	NM_014239	115.57	370.72	3.21	2.26	255.16	*	370.72	280.57	-1.32	-0.93	-90.16	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8088803	EIF4E3	NM_173359	212.81	109.27	-1.95	-1.34	-103.54	*	109.27	130.84	1.2	0.9	21.57	
7999387	EMP2	NM_001424	526.44	281.49	-1.87	-1.3	-244.95	*	281.49	368.74	1.31	0.75	87.25	
8112615	ENC1	NM_003633	95.69	256.95	2.69	1.76	161.27	*	256.95	181.47	-1.42	-1.03	-75.48	
7971311	ENOX1	NM_017993	78.55	50.42	-1.56	-1.06	-28.13	*	50.42	54.8	1.09	0.73	4.38	
8095723	EPGN	NM_001013442	201.09	410.91	2.04	0.56	209.82	*	410.91	492.17	1.2	0.13	81.26	
8081081	EPHA3	NM_005233	159.52	367.91	2.31	1.38	208.39	*	367.91	428.39	1.16	0.92	60.48	
8018860	EPR1	NR_002219	52.47	120.44	2.3	0.33	67.97	*	120.44	121.13	1.01	0	0.69	
8055969	ERMN	NM_001009959	48.65	91.7	1.88	1.04	43.05	*	91.7	70.67	-1.3	-0.81	-21.04	
8145624	EXTL3	NM_001440	265.19	127.47	-2.08	-1.39	-137.73	*	127.47	147.25	1.16	1	19.78	
8106393	F2R	NM_001992	145.65	282.75	1.94	1.07	137.11	*	282.75	273.73	-1.03	-0.55	-9.03	
8112731	F2RL2	NM_004101	95.87	197.29	2.06	0.37	101.42	*	197.29	175.01	-1.13	-0.21	-22.27	
8110123	FAM153B	NM_001079529	88.34	49.81	-1.77	-0.9	-38.53	*	49.81	55.44	1.11	0.81	5.62	
8097801	FAM160A1	NM_001109977	58.01	28.45	-2.04	-1.06	-29.56	*	28.45	30.51	1.07	0.6	2.06	
8143127	FAM180A	AY358803	96.59	166.99	1.73	1.02	70.4	*	166.99	216.24	1.29	0.78	49.24	
8017867	FAM20A	NM_017565	107.03	58.8	-1.82	-0.7	-48.23	*	58.8	78.83	1.34	0.4	20.03	
7919591	FAM72A	ENST00000369175	20.6	52.65	2.56	1.4	32.05	*	52.65	38.94	-1.35	-0.75	-13.71	
8073775	FBLN1	NM_006486	422.5	215.11	-1.96	-1.21	-207.39	*	215.11	234.75	1.09	0.67	19.63	
7980908	FBLN5	NM_006329	533.42	339.65	-1.57	-1	-193.77	*	339.65	472.6	1.39	0.7	132.94	
8150002	FBXO16	NM_172366	58.47	99.71	1.71	1.24	41.24	*	99.71	95.38	-1.05	-0.79	-4.33	
8152703	FBXO32	NM_058229	351.21	180.73	-1.94	-1.25	-170.48	*	180.73	181.01	1	0.62	0.28	
8140420	FDPSL2A	NR_003262	81.39	124.91	1.53	1.1	43.52	*	124.91	140.09	1.12	0.62	15.18	
8097829	FHDC1	NM_033393	92.21	51.53	-1.79	-1.26	-40.68	*	51.53	70.68	1.37	0.95	19.15	
7920165	FLG	NM_002016	239.52	78.77	-3.04	-0.98	-160.75	*	78.77	102.94	1.31	0.64	24.17	
8131479	FLJ20323	NM_019005	245.11	551.06	2.25	1.62	305.95	*	551.06	709.21	1.29	0.9	158.15	
8079167	FLJ36157	ENST00000309765	474.82	281.95	-1.68	-1.12	-192.87	*	281.95	297.82	1.06	0.87	15.87	
7976073	FLRT2	NM_013231	193.19	310.35	1.61	1.1	117.16	*	310.35	326	1.05	0.64	15.65	
8065071	FLRT3	NM_198391	53.62	105.83	1.97	1.09	52.21	*	105.83	75.2	-1.41	-0.75	-30.63	
7910923	FMN2	NM_020066	50.5	104	2.06	1.54	53.5	*	104	87.33	-1.19	-0.9	-16.68	
8010841	FN3K	NM_022158	104.87	60.02	-1.75	-1.31	-44.85	*	60.02	60.61	1.01	0.67	0.59	
8018646	FOXJ1	NM_001454	161.39	50.66	-3.19	0	-110.73	*	50.66	56.83	1.12	0.88	6.16	
8065576	FOXS1	NM_004118	121.43	60.9	-1.99	-0.72	-60.54	*	60.9	57.62	-1.06	-0.64	-3.28	
8057506	FRZB	NM_001463	20.43	617.01	30.2	11.42	596.58	*	617.01	513.31	-1.2	-0.43	-103.71	
8010614	FSCN2	NM_012418	103.32	43.8	-2.36	0	-59.52	*	43.8	42.4	-1.03	-0.78	-1.4	
8172244	FUNDC1	NM_173794	702.8	362.75	-1.94	-0.15	-340.05	*	362.75	374.29	1.03	0.74	11.54	
7909441	G0S2	NM_015714	634.43	389.59	-1.63	-1.11	-244.84	*	389.59	359.24	-1.08	-0.73	-30.35	
8167573	GAGE12B	NM_001127345	441.44	280.3	-1.57	-1.08	-161.13	*	280.3	287.86	1.03	0.76	7.55	
8098328	GALNT7	NM_017423	293.53	453.52	1.55	1.14	160	*	453.52	643.88	1.42	1.04	190.36	
7970329	GAS6	NM_000820	614.04	189.6	-3.24	-2.07	-424.44	*	189.6	232.93	1.23	0.93	43.33	
7936494	GFRA1	NM_005264	79.23	40.4	-1.96	-1.33	-38.83	*	40.4	36.19	-1.12	-0.62	-4.21	
8115664	GLRXL	NM_001123388	315.12	96.57	-3.26	0	-218.54	*	96.57	108.86	1.13	0.98	12.29	
8117225	GMNN	NM_015895	81.6	142.85	1.75	1.15	61.25	*	142.85	119.22	-1.2	-0.79	-23.63	
7936322	GPAM	NM_020918	125.07	376.49	3.01	0.68	251.42	*	376.49	389.3	1.03	0.33	12.81	
8141463	GPC2	NM_152742	39.78	72	1.81	0.83	32.23	*	72	47.08	-1.53	-0.65	-24.92	
8078386	GPD1L	NM_015141	29.91	64.83	2.17	1.32	34.92	*	64.83	71.64	1.11	0.48	6.81	
7999909	GPRC5B	NM_016235	74.88	316.64	4.23	2.09	241.76	*	316.64	432.69	1.37	0.66	116.06	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7925452	GREM2	NM_022469	104.18	502.09	4.82	3.27	397.91	*	502.09	490.52	-1.02	-0.73	-11.57	
8169717	GRIA3	NM_007325	299.9	516.04	1.72	1.09	216.14	*	516.04	485.05	-1.06	-0.68	-30.98	
8121225	GRIK2	NM_175768	196.16	335.48	1.71	0.85	139.32	*	335.48	337.79	1.01	0.43	2.31	
8072926	H1F0	NM_005318	768.04	507.07	-1.51	-0.8	-260.97	*	507.07	540.19	1.07	0.55	33.12	
8152617	HAS2	NM_005328	1221.43	565.64	-2.16	-1.16	-655.79	*	565.64	623.7	1.1	0.49	58.05	
8090193	HEG1	NM_020733	627.93	351.09	-1.79	-1.38	-276.84	*	351.09	325.82	-1.08	-0.89	-25.26	
8151457	HEY1	NM_012258	24.24	693.47	28.61	10.52	669.23	*	693.47	567.06	-1.22	-0.5	-126.41	
8121850	HEY2	NM_012259	29.04	120.75	4.16	2.54	91.71	*	120.75	88.83	-1.36	-0.95	-31.92	
8118548	HLA-DRA	NM_019111	66.84	30.29	-2.21	-1.01	-36.55	*	30.29	31.68	1.05	0.48	1.38	
8178193	HLA-DRA	NM_019111	131.94	46.99	-2.81	-1.23	-84.95	*	46.99	40.34	-1.16	-0.45	-6.66	
8179481	HLA-DRA	NM_019111	68.2	30.85	-2.21	-1.04	-37.35	*	30.85	31.82	1.03	0.47	0.97	
8178802	HLA-DRB3	NM_022555	185.79	123.49	-1.5	-0.76	-62.3	*	123.49	121.16	-1.02	-0.46	-2.33	
8178811	HLA-DRB3	NM_022555	214.31	139.22	-1.54	-0.8	-75.08	*	139.22	138.3	-1.01	-0.48	-0.93	
8180003	HLA-DRB3	NM_022555	204.74	133.21	-1.54	-0.8	-71.53	*	133.21	132.58	-1	-0.49	-0.64	
8125436	HLA-DRB5	NM_002125	192.8	104.21	-1.85	-1.03	-88.59	*	104.21	104.28	1	0.53	0.08	
7908204	HMCN1	NM_031935	319.06	604.55	1.89	0.85	285.48	*	604.55	670.51	1.11	0.52	65.96	
7945245	HNT	NM_016522	264.38	174.14	-1.52	-0.85	-90.25	*	174.14	219.58	1.26	0.63	45.44	
7991034	HOMER2	NM_199330	87.87	299.78	3.41	2.84	211.91	*	299.78	243.34	-1.23	-1.12	-56.44	
8016463	HOXB6	NM_018952	81.88	149.7	1.83	1.1	67.82	*	149.7	149.16	-1	-0.57	-0.54	
8155167	HRCT1	NM_001039792	242.68	138.99	-1.75	-1.21	-103.69	*	138.99	164.21	1.18	0.91	25.22	
8097335	HSPA4L	NM_014278	250.69	121.22	-2.07	-1.58	-129.47	*	121.22	127.71	1.05	0.79	6.49	
8061564	ID1	NM_181353	33.7	157.41	4.67	3.24	123.71	*	157.41	158.54	1.01	0.87	1.13	
8040103	ID2	NM_002166	65.18	395.25	6.06	3.74	330.07	*	395.25	487.64	1.23	1.01	92.39	
8088480	ID2	NM_002166	56.27	171.83	3.05	1.98	115.56	*	171.83	186.65	1.09	0.88	14.83	
7913655	ID3	NM_002167	31.88	161.92	5.08	3.72	130.04	*	161.92	198.88	1.23	0.97	36.95	
8117120	ID4	NM_001546	186.41	528.71	2.84	1.72	342.3	*	528.71	722.05	1.37	1.04	193.34	
8124848	IER3	NM_003897	194.81	128.06	-1.52	-1.03	-66.75	*	128.06	152.22	1.19	0.39	24.16	
8178435	IER3	NM_003897	211.58	139.56	-1.52	-1.01	-72.02	*	139.56	166.25	1.19	0.37	26.69	
8179704	IER3	NM_003897	194.81	128.06	-1.52	-1.03	-66.75	*	128.06	152.22	1.19	0.39	24.16	
7902541	IFI44L	NM_006820	77.53	137.46	1.77	0.16	59.93	*	137.46	103.12	-1.33	-0.12	-34.34	
7929047	IFIT2	NM_001547	137.47	83.98	-1.64	-0.89	-53.49	*	83.98	65.8	-1.28	-0.92	-18.18	
7937335	IFITM1	NM_003641	926.62	515.3	-1.8	-0.78	-411.32	*	515.3	399.72	-1.29	-0.05	-115.58	
8068280	IFNGR2	NM_005534	179.61	272.35	1.52	1.03	92.74	*	272.35	349.03	1.28	0.81	76.68	
7965873	IGF1	NM_001111283	53.48	296.75	5.55	2.76	243.27	*	296.75	278.57	-1.07	-0.59	-18.19	
8138566	IGF2BP3	NM_006547	38.39	77.9	2.03	0.96	39.5	*	77.9	99.46	1.28	0.66	21.56	
8132694	IGFBP1	NM_000596	221.55	124.09	-1.79	-1.27	-97.45	*	124.09	123.58	-1	-0.81	-0.51	
8037755	IGFL3	NM_207393	131.44	67.3	-1.95	-1.69	-64.15	*	67.3	64.68	-1.04	-0.9	-2.61	
8100827	IGJ	NM_144646	56.93	30.94	-1.84	-0.69	-25.99	*	30.94	31.85	1.03	0.59	0.91	
7918913	IGSF3	NM_001542	97.01	53.9	-1.8	-1.18	-43.11	*	53.9	63.49	1.18	0.96	9.59	
8039484	IL11	NM_000641	174.31	427.62	2.45	1.44	253.31	*	427.62	313.08	-1.37	-0.76	-114.54	
8169580	IL13RA1	NM_001560	510.7	958.44	1.88	1.36	447.74	*	958.44	915.07	-1.05	-0.76	-43.37	
8131803	IL6	NM_000600	703.06	408.53	-1.72	-0.79	-294.53	*	408.53	352.56	-1.16	-0.05	-55.96	
8138542	IL6 // LOC541472	ENST00000325042	178.8	102.36	-1.75	-0.65	-76.44	*	102.36	72.28	-1.42	0	-30.08	
7930927	INPP5F	NM_014937	285.25	454.44	1.59	1.16	169.2	*	454.44	511.1	1.12	0.77	56.66	
7993713	IQCK	NM_153208	28.05	62.51	2.23	1.27	34.45	*	62.51	89.59	1.43	0.85	27.09	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8059470	IRS1	NM_005544	54.32	85.59	1.58	0.97	31.27	*	85.59	75.57	-1.13	-0.71	-10.02	
8105267	ITGA2	NM_002203	294.12	446.76	1.52	0.58	152.64	*	446.76	430.03	-1.04	-0.39	-16.73	
8008237	ITGA3	NM_002204	247.7	127.65	-1.94	-1.37	-120.05	*	127.65	131.31	1.03	0.73	3.67	
8046695	ITGA4	NM_000885	226.25	446.42	1.97	1.49	220.17	*	446.42	359.9	-1.24	-0.87	-86.53	
7922889	IVNS1ABP	NM_006469	634.97	1114.92	1.76	1.35	479.96	*	1114.92	1343.96	1.21	0.85	229.04	
8064978	JAG1	NM_000214	188.55	538.59	2.86	2.36	350.04	*	538.59	376.06	-1.43	-1.07	-162.52	
8068024	JAM2	NM_021219	355.05	171.72	-2.07	-1.63	-183.33	*	171.72	222.64	1.3	1.11	50.92	
8171248	KAL1	NM_000216	130.84	322.51	2.46	0.64	191.67	*	322.51	376.1	1.17	0.53	53.59	
7929932	KAZALD1	NM_030929	107.35	399.34	3.72	2.68	291.99	*	399.34	267.61	-1.49	-1.14	-131.73	
7909730	KCNK2	NM_001017425	698.51	333.06	-2.1	-1.73	-365.45	*	333.06	318.16	-1.05	-0.62	-14.9	
8108905	KCTD16	NM_020768	51.39	96.97	1.89	0.72	45.58	*	96.97	109.76	1.13	0.49	12.79	
7971369	KCTD4	NM_198404	62.26	35.18	-1.77	-0.88	-27.07	*	35.18	35.63	1.01	0.83	0.44	
7989647	KIAA0101	NM_014736	35.26	72.16	2.05	0	36.9	*	72.16	58.9	-1.23	0	-13.26	
7985317	KIAA1199	NM_018689	1142.9	223.71	-5.11	-2.04	-919.19	*	223.71	311.96	1.39	0.63	88.24	
8009602	KIF19	NM_153209	135.03	65.37	-2.07	-1.29	-69.67	*	65.37	69.06	1.06	0.91	3.69	
8118669	KIFC1	NM_002263	100.01	159	1.59	0	58.99	*	159	115.94	-1.37	0	-43.06	
8179564	KIFC1	NM_002263	107.65	171.43	1.59	0	63.78	*	171.43	124.89	-1.37	0	-46.54	
7969414	KLF5	NM_001730	441.9	237.02	-1.86	-1.32	-204.88	*	237.02	245.89	1.04	0.89	8.87	
8101624	KLHL8	NM_020803	103.25	194.82	1.89	1.19	91.57	*	194.82	265.85	1.36	1.02	71.03	
7961151	KLRK1	NM_007360	20.49	64.39	3.14	0.66	43.9	*	64.39	53.94	-1.19	-0.23	-10.45	
8072170	KREMEN1	NM_001039570	58.44	90.29	1.54	0.86	31.84	*	90.29	69.12	-1.31	-0.73	-21.17	
8015376	KRT16	NM_005557	185.96	89.66	-2.07	-1.28	-96.3	*	89.66	87.69	-1.02	-0.67	-1.97	
8015349	KRT19	NM_002276	145.46	50.1	-2.9	-0.47	-95.36	*	50.1	65.83	1.31	0.7	15.73	
8015268	KRT34	NM_021013	45.83	103.97	2.27	0.6	58.14	*	103.97	69.79	-1.49	-0.37	-34.18	
7963545	KRT79	NM_175834	89.04	57.28	-1.55	-1.04	-31.76	*	57.28	57	-1	-0.84	-0.28	
7963359	KRT83	NM_002282	167.06	84.38	-1.98	-1.29	-82.68	*	84.38	109.29	1.3	0.96	24.92	
8069161	KRTAP12-3	NM_198697	395.26	204.31	-1.93	-1.36	-190.95	*	204.31	228.89	1.12	0.96	24.57	
8069800	KRTAP24-1	NM_001085455	104.86	57.44	-1.83	-1.22	-47.43	*	57.44	65.48	1.14	0.97	8.04	
8020551	LAMA3	NM_198129	65.9	31.06	-2.12	-1.71	-34.84	*	31.06	41.99	1.35	1.02	10.93	
7920193	LCE1C	NM_178351	399.57	181.47	-2.2	-1.2	-218.1	*	181.47	212.36	1.17	0.92	30.89	
8031253	LILRP2	NR_003061	133.74	66.89	-2	-1.36	-66.85	*	66.89	69.42	1.04	0.76	2.53	
7965156	LIN7A	NM_004664	86.99	172.53	1.98	1.7	85.54	*	172.53	193.63	1.12	0.84	21.1	
8030212	LIN7B	NM_022165	237.55	568.38	2.39	1.96	330.83	*	568.38	599.5	1.05	0.74	31.13	
7939492	LOC387763	ENST00000339446	261.23	109.54	-2.38	-1.52	-151.7	*	109.54	122.34	1.12	0.72	12.8	
7919580	LOC440570 // LOC440570	AK125737	119.52	74.74	-1.6	-1.07	-44.78	*	74.74	63.38	-1.18	-0.93	-11.36	
7919596	LOC440570 // LOC440570	AK125737	119.52	74.74	-1.6	-1.07	-44.78	*	74.74	63.38	-1.18	-0.93	-11.36	
8022653	LOC728606	NR_024259	78.96	38.73	-2.04	-1.49	-40.22	*	38.73	43.94	1.13	0.96	5.21	
7935553	LOXL4	NM_032211	355.21	119.32	-2.98	-1.52	-235.89	*	119.32	110.88	-1.08	-0.66	-8.43	
8142765	LRRC4	NM_022143	136.87	86.9	-1.58	-1.19	-49.97	*	86.9	95.06	1.09	0.67	8.17	
8135488	LRRN3	NM_001099660	50.41	87.55	1.74	1	37.14	*	87.55	101.01	1.15	0.78	13.46	
8153359	LY6D	NM_003695	143.93	81.62	-1.76	-0.94	-62.3	*	81.62	87.85	1.08	0.97	6.23	
8138466	MACC1	NM_182762	67.17	38.45	-1.75	-1.04	-28.72	*	38.45	35.98	-1.07	-0.84	-2.46	
8155754	MAMDC2	NM_153267	36.53	65.28	1.79	0.9	28.75	*	65.28	92.51	1.42	0.3	27.24	
7961365	MANSC1	NM_018050	170.84	105.4	-1.62	-1.09	-65.44	*	105.4	119.1	1.13	0.85	13.7	
8005707	MAP2K3	NM_002756	191.78	94.73	-2.02	-1.03	-97.05	*	94.73	105.3	1.11	0.85	10.57	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8147516	MATN2	NM_002380	264.74	168.81	-1.57	-0.51	-95.93	*	168.81	126.15	-1.34	-0.13	-42.66	
8075659	MB	NM_203377	84.11	54.83	-1.53	-0.93	-29.28	*	54.83	57.49	1.05	0.78	2.66	
7952205	MCAM	NM_006500	84.78	215.93	2.55	1.66	131.15	*	215.93	224.62	1.04	0.64	8.69	
8136248	MEST	NM_002402	292.59	120.01	-2.44	-1.07	-172.58	*	120.01	138.48	1.15	0.63	18.47	
7912887	MFAP2	NM_002403	290.15	178.51	-1.63	-0.92	-111.64	*	178.51	194.53	1.09	0.66	16.02	
8047062	MGC13057	NM_001042519	48.25	232.99	4.83	2.59	184.74	*	232.99	197.42	-1.18	-0.65	-35.57	
8169073	MGC39900	NM_194324	79.98	123.23	1.54	0.79	43.25	*	123.23	93.68	-1.32	-0.71	-29.54	
8179238	MICA	NM_000247	161.03	259.62	1.61	0.86	98.6	*	259.62	262.63	1.01	0.57	3	
7905329	MLLT11	NM_006818	316.42	1056.45	3.34	2.65	740.02	*	1056.45	817.4	-1.29	-1.05	-239.05	
7951271	MMP1	NM_002421	48.45	81.06	1.67	0.06	32.6	*	81.06	62.23	-1.3	-0.05	-18.82	
8151684	MMP16	AL136588	83.39	153.14	1.84	1.22	69.75	*	153.14	199.14	1.3	0.82	46	
8151686	MMP16	NM_005941	148.47	346.6	2.33	1.9	198.14	*	346.6	334.31	-1.04	-0.82	-12.29	
7951284	MMP3	NM_002422	23.91	136.42	5.71	0	112.52	*	136.42	110.59	-1.23	0	-25.83	
8097857	MND1	NM_032117	70.32	293.89	4.18	2.68	223.57	*	293.89	300.18	1.02	0.66	6.29	
7952036	MPZL3	NM_198275	90.75	160.47	1.77	1.12	69.73	*	160.47	113.78	-1.41	-0.94	-46.69	
7995806	MT1A	NM_005946	148.56	256.26	1.72	0.6	107.7	*	256.26	263.07	1.03	0.61	6.82	
8152764	MTSS1	NM_014751	86.92	40.12	-2.17	-1.38	-46.8	*	40.12	33.48	-1.2	-0.84	-6.65	
8135033	MUC12	ENST00000379443	38.7	64.4	1.66	1.19	25.7	*	64.4	57.71	-1.12	-0.64	-6.68	
8088047	MUSTN1	NM_205853	488.29	293.41	-1.66	-0.98	-194.88	*	293.41	361.78	1.23	0.99	68.37	
8171172	MXRA5	NM_015419	251.45	563.56	2.24	0.4	312.11	*	563.56	753.38	1.34	0.18	189.82	
8151101	MYBL1	NM_001080416	486.85	212.6	-2.29	-1.03	-274.25	*	212.6	195.27	-1.09	-0.65	-17.33	
7957966	MYBPC1	NM_002465	85.68	41.61	-2.06	-1.43	-44.07	*	41.61	43.26	1.04	0.81	1.65	
8014115	MYO1D	NM_015194	381.46	249.85	-1.53	-0.97	-131.61	*	249.85	252.13	1.01	0.58	2.27	
7943051	NAALAD2	NM_005467	19.18	48.67	2.54	2.05	29.5	*	48.67	56.08	1.15	0.73	7.4	
8139460	NACAD	AB002361	83.46	135.44	1.62	1.05	51.98	*	135.44	183.21	1.35	0.91	47.77	
8001197	NETO2	NM_018092	304.61	194.67	-1.56	-0.83	-109.93	*	194.67	244.61	1.26	0.59	49.93	
8014865	NEUROD2	NM_006160	147.37	80.82	-1.82	-1.31	-66.55	*	80.82	96.85	1.2	1.04	16.03	
8160138	NFIB	NM_005596	123.19	60.71	-2.03	-1.52	-62.48	*	60.71	56.68	-1.07	-0.8	-4.03	
8117663	NKAPL	NM_001007531	58.13	88.99	1.53	0.8	30.86	*	88.99	114.89	1.29	0.67	25.9	
8055702	NMI	NM_004688	415.68	254.73	-1.63	-1.07	-160.95	*	254.73	208.11	-1.22	-0.6	-46.62	
7922756	NMNAT2	NM_015039	80.53	138.01	1.71	0.65	57.48	*	138.01	175.84	1.27	0.78	37.83	
8008627	NOG	NM_005450	51.39	569.37	11.08	5.1	517.98	*	569.37	582.45	1.02	0.64	13.08	
8022531	NPC1	NM_000271	449.42	262.6	-1.71	-0.91	-186.82	*	262.6	314.88	1.2	1	52.28	
8139367	NPC1L1	NM_013389	162.48	99.24	-1.64	-0.99	-63.25	*	99.24	113.37	1.14	0.69	14.14	
7976012	NRXN3	NM_004796	56.38	27.07	-2.08	-1.37	-29.31	*	27.07	31.71	1.17	0.93	4.64	
7965573	NTN4	NM_021229	477.29	309.88	-1.54	-0.76	-167.41	*	309.88	337.87	1.09	0.67	27.99	
8102713	NUDT6	NM_007083	95.5	155.28	1.63	0.81	59.78	*	155.28	129.92	-1.2	-0.63	-25.36	
7982889	NUSAP1	NM_016359	58.73	92.06	1.57	0.31	33.33	*	92.06	91.87	-1	-0.19	-0.2	
8162373	OGN	NM_033014	24.21	80.93	3.34	2.2	56.72	*	80.93	70.12	-1.15	-0.6	-10.82	
7921882	OLFML2B	NM_015441	199.76	509.14	2.55	1.46	309.39	*	509.14	441.86	-1.15	-0.7	-67.28	
7911263	OR2M5	NM_001004690	66.89	41.33	-1.62	-1.19	-25.56	*	41.33	36.14	-1.14	-0.79	-5.2	
8161166	OR2S2	NM_019897	109.76	64.5	-1.7	-0.91	-45.25	*	64.5	61.42	-1.05	-0.81	-3.08	
8020354	OR4K15	NM_001005486	67.41	34.05	-1.98	-1.13	-33.36	*	34.05	38.31	1.12	0.83	4.25	
7946069	OR51B2	NM_033180	89.03	53.13	-1.68	-1.01	-35.89	*	53.13	37.79	-1.41	-1.04	-15.34	
7938072	OR56B4	NM_001005181	80.71	37.49	-2.15	-0.61	-43.21	*	37.49	45.52	1.21	1.01	8.02	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7939950	OR5D16	NM_001005496	63.82	38.49	-1.66	-1.12	-25.33	*	38.49	42.34	1.1	0.75	3.85	
8105040	OSMR	NM_003999	265.06	173.03	-1.53	-1.28	-92.03	*	173.03	244.5	1.41	0.98	71.47	
8085138	OXTR	NM_000916	565.85	237.76	-2.38	-0.45	-328.1	*	237.76	314.43	1.32	0.37	76.68	
8159265	PAEP	NM_001018049	258.38	136.27	-1.9	-1.19	-122.11	*	136.27	164.58	1.21	1.04	28.32	
8169389	PAK3	NM_002578	61.98	34.12	-1.82	-1.08	-27.86	*	34.12	55.36	1.62	1.07	21.24	
7943218	PANX1	NM_015368	486.63	275.96	-1.76	-1.26	-210.67	*	275.96	212.18	-1.3	-0.77	-63.78	
7981943	PAR5	NR_022008	75.08	143.99	1.92	1.11	68.91	*	143.99	110.65	-1.3	-0.83	-33.34	
8082100	PARP14	NM_017554	211.51	121.34	-1.74	-1.22	-90.17	*	121.34	123.98	1.02	0.4	2.65	
7971922	PCDH9	NM_203487	59.23	117.84	1.99	1.4	58.61	*	117.84	128.18	1.09	0.51	10.34	
8108737	PCDHB13	NM_018933	36.81	65.21	1.77	1.11	28.4	*	65.21	53.31	-1.22	-0.78	-11.9	
8108697	PCDHB5	NM_015669	197.91	303.42	1.53	0.58	105.51	*	303.42	223.18	-1.36	-0.54	-80.24	
8138888	PDE1C	NM_005020	304.05	116.79	-2.6	-1.31	-187.26	*	116.79	93.14	-1.25	-0.64	-23.64	
7954293	PDE3A	NM_000921	58.79	185.23	3.15	2.56	126.44	*	185.23	145.57	-1.27	-0.91	-39.66	
8095080	PDGFRA	NM_006206	856.72	469.74	-1.82	-1.09	-386.98	*	469.74	481.07	1.02	0.65	11.33	
8144802	PDGFRL	NM_006207	94.82	60.45	-1.57	-0.73	-34.37	*	60.45	84.8	1.4	0.44	24.35	
8104022	PDLIM3	NM_014476	112.22	43.79	-2.56	-1.8	-68.43	*	43.79	67.8	1.55	1.28	24.01	
8134339	PEG10	NM_015068	54.51	98.68	1.81	0.8	44.17	*	98.68	95.58	-1.03	-0.42	-3.1	
7925876	PFKP	NM_002627	83.22	136.55	1.64	0.65	53.33	*	136.55	136.59	1	0.6	0.05	
7980233	PGF	NM_002632	45.93	198.83	4.33	2.44	152.89	*	198.83	145.5	-1.37	-0.79	-53.33	
8081590	PHLDB2	NM_001134439	468.9	203.26	-2.31	-1.68	-265.64	*	203.26	222.93	1.1	0.6	19.67	
8133818	PHTF2	NM_001127358	50.65	98.92	1.95	1.08	48.26	*	98.92	144.07	1.46	0.9	45.15	
8121768	PKIB	NM_181794	181.87	30.33	-6	-4.31	-151.54	*	30.33	46.38	1.53	0.89	16.05	
7948987	PLA2G16	NM_007069	393.42	158.24	-2.49	-1.67	-235.18	*	158.24	189.82	1.2	0.85	31.58	
7928429	PLAU	NM_002658	192.4	59.5	-3.23	-1.64	-132.9	*	59.5	68.72	1.15	0.83	9.22	
8047248	PLCL1	NM_001114661	72.27	172.63	2.39	1.32	100.36	*	172.63	179.83	1.04	0.65	7.21	
8014768	PLXDC1	NM_020405	104.44	58.29	-1.79	-1.12	-46.16	*	58.29	58.09	-1	-0.78	-0.2	
8021470	PMAIP1	NM_021127	87.05	49.52	-1.76	-1.08	-37.53	*	49.52	30.59	-1.62	-0.67	-18.93	
7965867	PMCH	NM_002674	37.38	68.44	1.83	1.18	31.06	*	68.44	51.16	-1.34	-1.04	-17.28	
8149877	PNMA2	NM_007257	57.35	25.48	-2.25	-0.86	-31.87	*	25.48	31.04	1.22	0.69	5.56	
7935865	POLL	NM_013274	91.22	59.18	-1.54	-0.82	-32.04	*	59.18	52.36	-1.13	-0.75	-6.82	
8148315	POU5F1P1	NR_002304	87.99	34.56	-2.55	-0.08	-53.43	*	34.56	29.38	-1.18	-0.67	-5.18	
8036473	PPP1R14A	NM_033256	220.75	140.95	-1.57	-0.26	-79.8	*	140.95	175.05	1.24	0.28	34.1	
7908312	PRG4	NM_005807	87.83	243.66	2.77	1.55	155.83	*	243.66	181.29	-1.34	-0.74	-62.37	
8135378	PRKAR2B	NM_002736	29.31	62.56	2.13	1.36	33.26	*	62.56	66.91	1.07	0.46	4.34	
7927606	PRKG1	NM_001098512	251.16	165.4	-1.52	-0.36	-85.75	*	165.4	163.72	-1.01	-0.29	-1.68	
8008784	PRR11	NM_018304	48.23	92.23	1.91	1.08	44	*	92.23	75.9	-1.22	-0.61	-16.33	
7907222	PRRX1	NM_006902	468.06	885.41	1.89	1.29	417.36	*	885.41	1077.94	1.22	0.86	192.52	
7910146	PSEN2	NM_000447	178.26	117.3	-1.52	-1.13	-60.96	*	117.3	115.96	-1.01	-0.64	-1.34	
8118571	PSMB9	NM_002800	276.79	148.42	-1.86	-0.9	-128.37	*	148.42	125.52	-1.18	-0.23	-22.9	
8178211	PSMB9	NM_002800	276.79	148.42	-1.86	-0.9	-128.37	*	148.42	125.52	-1.18	-0.23	-22.9	
8179495	PSMB9	NM_002800	276.79	148.42	-1.86	-0.9	-128.37	*	148.42	125.52	-1.18	-0.23	-22.9	
8164580	PTGES	NM_004878	85.93	151.24	1.76	1.24	65.31	*	151.24	162.8	1.08	0.81	11.56	
7922976	PTGS2	NM_000963	169.91	415.5	2.45	0.56	245.59	*	415.5	519.83	1.25	0.27	104.32	
7962000	PTHLH	NM_198965	33.01	203.67	6.17	0.71	170.66	*	203.67	174.76	-1.17	-0.13	-28.91	
7931353	PTPRE	NM_006504	101.3	59.14	-1.71	-1.27	-42.15	*	59.14	71.12	1.2	0.87	11.97	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8021301	RAB27B	NM_004163	222.03	608.06	2.74	1.55	386.03	*	608.06	458.15	-1.33	-0.75	-149.91	
8091723	RARRES1	NM_206963	185.28	97.65	-1.9	-0.58	-87.63	*	97.65	103.89	1.06	0.59	6.24	
8013112	RASD1	NM_016084	616.8	238.01	-2.59	-1.67	-378.79	*	238.01	328.55	1.38	0.98	90.53	
8106660	RASGRF2	NM_006909	133.72	74.49	-1.8	-1.39	-59.23	*	74.49	69.72	-1.07	-0.9	-4.77	
8095043	RASL11B	NM_023940	17.65	112.26	6.36	1.82	94.61	*	112.26	97.99	-1.15	-0.31	-14.27	
7965226	RASSF9	NM_005447	77.69	125.58	1.62	1.18	47.89	*	125.58	107.86	-1.16	-0.79	-17.72	
8117045	RBM24	NM_153020	93.12	227.01	2.44	1.8	133.89	*	227.01	260.24	1.15	0.85	33.23	
8062948	RBPJL	NM_014276	109.43	69.72	-1.57	-0.65	-39.71	*	69.72	61.27	-1.14	-0.75	-8.45	
8029580	RELB	NM_006509	208.91	116.04	-1.8	-1.25	-92.88	*	116.04	111.07	-1.04	-0.79	-4.97	
7975482	RGS6	NM_004296	121.09	66.36	-1.82	-1.05	-54.73	*	66.36	78.3	1.18	0.91	11.94	
8120613	RIMS1	NM_014989	179.06	97.25	-1.84	-0.51	-81.81	*	97.25	130.44	1.34	0.77	33.19	
8169174	RNF128	NM_024539	97.57	54.52	-1.79	-0.86	-43.04	*	54.52	45.94	-1.19	-0.78	-8.58	
8023598	RNF152	NM_173557	66.08	109.94	1.66	1.12	43.86	*	109.94	137.81	1.25	0.6	27.88	
8176730	RPS4Y2	NM_001039567	60.71	95.45	1.57	0.39	34.74	*	95.45	89.51	-1.07	-0.27	-5.94	
8040223	RRM2	NM_001034	52.2	83.99	1.61	0	31.79	*	83.99	78.66	-1.07	0	-5.33	
8152314	RSPO2	NM_178565	17.27	131.74	7.63	0	114.47	*	131.74	105.82	-1.24	0	-25.92	
8120043	RUNX2	NM_001024630	162.05	263.46	1.63	1.07	101.41	*	263.46	227.52	-1.16	-0.75	-35.95	
7920285	S100A2	NM_005978	604.76	402.34	-1.5	-0.61	-202.41	*	402.34	463.5	1.15	0.85	61.16	
8122634	SAMD5	NM_001030060	27.53	75.56	2.74	2.04	48.02	*	75.56	75.7	1	0.63	0.15	
8056491	SCN9A	NM_002977	98.04	172	1.75	0.77	73.96	*	172	124.52	-1.38	-0.59	-47.48	
8066513	SDC4	NM_002999	351.4	122.26	-2.87	-2.34	-229.14	*	122.26	88.5	-1.38	-1.1	-33.76	
7983527	SEMA6D	NM_153618	50.95	163.64	3.21	1.91	112.69	*	163.64	169.24	1.03	0.67	5.61	
8021623	SERPINB7	NM_003784	74.65	44.68	-1.67	-0.45	-29.97	*	44.68	46.57	1.04	0.25	1.89	
8021653	SERPINB8	NM_002640	187.31	306.78	1.64	0.97	119.46	*	306.78	323.05	1.05	0.76	16.27	
8003667	SERPINF1	NM_002615	381.36	173.42	-2.2	-1.82	-207.94	*	173.42	164.72	-1.05	-0.79	-8.7	
7940028	SERPING1	NM_000062	817.49	435.54	-1.88	-1.36	-381.95	*	435.54	429.96	-1.01	-0.62	-5.58	
7909503	SERTAD4	NM_019605	148.1	55.7	-2.66	-0.93	-92.41	*	55.7	72.94	1.31	0.72	17.25	
8129677	SGK1	NM_005627	135.39	369.82	2.73	1.72	234.43	*	369.82	307.15	-1.2	-0.77	-62.67	
8096733	SGMS2	NM_001136258	350.49	202.54	-1.73	-0.98	-147.95	*	202.54	239.2	1.18	0.78	36.65	
8112409	SGTB	NM_019072	168.81	291.01	1.72	1.28	122.21	*	291.01	320.9	1.1	0.93	29.89	
8095834	SHROOM3	NM_020859	43.46	73.01	1.68	1.01	29.55	*	73.01	64.94	-1.12	-0.68	-8.07	
7933750	SLC16A9	NM_194298	22.08	84.68	3.84	1.93	62.6	*	84.68	107.23	1.27	0.82	22.55	
8119974	SLC29A1	NM_001078175	314.86	151.98	-2.07	-0.47	-162.89	*	151.98	103.07	-1.47	-0.84	-48.9	
7962327	SLC2A13	NM_052885	88.46	142.3	1.61	1.13	53.84	*	142.3	155.37	1.09	0.68	13.07	
8068361	SLC5A3	NM_006933	302.16	177.23	-1.7	-0.42	-124.92	*	177.23	234.6	1.32	0.43	57.37	
8102800	SLC7A11	NM_014331	605.01	909.3	1.5	0.55	304.29	*	909.3	670.05	-1.36	-0.48	-239.25	
8003298	SLC7A5	NM_003486	181.61	302.77	1.67	0.52	121.17	*	302.77	242.67	-1.25	-0.37	-60.1	
7984364	SMAD3	NM_005902	472.36	251.21	-1.88	-1.55	-221.14	*	251.21	240.4	-1.05	-0.89	-10.82	
7971015	SMAD9	NM_001127217	57.31	120.54	2.1	1.57	63.22	*	120.54	105.96	-1.14	-0.88	-14.58	
8063382	SNAI1	NM_005985	96.79	260.49	2.69	1.77	163.69	*	260.49	256.42	-1.02	-0.68	-4.07	
8150698	SNAI2	NM_003068	1125.19	1766.06	1.57	1.16	640.88	*	1766.06	2016.22	1.14	0.86	250.16	
7902398	SNORD45A	NR_002749	22.42	57.84	2.58	1.87	35.42	*	57.84	40.76	-1.42	-1.06	-17.08	
8114468	SNORD63	NR_002913	64.05	100.67	1.57	0.7	36.62	*	100.67	84.28	-1.19	-0.54	-16.39	
7981958	SNRPN // SNORD116-5	NR_003320	116.94	195.25	1.67	0.92	78.3	*	195.25	173.5	-1.13	-0.95	-21.75	
7981962	SNRPN // SNORD116-5	NR_003320	116.94	195.25	1.67	0.92	78.3	*	195.25	173.5	-1.13	-0.95	-21.75	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7957551	SOCS2	NM_003877	48.48	214.12	4.42	1.74	165.64	*	214.12	150.97	-1.42	-0.53	-63.15	
8130556	SOD2	NM_001024465	740.72	368.18	-2.01	-1.43	-372.53	*	368.18	373.67	1.01	0.74	5.49	
8094372	SOD3	NM_003102	298.17	171	-1.74	-1.21	-127.18	*	171	169.16	-1.01	-0.79	-1.83	
7897449	SPSB1	NM_025106	114.59	53.28	-2.15	-1.63	-61.32	*	53.28	62.1	1.17	0.86	8.82	
7983512	SQRDL	NM_021199	620.82	238.62	-2.6	-1.82	-382.2	*	238.62	288.12	1.21	0.76	49.51	
8063839	SS18L1	NM_198935	324.93	73.11	-4.44	0	-251.82	*	73.11	75.29	1.03	0.87	2.18	
8147030	STMN2	NM_007029	25.11	57.03	2.27	0.97	31.92	*	57.03	73.43	1.29	0.53	16.4	
8041940	STON1-GTF2A1L	NM_172311	75.88	191.25	2.52	1.63	115.37	*	191.25	196.23	1.03	0.72	4.98	
8164013	STRBP	NM_018387	156.95	90.14	-1.74	-1.33	-66.81	*	90.14	75.23	-1.2	-0.89	-14.91	
8025255	STXBP2	NM_006949	182.24	104.71	-1.74	-1.07	-77.53	*	104.71	113.77	1.09	0.8	9.06	
8160712	SUGT1P	NR_003667	27.55	63.76	2.31	1.62	36.21	*	63.76	52.02	-1.23	-0.93	-11.75	
8163202	SVEP1	NM_153366	177.34	58.86	-3.01	-1.98	-118.49	*	58.86	70.61	1.2	0.79	11.75	
7932796	SVIL	NM_021738	383.38	214.84	-1.78	-1.41	-168.54	*	214.84	295.17	1.37	1.03	80.33	
7917322	SYDE2	NM_032184	71.5	146.85	2.05	1.44	75.35	*	146.85	111.37	-1.32	-0.9	-35.48	
7909494	SYT14	NM_153262	76.02	255.11	3.36	1.18	179.09	*	255.11	192.66	-1.32	-0.46	-62.45	
8100699	SYT14L	NM_001014372	20.45	69.77	3.41	1.46	49.32	*	69.77	57.69	-1.21	-0.5	-12.09	
8094476	TBC1D19	NM_018317	193.96	525.87	2.71	2.02	331.91	*	525.87	519.94	-1.01	-0.75	-5.93	
7966690	TBX3	NM_016569	84.29	195.92	2.32	1.59	111.63	*	195.92	189.1	-1.04	-0.81	-6.82	
8120082	TDRD6	NM_001010870	64.76	39.32	-1.65	-1.05	-25.44	*	39.32	35.43	-1.11	-0.83	-3.89	
8154692	TEK	NM_000459	73.56	40.17	-1.83	-0.62	-33.39	*	40.17	37.13	-1.08	-0.41	-3.04	
8037005	TGFB1	NM_000660	133.11	263.57	1.98	1.57	130.46	*	263.57	239.7	-1.1	-0.8	-23.87	
8066214	TGM2	NM_004613	425.24	208.11	-2.04	-0.71	-217.13	*	208.11	236.52	1.14	0.34	28.41	
8130867	THBS2	NM_003247	1146.02	668.93	-1.71	-1.18	-477.08	*	668.93	837.24	1.25	0.67	168.3	
7971813	THSD1	NM_018676	142.94	63.7	-2.24	-1.84	-79.24	*	63.7	76.96	1.21	0.92	13.26	
8091411	TM4SF1	NM_014220	883.35	384.93	-2.29	-1.86	-498.42	*	384.93	560.56	1.46	0.85	175.63	
8093104	TM4SF19	NM_138461	78.96	51.6	-1.53	-0.88	-27.36	*	51.6	48.09	-1.07	-0.66	-3.51	
7900409	TMCO2	NM_001008740	77.04	41.29	-1.87	-1.13	-35.76	*	41.29	43.55	1.05	0.67	2.26	
7966122	TMEM119	NM_181724	273.2	111.13	-2.46	-0.99	-162.07	*	111.13	128	1.15	0.41	16.87	
8141228	TMEM130	NM_001134450	197.03	63.14	-3.12	-2.23	-133.89	*	63.14	56.64	-1.11	-0.78	-6.5	
8161701	TMEM2	NM_013390	192.5	290.44	1.51	0.9	97.94	*	290.44	268.78	-1.08	-0.63	-21.66	
8152512	TNFRSF11B	NM_002546	698.02	162.46	-4.3	-1.73	-535.55	*	162.46	215.02	1.32	0.66	52.56	
7968015	TNFRSF19	NM_148957	138.46	73.97	-1.87	-1.27	-64.5	*	73.97	54.6	-1.35	-0.71	-19.37	
7937749	TNNT3	NM_006757	339.96	166.17	-2.05	-1.53	-173.79	*	166.17	195.68	1.18	0.7	29.5	
8150962	TOX	NM_014729	103.18	177.52	1.72	1.39	74.34	*	177.52	152.19	-1.17	-0.82	-25.33	
8133155	TPST1	NM_003596	265.32	652.47	2.46	2.11	387.15	*	652.47	583.18	-1.12	-1.03	-69.29	
8127051	TRAM2	NM_012288	479.52	272.77	-1.76	-1.32	-206.75	*	272.77	235.22	-1.16	-1.03	-37.55	
8148304	TRIB1	NM_025195	184.76	121.26	-1.52	-1.1	-63.49	*	121.26	132.19	1.09	0.54	10.92	
8178338	TRIM10	NM_006778	113.03	66.82	-1.69	-0.79	-46.21	*	66.82	87.22	1.31	0.93	20.4	
8097841	TRIM2	NM_015271	102.54	231.52	2.26	1.57	128.98	*	231.52	192.1	-1.21	-0.87	-39.42	
8063444	TSHZ2	AF230201	95.31	55.01	-1.73	-0.66	-40.3	*	55.01	50.25	-1.09	-0.38	-4.76	
7954653	TSPAN11	AY358804	76.61	141.64	1.85	1.27	65.02	*	141.64	114.1	-1.24	-0.86	-27.54	
8131600	TSPAN13	NM_014399	123.35	270.03	2.19	1.01	146.68	*	270.03	225.78	-1.2	-0.54	-44.25	
7928046	TSPAN15	NM_012339	76.93	233.7	3.04	1.61	156.77	*	233.7	160.46	-1.46	-0.84	-73.24	
7918857	TSPAN2	NM_005725	324.93	741.65	2.28	0.62	416.73	*	741.65	676.28	-1.1	-0.29	-65.37	
8177261	TTTY10	NR_001542	89.19	51.4	-1.74	-1.07	-37.8	*	51.4	49.04	-1.05	-0.78	-2.35	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7905428	TUFT1	NM_020127	125.9	67.22	-1.87	-0.81	-58.68	*	67.22	56.22	-1.2	-0.65	-11	
8129924	TXLNB	NM_153235	86.51	51.41	-1.68	-1.15	-35.1	*	51.41	52.58	1.02	0.72	1.17	
8100519	TXNDC9	BC024223	47.88	96.28	2.01	1.16	48.4	*	96.28	97.22	1.01	0.8	0.94	
7904726	TXNIP	NM_006472	1806.31	800.07	-2.26	-1.74	-1006.25	*	800.07	912.86	1.14	0.89	112.79	
7923426	UBE2T	NM_014176	58.01	103.26	1.78	1.52	45.25	*	103.26	120.63	1.17	0.79	17.37	
8157216	UGCG	NM_003358	296.13	173.58	-1.71	-1.31	-122.55	*	173.58	170.74	-1.02	-0.88	-2.83	
8100760	UGT2A3	NM_024743	50.95	23.55	-2.16	-1.06	-27.4	*	23.55	32.3	1.37	0.56	8.74	
7986248	UNQ6190	AY358245	383.62	189.71	-2.02	-1.21	-193.91	*	189.71	192.88	1.02	0.78	3.17	
8073743	UPK3A	NM_006953	124.09	57.02	-2.18	-0.71	-67.08	*	57.02	65.74	1.15	0.94	8.72	
8132725	UPP1	NM_003364	70.03	43.54	-1.61	-1.06	-26.49	*	43.54	40.11	-1.09	-0.87	-3.43	
7962689	VDR	NM_001017535	98.17	54.26	-1.81	-1.03	-43.91	*	54.26	72	1.33	0.79	17.73	
8103822	VEGFC	NM_005429	571.19	983.45	1.72	1.21	412.26	*	983.45	1167.45	1.19	0.91	184	
8098470	WWC2	NM_024949	548.87	929.67	1.69	1.26	380.8	*	929.67	972.83	1.05	0.66	43.16	
8106730	XRCC4	NM_022550	291.38	621.05	2.13	0.73	329.67	*	621.05	607.92	-1.02	-0.34	-13.14	
7943715	ZC3H12C	NM_033390	115.11	67.01	-1.72	-1.21	-48.1	*	67.01	85.29	1.27	1.04	18.28	
8083233	ZIC1	NM_003412	96.95	145.77	1.5	0.39	48.81	*	145.77	109.1	-1.34	-0.34	-36.67	
8137112	ZNF212	NM_012256	111.22	65.97	-1.69	-1.1	-45.25	*	65.97	72.53	1.1	0.78	6.56	
8133062	ZNF273	NM_021148	62.27	129.98	2.09	1.48	67.71	*	129.98	101.89	-1.28	-0.88	-28.08	
8085774	ZNF385D	NM_024697	176.78	63.31	-2.79	-0.95	-113.47	*	63.31	91.44	1.44	0.34	28.13	
8079198	ZNF660	NM_173658	59.36	124.42	2.1	0.95	65.06	*	124.42	90.01	-1.38	-0.62	-34.4	

Genes Differentially Expressed in OSX Null hMSCs from All Three Donors

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7960947	A2M	NM_000014	109.24	78.51	-1.39	-0.8	-30.73		78.51	44.6	-1.76	-0.67	-33.9	*
7975066	AKAP5	NM_004857	33.24	47.66	1.43	0.81	14.42		47.66	80.48	1.69	1.01	32.82	*
7983679	AP4E1	NM_007347	155.18	212.34	1.37	0.93	57.15		212.34	120.38	-1.76	-1.27	-91.96	*
8073088	APOBEC3G	NM_021822	58.9	67.36	1.14	0.07	8.46		67.36	39.12	-1.72	-0.1	-28.24	*
8059854	ARL4C	NM_005737	399.72	537.56	1.34	1.04	137.84		537.56	231.9	-2.32	-1.85	-305.67	*
8003814	ASPA	NM_000049	51.67	42.2	-1.22	-0.36	-9.47		42.2	17.11	-2.47	0	-25.08	*
8147756	BAALC	NM_024812	83.07	85.21	1.03	0.36	2.14		85.21	50.86	-1.68	-0.58	-34.35	*
7939215	C11orf41	NM_012194	194.38	146.55	-1.33	-0.86	-47.83		146.55	90.08	-1.63	-0.93	-56.47	*
8108163	C5orf24	NM_152409	284.08	313.4	1.1	0.8	29.32		313.4	638.74	2.04	1.59	325.34	*
7951408	CARD16	NM_052889	211.11	167.76	-1.26	-0.84	-43.35		167.76	92.7	-1.81	-0.83	-75.05	*
8056890	CHN1	NM_001822	108.37	125.65	1.16	0.66	17.27		125.65	290.97	2.32	1.23	165.32	*
7919800	CTSS	NM_004079	65.14	77.48	1.19	0.3	12.34		77.48	49.17	-1.58	-0.39	-28.3	*
7995552	CYLD	NM_015247	216.76	247.17	1.14	0.85	30.4		247.17	478.04	1.93	1.61	230.87	*
7974697	DAAM1	NM_014992	131.51	104.61	-1.26	-0.86	-26.9		104.61	179.41	1.72	1.13	74.8	*
8148059	DEPDC6	NM_022783	182.15	132.67	-1.37	-0.6	-49.48		132.67	219.23	1.65	1.02	86.56	*
8135480	DNAJB9	NM_012328	235.72	258.07	1.09	0.73	22.35		258.07	570.05	2.21	1.37	311.98	*
7922130	DPT	NM_001937	164.29	185.06	1.13	0	20.77		185.06	73.97	-2.5	0	-111.09	*
8023727	DSEL	NM_032160	521.97	441.92	-1.18	-0.89	-80.05		441.92	905.84	2.05	1.67	463.93	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7943293	ENDOD1	NM_015036	100.42	92.31	-1.09	-0.73	-8.11		92.31	255.86	2.77	2.12	163.55	*
8149793	ENTPD4	NM_004901	238.03	299.31	1.26	0.97	61.28		299.31	508.17	1.7	1.35	208.86	*
8091972	EVI1	NM_001105078	101.17	134.37	1.33	0.59	33.19		134.37	203.73	1.52	0.73	69.36	*
7918026	EXTL2	NM_001439	180.71	227.75	1.26	0.89	47.04		227.75	404.9	1.78	1.43	177.15	*
7914342	FABP3	NM_004102	303.82	210.58	-1.44	-0.57	-93.25		210.58	369.53	1.75	0	158.96	*
8046895	FAM171B	NM_177454	560.78	554.39	-1.01	-0.46	-6.38		554.39	853.44	1.54	0.94	299.05	*
7928909	FAM35A	NM_019054	60.53	75.14	1.24	0.74	14.6		75.14	124.47	1.66	1.11	49.33	*
7930882	FAM45A	NM_207009	240.15	226.8	-1.06	-0.75	-13.35		226.8	680.5	3	2.17	453.7	*
8169928	FAM45A	NM_207009	80.8	91.37	1.13	0.39	10.57		91.37	300.76	3.29	2.03	209.39	*
7989611	FAM96A	NM_032231	244.12	266.59	1.09	0.89	22.47		266.59	130.43	-2.04	-1.6	-136.16	*
7939052	FIBIN	NM_203371	53.38	36.67	-1.46	-0.98	-16.71		36.67	73.75	2.01	1.28	37.08	*
8147766	FZD6	NM_003506	276.6	235.69	-1.17	-0.71	-40.91		235.69	424.29	1.8	1.14	188.6	*
8081810	GAP43	NM_001130064	295.41	408.98	1.38	0.78	113.57		408.98	633.95	1.55	0.86	224.97	*
8112622	GFM2	NM_032380	189.56	281.23	1.48	0.93	91.67		281.23	427.03	1.52	1.11	145.8	*
8138857	GGCT	NM_024051	277.4	255.97	-1.08	-0.9	-21.43		255.97	595.03	2.32	1.88	339.06	*
8061471	GINS1	NM_021067	87.04	113.89	1.31	0.78	26.86		113.89	63.74	-1.79	-1.03	-50.15	*
8086028	GLB1	NM_000404	115.29	168.61	1.46	1.22	53.32		168.61	425.33	2.52	2.13	256.72	*
8036710	GMFG	NM_004877	84.67	118.12	1.4	0.68	33.45		118.12	78.07	-1.51	-0.71	-40.05	*
8043900	hCG_1790474	NM_001101386	93.06	123.64	1.33	0.92	30.58		123.64	78.15	-1.58	-1.03	-45.48	*
8089851	HGD	NM_000187	64.44	54.91	-1.17	-0.3	-9.53		54.91	98.4	1.79	0.58	43.49	*
8093278	HGD	NM_000187	64.44	54.91	-1.17	-0.3	-9.53		54.91	98.4	1.79	0.58	43.49	*
8042942	HK2	NM_000189	107.16	98.23	-1.09	-0.82	-8.93		98.23	177.19	1.8	1.27	78.96	*
7976443	IFI27	NM_001130080	187.78	244.06	1.3	0.3	56.28		244.06	130.15	-1.88	-0.47	-113.9	*
8056285	IFIH1	NM_022168	186.68	139.96	-1.33	-0.74	-46.72		139.96	91.16	-1.54	-0.33	-48.79	*
8095680	IL8	NM_000584	51.16	69.81	1.36	0.5	18.66		69.81	112.76	1.62	0	42.94	*
7902074	LEPR	NM_002303	230.16	190.54	-1.21	-0.98	-39.63		190.54	423.14	2.22	2.06	232.6	*
8108475	LOC492311	NM_001007189	269.98	228.05	-1.18	-0.77	-41.93		228.05	373.02	1.64	1.05	144.97	*
7985555	LOC727963	ENST00000379369	36.96	46.79	1.27	0.79	9.83		46.79	17.96	-2.6	-1.24	-28.83	*
8129804	MAP3K5	NM_005923	60.3	86.6	1.44	1.08	26.29		86.6	143.6	1.66	1.29	57.01	*
8060813	MCM8	NM_032485	134.44	198.65	1.48	0.72	64.21		198.65	118.18	-1.68	-0.81	-80.47	*
7986411	MEF2A	NM_005587	419.57	418.4	-1	-0.76	-1.17		418.4	277.98	-1.51	-1.03	-140.42	*
8129573	MOXD1	NM_015529	306.48	210.12	-1.46	-0.66	-96.36		210.12	332.46	1.58	0.64	122.34	*
8142814	OPN1SW	NM_001708	57.45	55.04	-1.04	-0.67	-2.4		55.04	100.06	1.82	1.17	45.01	*
8173933	PCDH19	NM_001105243	30.91	38.98	1.26	0.87	8.07		38.98	73.9	1.9	0.78	34.92	*
7950391	PGM2L1	NM_173582	315.74	329.58	1.04	0.67	13.84		329.58	199.8	-1.65	-0.98	-129.78	*
8037374	PLAUR	NM_002659	254.47	246.02	-1.03	-0.68	-8.45		246.02	387.43	1.57	0.79	141.42	*
8101284	PRKG2	NM_006259	42.46	60.57	1.43	0.42	18.11		60.57	100.88	1.67	0.58	40.31	*
7903457	PRMT6	NM_018137	96.24	114	1.18	0.93	17.77		114	186.54	1.64	1.23	72.54	*
8161865	PRUNE2	NM_015225	303.02	277.08	-1.09	-0.66	-25.94		277.08	421.06	1.52	0.93	143.98	*
7935990	PSD	NM_002779	86.88	81.12	-1.07	-0.78	-5.76		81.12	53.36	-1.52	-1.04	-27.76	*
8037283	PSG4	NM_002780	141.92	154.02	1.09	0	12.09		154.02	254.59	1.65	0	100.58	*
8037272	PSG5	NM_002781	91.9	120.26	1.31	0	28.37		120.26	199.96	1.66	0	79.7	*
8037251	PSG7	NM_002783	167.07	169.7	1.02	0	2.63		169.7	267.04	1.57	0	97.33	*
8037290	PSG9	NM_002784	79.17	75.79	-1.04	-0.17	-3.38		75.79	134.22	1.77	0	58.43	*
8159521	PTGDS	NM_000954	203.99	147.17	-1.39	-0.59	-56.82		147.17	91.52	-1.61	-0.67	-55.65	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8085665	RFTN1	NM_015150	161.58	188.33	1.17	0.65	26.75		188.33	346.3	1.84	1.24	157.97	*
7906919	RGS4	NM_001102445	847.96	627.1	-1.35	-0.68	-220.86		627.1	977.72	1.56	0.73	350.62	*
8110499	RUFY1	NM_025158	543.56	443.18	-1.23	-0.96	-100.38		443.18	240.59	-1.84	-1.48	-202.59	*
8118890	SCUBE3	NM_152753	203.06	245.56	1.21	0.65	42.5		245.56	532.4	2.17	0.57	286.84	*
7899043	SEPN1	NM_020451	108.83	81.51	-1.34	-1.08	-27.31		81.51	167.05	2.05	1.79	85.54	*
7918622	SLC16A1	NM_003051	182.56	190.32	1.04	0.65	7.76		190.32	328.97	1.73	1.17	138.65	*
8157264	SLC31A2	NM_001860	281.95	235.74	-1.2	-0.75	-46.21		235.74	154.75	-1.52	-1.1	-80.99	*
8095585	SLC4A4	NM_001098484	139.12	180.28	1.3	0.82	41.16		180.28	271.69	1.51	1.09	91.42	*
8060997	SPTLC3	NM_018327	126.46	95.14	-1.33	-0.52	-31.31		95.14	149.95	1.58	0.13	54.81	*
8106597	SPZ1	NM_032567	26.26	21.66	-1.21	-0.78	-4.61		21.66	109.82	5.07	0	88.16	*
8113358	ST8SIA4	NM_005668	70.03	50.42	-1.39	-0.52	-19.62		50.42	118.56	2.35	1.04	68.14	*
7964119	STAT2	NM_005419	139.45	140.59	1.01	0.8	1.13		140.59	243.61	1.73	1.43	103.03	*
8000590	SULT1A1	NM_177534	98.41	114.83	1.17	0.25	16.42		114.83	75.59	-1.52	-0.34	-39.23	*
7938544	TEAD1	NM_021961	402.42	448.13	1.11	0.8	45.71		448.13	865.91	1.93	1.53	417.78	*
8057599	TFPI	NM_006287	207.94	188.47	-1.1	-0.68	-19.47		188.47	292.67	1.55	1.16	104.2	*
7920664	THBS3	NM_007112	129.45	87.52	-1.48	-0.91	-41.93		87.52	134.64	1.54	0.91	47.12	*
7993588	TMC7	NM_024847	82.37	70.9	-1.16	-0.62	-11.47		70.9	168.69	2.38	1.16	97.79	*
7970301	TMCO3	NM_017905	177.92	199.73	1.12	0.76	21.81		199.73	386.75	1.94	1.56	187.02	*
8045688	TNFAIP6	NM_007115	237.93	253.98	1.07	0.36	16.05		253.98	165.37	-1.54	-0.45	-88.61	*
8102594	TNIP3	NM_024873	47	57.23	1.22	0.68	10.23		57.23	86.4	1.51	0.92	29.17	*
8019842	TYMS	NM_001071	234.83	163.45	-1.44	-0.65	-71.38		163.45	300.76	1.84	0.46	137.31	*
8100328	USP46	NM_022832	221.68	280.01	1.26	1.13	58.32		280.01	130.29	-2.15	-1.56	-149.71	*
8041467	VIT	NM_053276	160.48	197.37	1.23	0.54	36.89		197.37	104.68	-1.89	-0.83	-92.69	*
8004184	XAF1	NM_017523	89.71	106.78	1.19	1	17.06		106.78	57.65	-1.85	-1.38	-49.13	*
8153935	ZNF252	NR_023392	57.72	79.67	1.38	1.06	21.95		79.67	119.82	1.5	1.19	40.15	*
8167201	ZNF81	NM_007137	73.53	71.55	-1.03	-0.74	-1.98		71.55	112.76	1.58	0.87	41.21	*

Appendix 2.2 Differentially Expressed Genes in OSX Null hMSCs from Donors A and C

BMP6 Responsive Genes Differentially Expressed in OSX Null hMSCs from Donors A & C

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8145361	NEFM	NM_005382	112.06	1680.27	14.99	11.88	1568.21	*	1680.27	174.29	-9.64	-7.75	-1505.98	*
7963664	SP7	NM_152860	26.47	502.68	18.99	6.75	476.21	*	502.68	62.19	-8.08	-3.25	-440.49	*
7948322	OR5B17	NM_001005489	109.48	458.99	4.19	0	349.51	*	458.99	57.16	-8.03	0	-401.83	*
7898693	ALPL	NM_000478	44.95	337.84	7.52	0	292.89	*	337.84	47.66	-7.09	0	-290.18	*
8104901	IL7R	NM_002185	22.73	330.33	14.53	10.87	307.59	*	330.33	52.67	-6.27	-4.84	-277.66	*
8162388	OMD	NM_005014	21.92	786.15	35.86	27.3	764.23	*	786.15	125.36	-6.27	-3.54	-660.79	*
8105495	PART1	AF163475	31.02	116.97	3.77	1.92	85.95	*	116.97	23.7	-4.94	-2.51	-93.27	*
8175256	MGC16121	BC007360	82.23	345.15	4.2	1.05	262.91	*	345.15	72.38	-4.77	-1.19	-272.77	*
8162394	ASPN	NM_017680	64.05	543.64	8.49	3.2	479.59	*	543.64	133.53	-4.07	-1.4	-410.11	*
7972239	SLITRK6	NM_032229	24.32	170.93	7.03	4.65	146.61	*	170.93	50.31	-3.4	-1.75	-120.62	*
8045336	GPR39	NM_001508	121.4	780.78	6.43	3.99	659.38	*	780.78	265.48	-2.94	-2.08	-515.3	*
8088560	ADAMTS9	NM_182920	29.43	278.34	9.46	5.77	248.91	*	278.34	97.72	-2.85	-1.74	-180.61	*
7974341	GNG2	NM_053064	54.74	560.35	10.24	5.7	505.61	*	560.35	207.43	-2.7	-1.87	-352.92	*
8162908	GRIN3A	NM_133445	32.96	89.18	2.71	1.73	56.22	*	89.18	33.05	-2.7	-1.74	-56.13	*
8046906	GULP1	NM_016315	62.41	334.16	5.35	3.05	271.74	*	334.16	126.36	-2.64	-1.44	-207.8	*
8016841	TMEM100	NM_001099640	21.44	145.26	6.78	3.83	123.82	*	145.26	55.11	-2.64	-1.75	-90.15	*
8055314	LYPD1	NM_144586	110.89	382.63	3.45	2.21	271.74	*	382.63	146.34	-2.61	-2	-236.29	*
7989937	LCTL	NM_207338	80.69	173.29	2.15	0.81	92.6	*	173.29	67.35	-2.57	-1.05	-105.94	*
7957417	TMTC2	NM_152588	53.26	286.46	5.38	3.41	233.2	*	286.46	114.23	-2.51	-1.33	-172.23	*
8162373	OGN	NM_033014	19.34	90.92	4.7	3.45	71.58	*	90.92	36.57	-2.49	-1.96	-54.35	*
8059854	ARL4C	NM_005737	369.46	568.24	1.54	1.08	198.78	*	568.24	236.71	-2.4	-1.73	-331.53	*
8057506	FRZB	NM_001463	20.02	843.66	42.13	29.51	823.63	*	843.66	351.7	-2.4	-1.61	-491.96	*
7964687	C12orf56	NM_001099676	18.02	79.13	4.39	3.44	61.12	*	79.13	33.75	-2.34	-1.59	-45.38	*
8023401	CCDC68	NM_025214	53.82	576.8	10.72	5.57	522.99	*	576.8	250.72	-2.3	-1.11	-326.09	*
8081758	GRAMD1C	NM_017577	25.54	68.15	2.67	1.61	42.61	*	68.15	30.56	-2.23	-1.46	-37.59	*
8077366	LRRN1	NM_020873	118.7	249.38	2.1	1.02	130.68	*	249.38	115.97	-2.15	-0.88	-133.41	*
8140668	SEMA3A	NM_006080	108.79	208	1.91	1.5	99.22	*	208	97.64	-2.13	-1.64	-110.36	*
8021376	NEDD4L	NM_015277	98.74	193.33	1.96	1.16	94.59	*	193.33	91.78	-2.11	-1.25	-101.54	*
7940775	RARRES3	NM_004585	256.15	133.61	-1.92	-1.14	-122.54	*	133.61	63.77	-2.1	-0.59	-69.85	*
8092621	CRYGS	NM_017541	66.09	671.65	10.16	6.3	605.56	*	671.65	326.83	-2.06	-1.14	-344.82	*
8122045	AKAP7	NM_016377	56.47	171.8	3.04	2.13	115.32	*	171.8	84.27	-2.04	-1.26	-87.53	*
7986068	BLM	NM_000057	50.33	114.12	2.27	0.7	63.78	*	114.12	56.16	-2.03	-0.61	-57.96	*
8016609	DLX3	NM_005220	27.74	207.19	7.47	2.15	179.45	*	207.19	105.96	-1.96	-0.58	-101.24	*
7961182	KLRC2	NM_002260	16.24	153.48	9.45	0	137.24	*	153.48	79.08	-1.94	0	-74.4	*
8077270	CHL1	NM_006614	22.99	94.19	4.1	0.95	71.2	*	94.19	49.46	-1.9	-0.43	-44.72	*
8056323	FIGN	NM_018086	85.93	160.53	1.87	0.99	74.6	*	160.53	84.82	-1.89	-1.1	-75.72	*
8083233	ZIC1	NM_003412	83.54	143.1	1.71	0	59.56	*	143.1	76.17	-1.88	0	-66.93	*
7933772	ANK3	NM_020987	69.76	230.07	3.3	2.92	160.31	*	230.07	123.23	-1.87	-1.64	-106.84	*
7987385	MEIS2	NM_172316	225.28	440.55	1.96	1.09	215.26	*	440.55	236.04	-1.87	-1.11	-204.51	*
8099746	CCKAR	NM_000730	21.65	406.31	18.77	8.38	384.67	*	406.31	218.3	-1.86	-0.78	-188.01	*
8155707	TJP2	NM_004817	124.42	323.65	2.6	1.25	199.23	*	323.65	173.67	-1.86	-0.97	-149.97	*
8011214	RTN4RL1	NM_178568	37.99	91.13	2.4	0.98	53.14	*	91.13	50.15	-1.82	-0.67	-40.98	*
8061471	GINS1	NM_021067	78.04	125.15	1.6	0.73	47.11	*	125.15	70.07	-1.79	-0.77	-55.07	*
8061013	ISM1	NM_080826	26.02	68.74	2.64	1.12	42.72	*	68.74	38.59	-1.78	-0.73	-30.15	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8060813	MCM8	NM_032485	147.41	233.55	1.58	0.62	86.14	*	233.55	131.42	-1.78	-0.68	-102.12	*
8036710	GMFG	NM_004877	88.27	147.5	1.67	0.95	59.23	*	147.5	83.34	-1.77	-0.91	-64.15	*
8056491	SCN9A	NM_002977	66.04	134.17	2.03	0.51	68.12	*	134.17	75.95	-1.77	-0.47	-58.22	*
7926875	BAMBI	NM_012342	350.51	1663.93	4.75	3.13	1313.42	*	1663.93	949.92	-1.75	-1.45	-714.01	*
8046695	ITGA4	NM_000885	193.44	488.18	2.52	2.31	294.74	*	488.18	279.52	-1.75	-1.65	-208.66	*
7917954	FRRS1	NM_001013660	155.9	303.18	1.94	1.61	147.28	*	303.18	175.7	-1.73	-1.55	-127.49	*
7985786	ACAN	NM_013227	34.26	301.23	8.79	0	266.97	*	301.23	176.26	-1.71	0	-124.97	*
8096116	AGPAT9	NM_032717	96.31	167.45	1.74	0.66	71.14	*	167.45	98.17	-1.71	-0.61	-69.29	*
8149071	ANGPT2	NM_001147	40.75	158.25	3.88	1.15	117.51	*	158.25	92.37	-1.71	-0.44	-65.89	*
8088866	CNTN3	NM_020872	50.46	117.73	2.33	0	67.28	*	117.73	68.69	-1.71	0	-49.05	*
7957551	SOCS2	NM_003877	48.14	281.04	5.84	3.14	232.9	*	281.04	165.06	-1.7	-0.79	-115.98	*
7980485	DIO2	NM_013989	10.55	839.13	79.54	34.85	828.58	*	839.13	502.49	-1.67	-0.89	-336.64	*
7903227	PALMD	NM_017734	113.97	445	3.9	1.02	331.03	*	445	267.23	-1.67	-0.43	-177.77	*
8170364	AFF2	NM_002025	97.34	327.15	3.36	1.46	229.81	*	327.15	196.55	-1.66	-0.89	-130.6	*
8157324	RGS3	NM_144488	72.22	132.7	1.84	0.92	60.48	*	132.7	80.58	-1.65	-0.79	-52.13	*
8119974	SLC29A1	NM_001078175	356.12	148.04	-2.41	0	-208.08	*	148.04	89.64	-1.65	-0.62	-58.4	*
7942332	FOLR1	NM_016730	55.35	87.54	1.58	0.72	32.18	*	87.54	53.36	-1.64	-0.75	-34.18	*
7930980	PPAPDC1A	NM_001030059	235.32	474.12	2.01	1.53	238.8	*	474.12	291.43	-1.63	-1.12	-182.68	*
8079198	ZNF660	NM_173658	56.32	153.97	2.73	1.28	97.66	*	153.97	94.51	-1.63	-0.73	-59.46	*
8162404	ECM2	NM_001393	135.53	257.1	1.9	0.97	121.57	*	257.1	158.28	-1.62	-0.81	-98.82	*
8141463	GPC2	NM_152742	39.96	87.72	2.2	0.95	47.76	*	87.72	54.24	-1.62	-0.62	-33.49	*
8156341	CENPP	NM_001012267	84.57	203.38	2.4	2.05	118.81	*	203.38	126.7	-1.61	-1.32	-76.68	*
7981427	CKB	NM_001823	84.02	196.11	2.33	0.76	112.09	*	196.11	121.54	-1.61	-0.5	-74.57	*
8143341	JHDM1D	NM_030647	75.87	127.61	1.68	1.04	51.74	*	127.61	79.04	-1.61	-1.07	-48.58	*
7929932	KAZALD1	NM_030929	106.19	449.93	4.24	2.96	343.74	*	449.93	278.94	-1.61	-1.35	-170.99	*
7950810	SYTL2	NM_206927	77.7	128.15	1.65	0.89	50.46	*	128.15	79.76	-1.61	-0.82	-48.39	*
7952036	MPZL3	NM_198275	100.58	190.68	1.9	1.43	90.1	*	190.68	118.94	-1.6	-1.33	-71.74	*
8141140	DLX5	NM_005221	172.15	1021.05	5.93	3.95	848.9	*	1021.05	640.5	-1.59	-1.08	-380.55	*
8150962	TOX	NM_014729	102.55	187.17	1.83	1.35	84.62	*	187.17	118.7	-1.58	-1.29	-68.47	*
7907160	ATP1B1	NM_001677	748.22	2086.66	2.79	2.11	1338.44	*	2086.66	1326.05	-1.57	-1.49	-760.61	*
8097841	TRIM2	NM_015271	84.26	260.08	3.09	2.57	175.82	*	260.08	165.55	-1.57	-1.34	-94.53	*
7917370	COL24A1	NM_152890	46.84	75.9	1.62	0.73	29.06	*	75.9	48.62	-1.56	-0.7	-27.28	*
8072735	APOL1	NM_145343	268.51	151.94	-1.77	-1.17	-116.57	*	151.94	97.94	-1.55	-0.67	-54	*
7917322	SYDE2	NM_032184	68.89	167.26	2.43	1.66	98.37	*	167.26	107.76	-1.55	-1.01	-59.5	*
7927631	DKK1	NM_012242	132.88	1433.13	10.78	3.32	1300.25	*	1433.13	928.68	-1.54	-0.46	-504.45	*
7977933	SLC7A8	NM_012244	236.91	403.62	1.7	0.69	166.7	*	403.62	262.43	-1.54	-0.6	-141.19	*
7903334	CDC14A	NM_003672	81.94	149.88	1.83	0.9	67.94	*	149.88	97.87	-1.53	-0.74	-52.01	*
8007799	CRHR1	AK295559	67.27	105.71	1.57	0.2	38.44	*	105.71	68.94	-1.53	-0.2	-36.77	*
8151457	HEY1	NM_012258	28.97	905.96	31.27	14.28	876.99	*	905.96	593.94	-1.53	-0.87	-312.02	*
8064978	JAG1	NM_000214	175.96	510.58	2.9	2.31	334.62	*	510.58	333.99	-1.53	-1	-176.59	*
7954293	PDE3A	NM_000921	54.66	177.19	3.24	2.49	122.53	*	177.19	115.44	-1.53	-1.2	-61.75	*
8177222	CD24	NM_013230	9.73	142.05	14.6	4.3	132.32	*	142.05	93.51	-1.52	-0.4	-48.54	*
7902541	IFI44L	NM_006820	87.25	174.19	2	0	86.94	*	174.19	114.27	-1.52	0	-59.92	*
8108697	PCDHB5	NM_015669	199.66	329.7	1.65	0.17	130.04	*	329.7	219.45	-1.5	-0.15	-110.25	*
7975390	SMOC1	NM_001034852	86.72	146.5	1.69	1.28	59.78	*	146.5	221.15	1.51	1.25	74.65	*
8095723	EPGN	NM_001013442	214.08	356.88	1.67	0	142.8	*	356.88	542.67	1.52	0	185.78	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8170119	FHL1	NM_001449	177.34	117.45	-1.51	-0.41	-59.89	*	117.45	181.15	1.54	0.63	63.7	*
8133818	PHTF2	NM_001127358	39.08	80.65	2.06	1.09	41.57	*	80.65	125.05	1.55	0.82	44.4	*
8153935	ZNF252	NR_023392	53.41	82.89	1.55	1.06	29.49	*	82.89	129.08	1.56	1.18	46.19	*
7953291	CD9	NM_001769	451	265.89	-1.7	-1.25	-185.11	*	265.89	417.5	1.57	1.36	151.61	*
7923547	CHI3L1	NM_001276	1833.36	427.67	-4.29	0	-1405.69	*	427.67	672.18	1.57	0	244.51	*
8085774	ZNF385D	NM_024697	199.09	68.1	-2.92	-0.21	-130.99	*	68.1	106.89	1.57	0	38.79	*
8091411	TM4SF1	NM_014220	888.38	380.45	-2.34	-1.61	-507.93	*	380.45	603.48	1.59	0.59	223.03	*
8046488	CDCA7	NM_031942	87.11	48.74	-1.79	-1.47	-38.37	*	48.74	78.27	1.61	1.01	29.52	*
7985317	KIAA1199	NM_018689	877.48	138.7	-6.33	-0.83	-738.77	*	138.7	224.77	1.62	1.35	86.06	*
7981514	AHNAK2	NM_138420	375.14	121.3	-3.09	-1.25	-253.84	*	121.3	197.35	1.63	0.39	76.06	*
7951077	SESN3	NM_144665	132.93	351.88	2.65	0.9	218.95	*	351.88	573.59	1.63	0.61	221.71	*
7983512	SQRDL	NM_021199	625.58	185.39	-3.37	-2.34	-440.19	*	185.39	306.21	1.65	0.9	120.82	*
8015349	KRT19	NM_002276	180.51	48.77	-3.7	0	-131.73	*	48.77	80.85	1.66	0.95	32.07	*
8088979	VGLL3	NM_016206	370.66	179.09	-2.07	-1.27	-191.57	*	179.09	297.47	1.66	1.23	118.38	*
7932796	SVIL	NM_021738	378.65	182.93	-2.07	-1.79	-195.72	*	182.93	306.19	1.67	1.24	123.26	*
7920165	FLG	NM_002016	189.22	60.93	-3.11	0	-128.29	*	60.93	103.73	1.7	0.34	42.81	*
7954065	GPRC5A	NM_003979	97.75	63.37	-1.54	0	-34.38	*	63.37	108.21	1.71	0	44.84	*
8124848	IER3	NM_003897	176.51	100.81	-1.75	-1.17	-75.7	*	100.81	171.93	1.71	0.06	71.11	*
8179704	IER3	NM_003897	176.51	100.81	-1.75	-1.17	-75.7	*	100.81	171.93	1.71	0.06	71.11	*
8178435	IER3	NM_003897	190.77	108.72	-1.75	-1.15	-82.04	*	108.72	188.86	1.74	0.03	80.13	*
7989501	CA12	NM_001218	348.94	191.53	-1.82	-0.58	-157.41	*	191.53	334.33	1.75	0.29	142.81	*
8113800	FBN2	NM_001999	50.32	90.83	1.8	0.85	40.5	*	90.83	158.5	1.75	0.83	67.67	*
8105040	OSMR	NM_003999	270.22	159.63	-1.69	-1.4	-110.59	*	159.63	280.51	1.76	1.31	120.87	*
8179519	HLA-DPB1	NM_002121	78.59	49.12	-1.6	-0.87	-29.46	*	49.12	87.18	1.77	1.04	38.05	*
7962689	VDR	NM_001017535	85.55	36.59	-2.34	-1.38	-48.95	*	36.59	64.97	1.78	1.12	28.38	*
8152617	HAS2	NM_005328	1121.76	362.25	-3.1	-1.32	-759.51	*	362.25	647.06	1.79	0.37	284.81	*
8169389	PAK3	NM_002578	69.82	33.99	-2.05	-0.95	-35.83	*	33.99	60.89	1.79	0.95	26.9	*
8001197	NETO2	NM_018092	234.75	140.59	-1.67	-1.05	-94.15	*	140.59	257.27	1.83	0.43	116.67	*
8138542	IL6 // LOC541472	ENST00000325042	175.43	38.03	-4.61	-0.57	-137.4	*	38.03	69.84	1.84	0.18	31.8	*
7902452	AK5	NM_174858	357.12	186.47	-1.92	-1.12	-170.66	*	186.47	346.16	1.86	0	159.69	*
8122222	PDE7B	NM_018945	217.06	132.66	-1.64	-1.16	-84.4	*	132.66	247.3	1.86	0.64	114.64	*
8135594	CAV1	NM_001753	1208.22	525.64	-2.3	-1.39	-682.58	*	525.64	984.44	1.87	0.18	458.8	*
8131803	IL6	NM_000600	684.06	177.01	-3.86	-1.43	-507.05	*	177.01	331.74	1.87	0.59	154.73	*
7984771	LOXL1	NM_005576	190.45	108.74	-1.75	-0.95	-81.71	*	108.74	203.77	1.87	1.17	95.03	*
7963024	LMBR1L	NM_018113	41.51	105.84	2.55	1.46	64.33	*	105.84	200.45	1.89	1.37	94.61	*
7933469	ARHGAP22	NM_021226	469.84	107.55	-4.37	-3.51	-362.28	*	107.55	205.77	1.91	1.63	98.22	*
8056222	DPP4	NM_001935	777.63	169.28	-4.59	-3.52	-608.35	*	169.28	324.52	1.92	0.59	155.24	*
7972713	EFNB2	NM_004093	67.51	40.79	-1.66	-1.12	-26.72	*	40.79	78.35	1.92	1.19	37.56	*
8086517	CDCP1	NM_022842	389.22	95.11	-4.09	-1.11	-294.11	*	95.11	184.87	1.94	0	89.76	*
7906919	RGS4	NM_001102445	747.01	462.95	-1.61	-0.42	-284.06	*	462.95	899.85	1.94	0.3	436.91	*
8054344	FLJ42986	AK298610	103.57	47.82	-2.17	-1.37	-55.75	*	47.82	93.65	1.96	0.7	45.83	*
7982366	SCG5	NM_003020	135.76	66.62	-2.04	-0.76	-69.14	*	66.62	131.21	1.97	1.3	64.59	*
7944722	UBASH3B	NM_032873	194.23	123.43	-1.57	-0.98	-70.8	*	123.43	243.14	1.97	1.21	119.71	*
8111552	C5orf33	NM_001085411	582.78	313.51	-1.86	-1.35	-269.28	*	313.51	627.85	2	1.44	314.35	*
7925413	MT1P2	AF333388	115.49	70.07	-1.65	-1.22	-45.42	*	70.07	143.54	2.05	1.62	73.46	*
7913237	CAMK2N1	NM_018584	359.33	117.01	-3.07	-1.28	-242.32	*	117.01	246.21	2.1	0.74	129.19	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8021081	SLC14A1	NM_001128588	630.39	267.87	-2.35	-0.71	-362.53	*	267.87	563.11	2.1	0	295.24	*
8014066	EVI2A	NM_001003927	123.04	43.8	-2.81	-0.55	-79.24	*	43.8	96.94	2.21	0	53.14	*
7945245	HNT	NM_016522	241.06	96.82	-2.49	-2.18	-144.25	*	96.82	222.26	2.3	0.98	125.44	*
7965335	DUSP6	NM_001946	132.89	50.55	-2.63	-2.04	-82.34	*	50.55	116.78	2.31	1.29	66.23	*
8095376	MT2A // MT2A	BT007315	574.34	345.85	-1.66	-1.12	-228.49	*	345.85	799	2.31	1.69	453.16	*
8152512	TNFRSF11B	NM_002546	653.06	81.2	-8.04	-0.9	-571.86	*	81.2	187.24	2.31	1.22	106.04	*
8095362	MT2A // MT2A	BT007315	676.93	389.21	-1.74	-1.17	-287.72	*	389.21	934.32	2.4	1.72	545.11	*
7903358	VCAM1	NM_001078	593.55	204.6	-2.9	-1.89	-388.96	*	204.6	509.64	2.49	1.89	305.04	*
8006433	CCL2	NM_002982	976.63	124.33	-7.86	-5.39	-852.31	*	124.33	320.99	2.58	1.88	196.66	*
8009502	KCNJ2	NM_000891	108.64	33.34	-3.26	-2.15	-75.3	*	33.34	88.49	2.65	0.52	55.15	*
8111569	RANBP3L	NM_145000	296.67	36.48	-8.13	-0.97	-260.19	*	36.48	98.69	2.71	0	62.21	*
7902527	PTGFR	NM_001039585	218.29	64.1	-3.41	0	-154.19	*	64.1	181.01	2.82	0	116.91	*
7918657	PTPN22	NM_015967	64.29	20	-3.21	-1.42	-44.29	*	20	57.18	2.86	0.41	37.18	*
8083690	IL12A	NM_000882	39.56	73.61	1.86	0	34.05	*	73.61	213.25	2.9	0	139.64	*
8066214	TGM2	NM_004613	365.99	63.32	-5.78	-0.39	-302.67	*	63.32	191.69	3.03	0	128.37	*
7908543	NEK7	NM_133494	362.64	171.2	-2.12	-0.5	-191.44	*	171.2	576.39	3.37	1.53	405.19	*
8104930	SLC1A3	NM_004172	228.25	41.6	-5.49	-0.35	-186.65	*	41.6	146.28	3.52	0	104.68	*

BMP6 Responsive Genes Differentially Expressed in hMSCs from Donors A & C

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7987315	ACTC1	NM_005159	50.15	1622.07	32.34	10.68	1571.92	*	1622.07	1156.87	-1.4	-0.55	-465.2	
8095110	KIT	NM_000222	8.06	167.15	20.73	10.03	159.08	*	167.15	180.33	1.08	0.8	13.18	
8008627	NOG	NM_005450	50.27	726.3	14.45	7.75	676.03	*	726.3	598.61	-1.21	-0.77	-127.7	
8152314	RSPO2	NM_178565	19.59	180.03	9.19	0	160.44	*	180.03	123.82	-1.45	0	-56.21	
7965873	IGF1	NM_001111283	40.09	306.7	7.65	1.94	266.61	*	306.7	267.45	-1.15	-0.3	-39.24	
8056784	DLX2	NM_004405	80.96	609.34	7.53	3.68	528.38	*	609.34	529.59	-1.15	-0.68	-79.75	
7939024	ANO3	NM_031418	18.62	139.1	7.47	4.89	120.48	*	139.1	191.36	1.38	0.53	52.25	
7925452	GREM2	NM_022469	78.4	504.07	6.43	4.55	425.67	*	504.07	379.44	-1.33	-1.07	-124.63	
7962000	PTHLH	NM_198965	37.72	234.83	6.23	0	197.1	*	234.83	191.85	-1.22	0	-42.98	
8040103	ID2	NM_002166	68.92	415.92	6.04	3.13	347	*	415.92	477.45	1.15	0.82	61.54	
8047062	MGC13057	NM_001042519	49.7	281.14	5.66	3.14	231.45	*	281.14	197.08	-1.43	-0.82	-84.06	
8097857	MND1	NM_032117	66.25	348.95	5.27	3.73	282.71	*	348.95	268.2	-1.3	-0.85	-80.75	
7980233	PGF	NM_002632	48.01	231.61	4.82	2.48	183.6	*	231.61	155.13	-1.49	-0.8	-76.48	
7933750	SLC16A9	NM_194298	21.37	97.36	4.56	1.63	75.99	*	97.36	101.2	1.04	0.59	3.84	
8142981	PODXL	NM_001018111	40.84	181.84	4.45	1.74	141	*	181.84	132.98	-1.37	-0.5	-48.86	
7999909	GPRC5B	NM_016235	81.46	360.15	4.42	1.72	278.69	*	360.15	358.74	-1	-0.45	-1.4	
7913655	ID3	NM_002167	36.44	160.22	4.4	2.97	123.79	*	160.22	210.14	1.31	0.91	49.92	
8145293	ADAM28	NM_014265	45.52	198.25	4.35	0	152.72	*	198.25	184.49	-1.07	0	-13.75	
8061564	ID1	NM_181353	34.67	150.55	4.34	2.71	115.89	*	150.55	152.19	1.01	0.87	1.64	
7962579	AMIGO2	NM_181847	93.39	392.76	4.21	0.1	299.37	*	392.76	396.69	1.01	0.14	3.93	
8121850	HEY2	NM_012259	33.96	137.96	4.06	2.56	104	*	137.96	95.51	-1.44	-1.03	-42.45	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8102587	C4orf31	NM_024574	133.6	535.98	4.01	1.93	402.38	*	535.98	376.06	-1.43	-0.73	-159.92	
7975760	EIF2B2	NM_014239	110.51	420.73	3.81	2.72	310.22	*	420.73	285.96	-1.47	-1.02	-134.78	
7909494	SYT14	NM_153262	65.51	248.47	3.79	0	182.97	*	248.47	177.96	-1.4	0	-70.51	
7928046	TSPAN15	NM_012339	54.07	201.13	3.72	1.48	147.06	*	201.13	135.02	-1.49	-0.57	-66.11	
7961151	KLRK1	NM_007360	20.86	77.2	3.7	0	56.34	*	77.2	68.1	-1.13	0	-9.1	
8095043	RASL11B	NM_023940	19.59	69.73	3.56	0.4	50.14	*	69.73	55.21	-1.26	-0.14	-14.52	
7983527	SEMA6D	NM_153618	55.41	196.99	3.56	2.36	141.58	*	196.99	144.06	-1.37	-1.14	-52.92	
7991034	HOMER2	NM_199330	87.11	309.17	3.55	2.76	222.06	*	309.17	241.98	-1.28	-1.12	-67.19	
8097692	EDNRA	NM_001957	172.53	603.31	3.5	1.68	430.78	*	603.31	417.77	-1.44	-0.89	-185.54	
7905329	MLLT11	NM_006818	310.49	1053.29	3.39	2.29	742.79	*	1053.29	804.04	-1.31	-0.92	-249.25	
7981958	SNRPN // SNORD116-5	NR_003320	61.68	205.83	3.34	2.61	144.15	*	205.83	180.61	-1.14	-0.93	-25.22	
7981962	SNRPN // SNORD116-5	NR_003320	61.68	205.83	3.34	2.61	144.15	*	205.83	180.61	-1.14	-0.93	-25.22	
8100699	SYT14L	NM_001014372	18.64	58.72	3.15	0	40.07	*	58.72	47.94	-1.22	0	-10.78	
8047248	PLCL1	NM_001114661	63.37	196.57	3.1	1.34	133.2	*	196.57	180.5	-1.09	-0.51	-16.07	
7921882	OLFML2B	NM_015441	204.68	627.72	3.07	1.97	423.04	*	627.72	461.87	-1.36	-1.11	-165.85	
7958352	BTBD11	NM_001018072	39.52	120.78	3.06	2.26	81.26	*	120.78	83.37	-1.45	-1.28	-37.42	
8088480	ID2	NM_002166	59.62	182.39	3.06	1.72	122.77	*	182.39	176.22	-1.04	-0.8	-6.17	
7902398	SNORD45A	NR_002749	21.83	66.1	3.03	2.35	44.26	*	66.1	42.16	-1.57	-1.32	-23.94	
8094476	TBC1D19	NM_018317	186.01	563.18	3.03	1.95	377.17	*	563.18	497.87	-1.13	-0.72	-65.31	
7930299	C10orf78	NM_145247	22.9	68.89	3.01	2.25	45.99	*	68.89	60.83	-1.13	-0.96	-8.06	
8063382	SNAI1	NM_005985	102.8	308.34	3	2.25	205.54	*	308.34	255.38	-1.21	-0.88	-52.97	
8117120	ID4	NM_001546	208.39	604.83	2.9	1.62	396.44	*	604.83	715.23	1.18	0.88	110.39	
8041940	STON1-GTF2A1L	NM_172311	73.43	210.83	2.87	1.51	137.39	*	210.83	173.47	-1.22	-0.72	-37.36	
7981949	SNRPN // SNORD116-1	NR_003316	59.68	169.71	2.84	2.29	110.03	*	169.71	133.19	-1.27	-1.02	-36.52	
8056343	COBLL1	NM_014900	66.1	186.84	2.83	0.57	120.74	*	186.84	133.8	-1.4	-0.28	-53.04	
8112615	ENC1	NM_003633	79.03	222.56	2.82	1.91	143.53	*	222.56	173.84	-1.28	-0.96	-48.73	
8171248	KAL1	NM_000216	133.95	370.72	2.77	0	236.77	*	370.72	387.42	1.05	0.25	16.7	
8021301	RAB27B	NM_004163	250.4	692.84	2.77	1.38	442.44	*	692.84	489.77	-1.41	-0.68	-203.07	
8107850	CHSY3	NM_175856	157.04	422.13	2.69	1.84	265.09	*	422.13	291.55	-1.45	-1.24	-130.58	
8030212	LIN7B	NM_022165	212.27	568.55	2.68	2.24	356.29	*	568.55	495.36	-1.15	-0.99	-73.19	
8122634	SAMD5	NM_001030060	29.01	77.07	2.66	1.74	48.06	*	77.07	65.82	-1.17	-0.69	-11.25	
8147030	STMN2	NM_007029	28.79	76.21	2.65	1.83	47.42	*	76.21	97.31	1.28	1.06	21.1	
8078386	GPD1L	NM_015141	27.95	73.43	2.63	1.41	45.47	*	73.43	83.87	1.14	0.36	10.44	
8164200	ANGPTL2	NM_012098	225.23	588.75	2.61	1.3	363.52	*	588.75	621.46	1.06	0.45	32.7	
8086752	SNORD13	NR_003041	233.92	607.58	2.6	1.01	373.66	*	607.58	524.44	-1.16	-0.53	-83.14	
8160712	SUGT1P	NR_003667	22.96	59.22	2.58	1.73	36.26	*	59.22	53.14	-1.11	-0.77	-6.09	
8111443	C1QTNF3	NM_181435	34.41	88.04	2.56	0	53.63	*	88.04	98.31	1.12	0	10.27	
7943051	NAALAD2	NM_005467	18.88	48.24	2.56	1.86	29.36	*	48.24	44.94	-1.07	-0.78	-3.3	
8081657	CD200	NM_001004196	34.33	87.49	2.55	0.49	53.15	*	87.49	69.31	-1.26	-0.23	-18.18	
8100519	TXNDC9	BC024223	33.48	83.58	2.5	1.29	50.11	*	83.58	99.33	1.19	1.01	15.75	
8067140	CYP24A1	NM_000782	18.9	47.06	2.49	0.21	28.16	*	47.06	43.7	-1.08	-0.09	-3.36	
8129677	SGK1	NM_005627	153.82	383.11	2.49	1.14	229.29	*	383.11	275.37	-1.39	-0.62	-107.74	
7919591	FAM72A	ENST00000369175	19.63	48.03	2.45	0.64	28.4	*	48.03	38.96	-1.23	-0.32	-9.07	
8035517	COMP	NM_000095	143.11	349.56	2.44	0.36	206.45	*	349.56	355.24	1.02	0.06	5.68	
7952205	MCAM	NM_006500	88.56	215.08	2.43	1.22	126.52	*	215.08	211.32	-1.02	-0.54	-3.77	
8106393	F2R	NM_001992	97.64	235.88	2.42	1.39	138.24	*	235.88	174.72	-1.35	-0.73	-61.16	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8027323	ZNF257	NM_033468	21.55	52.21	2.42	1.29	30.66	*	52.21	32.76	-1.59	-1.02	-19.45	
7918857	TSPAN2	NM_005725	304.07	731.56	2.41	0	427.49	*	731.56	654.36	-1.12	0	-77.19	
7981953	SNRPN // SNORD116-3	NR_003318	170.36	407.07	2.39	1.38	236.71	*	407.07	346.29	-1.18	-0.79	-60.78	
7981966	SNRPN // SNORD116-3	NR_003318	170.36	407.07	2.39	1.38	236.71	*	407.07	346.29	-1.18	-0.79	-60.78	
8117045	RBM24	NM_153020	100.88	239.19	2.37	1.55	138.31	*	239.19	225.58	-1.06	-0.79	-13.61	
8133062	ZNF273	NM_021148	63.5	149.4	2.35	1.84	85.9	*	149.4	107.62	-1.39	-1.01	-41.79	
7965867	PMCH	NM_002674	31.42	73.48	2.34	1.24	42.06	*	73.48	49.74	-1.48	-1.04	-23.73	
7966690	TBX3	NM_016569	83.62	195.39	2.34	1.25	111.77	*	195.39	185.98	-1.05	-0.68	-9.41	
8133155	TPST1	NM_003596	283.79	664.1	2.34	1.99	380.31	*	664.1	600.9	-1.11	-1.01	-63.21	
8134339	PEG10	NM_015068	48.01	111.15	2.32	0.53	63.14	*	111.15	85.71	-1.3	-0.27	-25.43	
8069689	ADAMTS5	NM_007038	165.62	380.25	2.3	2.02	214.63	*	380.25	419.56	1.1	0.97	39.31	
8112731	F2RL2	NM_004101	44.96	103.48	2.3	0.92	58.52	*	103.48	91.85	-1.13	-0.49	-11.64	
7981964	SNRPN // SNORD116-8	NR_003323	167.28	385.14	2.3	1.29	217.86	*	385.14	326.72	-1.18	-0.77	-58.42	
8135378	PRKAR2B	NM_002736	31.46	72.18	2.29	1.49	40.73	*	72.18	78.34	1.09	0.32	6.16	
8151686	MMP16	NM_005941	150.99	342.75	2.27	1.59	191.76	*	342.75	303.18	-1.13	-0.8	-39.57	
8081081	EPHA3	NM_005233	174.07	393.66	2.26	1.14	219.59	*	393.66	388.13	-1.01	-0.86	-5.53	
7971015	SMAD9	NM_001127217	60.28	135.8	2.25	1.8	75.52	*	135.8	108.38	-1.25	-1.09	-27.42	
8018860	EPR1	NR_002219	61.02	136.57	2.24	0	75.56	*	136.57	160.14	1.17	0	23.56	
7997642	CRISPLD2	NM_031476	49.13	108.58	2.21	1.46	59.45	*	108.58	81.25	-1.34	-1.06	-27.34	
8139460	NACAD	AB002361	72.75	160.76	2.21	1.76	88	*	160.76	181.73	1.13	0.64	20.97	
8102643	CCNA2	NM_001237	55.59	122.48	2.2	1.58	66.89	*	122.48	135.76	1.11	0.99	13.28	
8104825	BXDC2	NM_018321	397.63	872.32	2.19	1.3	474.69	*	872.32	1278.58	1.47	0.97	406.25	
7916853	DIRAS3	NM_004675	50.48	110.32	2.19	0.48	59.83	*	110.32	85.3	-1.29	-0.31	-25.02	
8016463	HOXB6	NM_018952	74.38	163.02	2.19	0.99	88.64	*	163.02	158.97	-1.03	-0.42	-4.05	
8039484	IL11	NM_000641	160.7	350.49	2.18	0.94	189.8	*	350.49	342.11	-1.02	-0.41	-8.38	
8097753	DCLK2	NM_001040260	66.94	145.13	2.17	0	78.19	*	145.13	125.21	-1.16	0	-19.92	
7993713	IQCK	NM_153208	31.34	67.75	2.16	0.84	36.4	*	67.75	80.95	1.19	0.47	13.2	
8065071	FLRT3	NM_198391	56.77	121.74	2.14	0.99	64.97	*	121.74	83.49	-1.46	-0.65	-38.26	
7965156	LIN7A	NM_004664	82.51	176.35	2.14	1.8	93.85	*	176.35	177.13	1	0.64	0.78	
7996393	CBFB	NM_001755	806.35	1714	2.13	1.76	907.65	*	1714	1244.16	-1.38	-1.05	-469.84	
8149825	STC1	NM_003155	49.24	103.88	2.11	1.23	54.64	*	103.88	74.85	-1.39	-0.91	-29.03	
8115851	STC2	NM_003714	109.69	231.99	2.11	1.47	122.3	*	231.99	233.56	1.01	0.93	1.57	
8131600	TSPAN13	NM_014399	103.68	219.2	2.11	0.42	115.51	*	219.2	183.87	-1.19	-0.23	-35.33	
8101429	PLAC8	NM_016619	34.09	71.49	2.1	0.98	37.4	*	71.49	56.67	-1.26	-0.6	-14.83	
8008784	PRR11	NM_018304	51.05	107.27	2.1	1.08	56.22	*	107.27	85.61	-1.25	-0.54	-21.66	
7981943	PAR5	NR_022008	72.45	151.62	2.09	0.84	79.17	*	151.62	111.41	-1.36	-0.63	-40.21	
7908312	PRG4	NM_005807	104.21	218.05	2.09	0.61	113.85	*	218.05	149.48	-1.46	-0.41	-68.57	
8139131	AMPH	NM_001635	47.01	97.87	2.08	1.11	50.86	*	97.87	67.58	-1.45	-0.69	-30.29	
7983969	CCNB2	NM_004701	46.82	96.53	2.06	0.21	49.71	*	96.53	93.66	-1.03	-0.1	-2.87	
7989647	KIAA0101	NM_014736	46.06	94.8	2.06	0	48.74	*	94.8	81.76	-1.16	0	-13.04	
7954653	TSPAN11	AY358804	80.71	166.41	2.06	1.66	85.7	*	166.41	118.72	-1.4	-1.13	-47.68	
8118890	SCUBE3	NM_152753	107.39	219.87	2.05	1.33	112.49	*	219.87	296.78	1.35	1.03	76.91	
8037005	TGFB1	NM_000660	126.49	256.18	2.03	1.33	129.7	*	256.18	244.35	-1.05	-0.6	-11.83	
8169580	IL13RA1	NM_001560	470.72	945.75	2.01	1.12	475.03	*	945.75	864.57	-1.09	-0.6	-81.18	
7967030	RNU4-1	NR_003925	39.4	79.09	2.01	1.39	39.69	*	79.09	79.78	1.01	0.72	0.69	
7961710	ABCC9	NM_005691	44.79	89.52	2	0.16	44.73	*	89.52	84.88	-1.05	-0.09	-4.65	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8101624	KLHL8	NM_020803	98.59	196.82	2	0.88	98.24	*	196.82	243.35	1.24	0.84	46.53	
8171892	NR0B1	NM_000475	32.12	64.11	2	0.69	32	*	64.11	41.18	-1.56	-0.52	-22.94	
7971922	PCDH9	NM_203487	58.69	115.75	1.97	1.06	57.05	*	115.75	92.06	-1.26	-0.66	-23.69	
8108737	PCDHB13	NM_018933	33.5	65.53	1.96	0.77	32.03	*	65.53	55.77	-1.18	-0.47	-9.76	
8132318	ANLN	NM_018685	49.91	97.15	1.95	0	47.25	*	97.15	120.65	1.24	0	23.5	
7910923	FMN2	NM_020066	47.35	92.43	1.95	1.55	45.09	*	92.43	79	-1.17	-1.01	-13.43	
7975076	HSPA2	NM_021979	145.81	283.99	1.95	1.03	138.18	*	283.99	235.54	-1.21	-0.87	-48.45	
7968800	DGKH	NM_178009	42.38	81.59	1.93	1.01	39.21	*	81.59	60.12	-1.36	-0.7	-21.47	
7922976	PTGS2	NM_000963	224.48	433.63	1.93	0	209.15	*	433.63	564.84	1.3	0	131.2	
8148955	C8orf33	NM_023080	191.84	368.95	1.92	0.86	177.11	*	368.95	338.04	-1.09	-0.46	-30.91	
7918751	DENND2C	BC063894	62.39	120.01	1.92	1.12	57.62	*	120.01	113.41	-1.06	-0.57	-6.59	
7985522	ADAMTSL3	NM_207517	47.38	90.51	1.91	0.81	43.13	*	90.51	123.72	1.37	0.71	33.21	
8121489	AMD1	NM_001634	327.33	626.11	1.91	1.42	298.78	*	626.11	551.22	-1.14	-0.79	-74.89	
8117225	GMNN	NM_015895	85.4	162.87	1.91	1.18	77.47	*	162.87	125.54	-1.3	-0.81	-37.33	
8131479	FLJ20323	NM_019005	248.51	473.25	1.9	1.33	224.74	*	473.25	609.2	1.29	0.99	135.95	
8095834	SHROOM3	NM_020859	47.33	90.04	1.9	1.64	42.71	*	90.04	63.91	-1.41	-1.1	-26.13	
7922474	KIAA0040	BC111699	37.7	71.28	1.89	0.91	33.58	*	71.28	89.29	1.25	0.34	18	
7914851	CLSPN	NM_022111	58.46	109.83	1.88	0.1	51.36	*	109.83	85.46	-1.29	-0.07	-24.37	
8143127	FAM180A	AY358803	80.24	150.98	1.88	0.71	70.74	*	150.98	216.94	1.44	0.57	65.96	
8145793	SNORD13	NR_003041	417.4	786.58	1.88	0.79	369.18	*	786.58	714.65	-1.1	-0.55	-71.93	
8065124	BFSP1	NM_001195	106.37	199.29	1.87	0.67	92.92	*	199.29	193	-1.03	-0.36	-6.29	
8150002	FBXO16	NM_172366	49.24	92	1.87	1.5	42.76	*	92	82.79	-1.11	-0.92	-9.22	
8160431	LOC554202	AK124391	69.4	129.67	1.87	1.3	60.27	*	129.67	92.93	-1.4	-0.97	-36.74	
8112409	SGTB	NM_019072	154.91	289.35	1.87	1.16	134.44	*	289.35	296.79	1.03	0.87	7.44	
8112376	CENPK	NM_022145	58.56	109.13	1.86	1.14	50.57	*	109.13	75.15	-1.45	-0.85	-33.98	
8108720	PCDHB9	NM_019119	48.43	90.09	1.86	1.27	41.66	*	90.09	68.61	-1.31	-0.93	-21.48	
7971104	TRPC4	NM_016179	35	65.02	1.86	1.02	30.03	*	65.02	42.57	-1.53	-0.85	-22.45	
8121685	DCBLD1	NM_173674	268.73	496.04	1.85	1.22	227.31	*	496.04	593.99	1.2	0.71	97.95	
8135033	MUC12	ENST00000379443	34.05	62.85	1.85	1.2	28.8	*	62.85	70.78	1.13	0.25	7.93	
8171172	MXRA5	NM_015419	154.86	287	1.85	1.03	132.14	*	287	363.77	1.27	0.92	76.77	
7907222	PRRX1	NM_006902	494.77	914.41	1.85	1.06	419.64	*	914.41	1070.61	1.17	0.6	156.2	
7936322	GPAM	NM_020918	113.01	207.09	1.83	0.62	94.09	*	207.09	255.61	1.23	0.26	48.51	
8098470	WWC2	NM_024949	500.12	916.21	1.83	1.1	416.09	*	916.21	831	-1.1	-0.59	-85.21	
8021695	DOK6	NM_152721	38.31	69.61	1.82	1.2	31.3	*	69.61	57.07	-1.22	-0.71	-12.54	
8028084	APLP1	NM_001024807	75.17	135.76	1.81	0.88	60.59	*	135.76	120.45	-1.13	-0.56	-15.3	
7930927	INPP5F	NM_014937	262.82	475.99	1.81	1.1	213.17	*	475.99	473.2	-1.01	-0.6	-2.79	
8105828	CCNB1	NM_031966	99.18	178.87	1.8	0.23	79.69	*	178.87	184.81	1.03	0	5.94	
7908204	HMCN1	NM_031935	322.84	580.01	1.8	0.08	257.17	*	580.01	583.29	1.01	0.16	3.28	
8161024	RMRP	NR_003051	376.1	673.49	1.79	1.3	297.39	*	673.49	619.39	-1.09	-0.63	-54.1	
8176730	RPS4Y2	NM_001039567	40.14	71.09	1.77	0	30.95	*	71.09	74.02	1.04	0	2.93	
8120043	RUNX2	NM_001024630	166.08	294.64	1.77	1.04	128.57	*	294.64	226.76	-1.3	-0.73	-67.88	
8097080	SYNPO2	NM_133477	64.18	112.47	1.75	0.73	48.29	*	112.47	101.26	-1.11	-0.56	-11.21	
7964834	CPM	NM_001874	37.17	64.68	1.74	0.75	27.51	*	64.68	41.46	-1.56	-0.77	-23.22	
8121911	C6orf173	NM_001012507	200.34	345.84	1.73	0.89	145.5	*	345.84	313.69	-1.1	-0.57	-32.15	
8104788	RAI14	NM_015577	292.74	506.35	1.73	0.86	213.61	*	506.35	488.98	-1.04	-0.51	-17.36	
8098204	CPE	NM_001873	187.69	322.56	1.72	0.62	134.87	*	322.56	240.4	-1.34	-0.48	-82.17	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8115831	DUSP1	NM_004417	216.36	369.38	1.71	1.23	153.02	*	369.38	354.85	-1.04	-0.82	-14.53	
7982889	NUSAP1	NM_016359	66.46	113.7	1.71	0.05	47.24	*	113.7	118.71	1.04	0	5.01	
8157092	TMEM38B	NM_018112	158.34	270.8	1.71	1.31	112.46	*	270.8	186.76	-1.45	-1.05	-84.04	
8081810	GAP43	NM_001130064	256.82	435.67	1.7	0.63	178.85	*	435.67	603.27	1.38	0.4	167.6	
8072170	KREMEN1	NM_001039570	58.58	99.75	1.7	0.64	41.16	*	99.75	72.68	-1.37	-0.52	-27.07	
8169073	MGC39900	NM_194324	82.94	141.37	1.7	0.68	58.43	*	141.37	96.14	-1.47	-0.63	-45.23	
8151684	MMP16	AL136588	83.72	142.56	1.7	0.73	58.85	*	142.56	175.95	1.23	0.57	33.38	
7925918	AKR1C1	NM_001353	61.66	104.15	1.69	1.22	42.49	*	104.15	106.5	1.02	0.56	2.34	
7979307	DLGAP5	NM_014750	39.48	66.88	1.69	0	27.4	*	66.88	95.38	1.43	0	28.5	
7965226	RASSF9	NM_005447	76.36	128.68	1.69	0.95	52.33	*	128.68	107.29	-1.2	-0.61	-21.39	
7923426	UBE2T	NM_014176	60.95	102.71	1.69	1.4	41.76	*	102.71	130.4	1.27	0.69	27.69	
8063458	DOK5	NM_018431	70.64	119.01	1.68	0	48.37	*	119.01	102.71	-1.16	0	-16.3	
7914127	IFI6	NM_002038	84.95	141.86	1.67	0.53	56.91	*	141.86	99.56	-1.42	-0.44	-42.3	
8179238	MICA	NM_000247	165.78	275.49	1.66	0.57	109.7	*	275.49	287.89	1.05	0.41	12.4	
8120932	PRSS35	NM_153362	38.18	63.32	1.66	0.98	25.14	*	63.32	50.55	-1.25	-0.87	-12.77	
8179564	KIFC1	NM_002263	136.4	224.74	1.65	0	88.34	*	224.74	174.42	-1.29	0	-50.32	
7912537	DHRS3	NM_004753	106	173.96	1.64	0.66	67.96	*	173.96	183.83	1.06	0.52	9.87	
7982377	GREM1	NM_013372	304.42	499.25	1.64	0.76	194.83	*	499.25	598.54	1.2	0.11	99.3	
7922889	IVNS1ABP	NM_006469	624.48	1021.76	1.64	1.08	397.28	*	1021.76	1185.85	1.16	0.73	164.08	
8118669	KIFC1	NM_002263	126.67	208.38	1.64	0	81.7	*	208.38	161.73	-1.29	0	-46.65	
8058857	IGFBP5	NM_000599	705.49	1146.89	1.63	0.5	441.4	*	1146.89	874.88	-1.31	-0.39	-272.02	
8113709	LOX	NM_002317	1429.09	2333.4	1.63	0.67	904.31	*	2333.4	2275.61	-1.03	-0.44	-57.79	
8102792	PCDH18	NM_019035	295.43	482.7	1.63	1.02	187.26	*	482.7	508.39	1.05	0.49	25.69	
8023528	ALPK2	NM_052947	83.38	135.4	1.62	0.88	52.03	*	135.4	95.2	-1.42	-0.89	-40.21	
8140420	FDPSL2A	NR_003262	77.86	125.08	1.61	0.86	47.22	*	125.08	163.38	1.31	0.62	38.3	
8055624	ZEB2	NM_014795	178.06	287.21	1.61	0.49	109.14	*	287.21	239.37	-1.2	-0.33	-47.84	
8169717	GRIA3	NM_007325	347.93	555.81	1.6	0.81	207.88	*	555.81	506.52	-1.1	-0.52	-49.29	
8160346	PTPLAD2	NM_001010915	90.74	144.76	1.6	0.55	54.01	*	144.76	119.1	-1.22	-0.38	-25.66	
7962327	SLC2A13	NM_052885	86.62	138.83	1.6	0.81	52.22	*	138.83	142.77	1.03	0.39	3.94	
7909708	CENPF	NM_016343	93.76	148.9	1.59	0.04	55.13	*	148.9	145.61	-1.02	-0.03	-3.29	
8174654	KLHL13	NM_033495	44.07	70.23	1.59	1.01	26.16	*	70.23	67.17	-1.05	-0.6	-3.06	
8040223	RRM2	NM_001034	66.06	105.03	1.59	0	38.97	*	105.03	99.68	-1.05	0	-5.35	
8140650	SEMA3E	NM_012431	42.45	67.62	1.59	0.57	25.18	*	67.62	57.51	-1.18	-0.45	-10.11	
8098328	GALNT7	NM_017423	272.17	430.34	1.58	0.97	158.17	*	430.34	574.63	1.34	0.86	144.3	
7929438	HELLS	NM_018063	50.18	79.16	1.58	0.5	28.98	*	79.16	64.2	-1.23	-0.39	-14.96	
7978407	PRKD1	NM_002742	343.98	544.02	1.58	0.99	200.04	*	544.02	638.3	1.17	0.48	94.28	
8150698	SNAI2	NM_003068	1198.49	1894.71	1.58	1.05	696.23	*	1894.71	2031.25	1.07	0.69	136.54	
8147079	LRRCC1	NM_033402	103.13	162.05	1.57	0.82	58.93	*	162.05	122.84	-1.32	-0.59	-39.21	
8123651	TUBB2B	NM_178012	77.45	121.68	1.57	0.82	44.23	*	121.68	100.47	-1.21	-0.69	-21.21	
8012918	CDRT4	NM_173622	62.12	96.7	1.56	0.57	34.59	*	96.7	116.77	1.21	0.57	20.07	
8058498	FZD5	NM_003468	84.15	131.16	1.56	1.36	47.01	*	131.16	142.26	1.08	0.91	11.11	
7929065	IFIT1	NM_001548	123.27	191.86	1.56	0.08	68.59	*	191.86	152.72	-1.26	-0.07	-39.14	
8113039	MEF2C	NM_002397	128.76	201.24	1.56	0.74	72.48	*	201.24	152.31	-1.32	-0.64	-48.93	
8059470	IRS1	NM_005544	59.27	91.86	1.55	0.71	32.59	*	91.86	78.95	-1.16	-0.54	-12.9	
8164580	PTGES	NM_004878	84.87	131.26	1.55	1.13	46.39	*	131.26	151.58	1.15	0.97	20.32	
7953428	CD4	NM_000616	61.63	94.72	1.54	1.09	33.09	*	94.72	81.38	-1.16	-0.85	-13.34	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7956271	HSD17B6	NM_003725	58.42	89.88	1.54	1.04	31.46	*	89.88	127.69	1.42	0.88	37.8	
8023598	RNF152	NM_173557	62.22	96.01	1.54	0.85	33.79	*	96.01	122.73	1.28	0.11	26.72	
8171758	SCARNA9L	NR_023358	319.03	489.96	1.54	0.25	170.93	*	489.96	376.87	-1.3	-0.21	-113.09	
8034512	SNORD41	NR_002751	69.63	107.14	1.54	0.7	37.51	*	107.14	140.08	1.31	0.78	32.94	
7976567	BDKRB1	NM_000710	68.36	104.61	1.53	0.78	36.26	*	104.61	156.32	1.49	0.94	51.71	
8146921	RDH10	NM_172037	195.08	298.15	1.53	0.76	103.07	*	298.15	229.02	-1.3	-0.74	-69.13	
7981951	SNRPN // SNORD116-2	NR_003317	245.73	372.89	1.52	0.62	127.17	*	372.89	454.56	1.22	0.66	81.67	
8106730	XRCC4	NM_022550	268.42	408.58	1.52	0.3	140.16	*	408.58	583.62	1.43	0	175.05	
8068280	IFNGR2	NM_005534	173.62	262.22	1.51	0.76	88.6	*	262.22	330.66	1.26	0.49	68.44	
8121949	LAMA2	NM_000426	120.03	181.63	1.51	1.02	61.6	*	181.63	141.55	-1.28	-1.14	-40.08	
8103822	VEGFC	NM_005429	560.26	844.76	1.51	0.96	284.5	*	844.76	1135.36	1.34	0.99	290.6	
8051197	CCDC121	NM_024584	104.03	68.87	-1.51	-0.74	-35.16	*	68.87	77.62	1.13	0.54	8.74	
8072926	H1F0	NM_005318	863.49	566.58	-1.52	-0.6	-296.91	*	566.58	581.76	1.03	0.32	15.18	
8135069	SERPINE1	NM_000602	828.42	543.72	-1.52	-0.58	-284.71	*	543.72	756.97	1.39	0.12	213.25	
7926786	APBB1IP	NM_019043	365.78	238.55	-1.53	-1.11	-127.24	*	238.55	289.5	1.21	0.67	50.95	
8107044	ERAP2	NM_022350	232.42	151.42	-1.53	-0.98	-81	*	151.42	130.29	-1.16	-0.81	-21.13	
8143772	RARRES2	NM_002889	140.68	91.88	-1.53	-0.92	-48.8	*	91.88	101.51	1.1	0.52	9.63	
8115147	CD74	NM_001025159	151	98	-1.54	-0.69	-53	*	98	84.34	-1.16	-0.33	-13.66	
8072124	CRYBA4	NM_001886	160.33	104.45	-1.54	-0.72	-55.89	*	104.45	89.3	-1.17	-0.46	-15.14	
8016382	SP6	NM_199262	103.85	67.23	-1.54	-1.02	-36.61	*	67.23	76.75	1.14	0.88	9.52	
8080640	SPATA12	NM_181727	81.7	53.17	-1.54	-0.63	-28.54	*	53.17	47.88	-1.11	-0.09	-5.28	
8049448	AGAP1	NM_001037131	352.46	227.89	-1.55	-0.74	-124.57	*	227.89	203.2	-1.12	-0.55	-24.69	
8055702	NMI	NM_004688	459.57	295.93	-1.55	-0.99	-163.64	*	295.93	257.42	-1.15	-0.52	-38.51	
7935865	POLL	NM_013274	107.38	69.48	-1.55	-0.8	-37.9	*	69.48	56.69	-1.23	-0.94	-12.79	
8025402	ANGPTL4	NM_139314	102.27	65.74	-1.56	-0.38	-36.53	*	65.74	61.36	-1.07	-0.68	-4.39	
7942769	DKFZp434E1119	AL834516	154.38	99.19	-1.56	-0.62	-55.19	*	99.19	70.27	-1.41	-0.84	-28.92	
8167573	GAGE12B	NM_001127345	493.54	315.88	-1.56	-1.1	-177.66	*	315.88	298.7	-1.06	-0.75	-17.18	
7932826	KIAA1462	NM_020848	169.96	109	-1.56	-1.11	-60.96	*	109	135.33	1.24	0.92	26.33	
8144802	PDGFRL	NM_006207	118.47	75.93	-1.56	-0.86	-42.54	*	75.93	104.86	1.38	0.34	28.93	
8164013	STRBP	NM_018387	158.99	101.61	-1.56	-1.15	-57.38	*	101.61	71.39	-1.42	-1.14	-30.22	
7909088	TMCC2	NM_014858	217.79	139.68	-1.56	-0.69	-78.1	*	139.68	146.43	1.05	0.59	6.74	
8052355	EFEMP1	NM_004105	1447.23	921.14	-1.57	-0.03	-526.09	*	921.14	949.98	1.03	0	28.84	
7912854	ESPNP	AL035288	144.17	91.81	-1.57	-0.83	-52.36	*	91.81	70.11	-1.31	-0.92	-21.7	
7937335	IFITM1	NM_003641	1080.51	690.18	-1.57	-0.65	-390.33	*	690.18	513.37	-1.34	0	-176.81	
8142765	LRRC4	NM_022143	149.56	95.42	-1.57	-1.19	-54.14	*	95.42	115.16	1.21	0.89	19.75	
7912887	MFAP2	NM_002403	227.38	144.71	-1.57	-1.09	-82.66	*	144.71	155.8	1.08	0.8	11.09	
8099633	PPARGC1A	NM_013261	76.17	48.39	-1.57	-0.97	-27.77	*	48.39	71.15	1.47	0.91	22.76	
8008454	ABCC3	NM_003786	86.66	54.91	-1.58	-1.15	-31.75	*	54.91	47.18	-1.16	-0.79	-7.73	
8065576	FOXS1	NM_004118	79.29	50.21	-1.58	-0.84	-29.08	*	50.21	52.78	1.05	0.61	2.57	
8048639	INHA	NM_002191	122.8	77.61	-1.58	-0.61	-45.2	*	77.61	82.81	1.07	0.61	5.2	
7994152	CACNG3	NM_006539	79.07	49.71	-1.59	-1.07	-29.37	*	49.71	65.73	1.32	1.08	16.02	
8049471	CXCR7	NM_020311	74.52	46.82	-1.59	-0.81	-27.69	*	46.82	53.89	1.15	0.5	7.07	
7960744	C1R	NM_001733	289.98	181.15	-1.6	-1.43	-108.83	*	181.15	182.11	1.01	0.64	0.95	
7949588	CD248	NM_020404	730.62	456.51	-1.6	-0.95	-274.11	*	456.51	415.57	-1.1	-0.56	-40.94	
8113641	CDO1	NM_001801	125.79	78.82	-1.6	-0.82	-46.97	*	78.82	84.98	1.08	0.58	6.16	
8083887	CLDN11	NM_005602	135.34	84.6	-1.6	-0.72	-50.74	*	84.6	103.18	1.22	0.62	18.58	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8093104	TM4SF19	NM_138461	91.16	56.53	-1.61	-0.86	-34.63	*	56.53	47.38	-1.19	-0.57	-9.15	
8171921	DMD	NM_000109	106.5	65.74	-1.62	0	-40.76	*	65.74	77.36	1.18	0.17	11.62	
8056408	GALNT3	NM_004482	104.41	64.6	-1.62	-0.71	-39.81	*	64.6	68.62	1.06	0.75	4.02	
8090193	HEG1	NM_020733	579.62	356.55	-1.63	-1.06	-223.07	*	356.55	330.44	-1.08	-0.79	-26.11	
8032588	LOC284422	NM_001136503	161.71	99.42	-1.63	-0.63	-62.29	*	99.42	88.96	-1.12	-0.78	-10.47	
8089714	LSAMP	NM_002338	118.38	72.14	-1.64	-0.99	-46.24	*	72.14	86.67	1.2	0.75	14.52	
7943218	PANX1	NM_015368	515.9	315.35	-1.64	-1.13	-200.55	*	315.35	249.83	-1.26	-0.72	-65.51	
8118571	PSMB9	NM_002800	310.19	189.51	-1.64	-0.7	-120.67	*	189.51	166.13	-1.14	-0.15	-23.38	
8178211	PSMB9	NM_002800	310.19	189.51	-1.64	-0.7	-120.67	*	189.51	166.13	-1.14	-0.15	-23.38	
8179495	PSMB9	NM_002800	310.19	189.51	-1.64	-0.7	-120.67	*	189.51	166.13	-1.14	-0.15	-23.38	
7940028	SERPING1	NM_000062	859.04	524.66	-1.64	-1.36	-334.38	*	524.66	480.21	-1.09	-0.82	-44.45	
8121319	SOBP	NM_018013	131.26	79.98	-1.64	-0.76	-51.27	*	79.98	116.29	1.45	0.73	36.31	
8127051	TRAM2	NM_012288	425.13	259	-1.64	-1.22	-166.13	*	259	233.11	-1.11	-1	-25.89	
8057954	C2orf66	AY358249	96.46	58.43	-1.65	-1.17	-38.03	*	58.43	54.7	-1.07	-0.82	-3.73	
7963545	KRT79	NM_175834	98.88	59.87	-1.65	-0.96	-39.01	*	59.87	53.33	-1.12	-0.92	-6.54	
8017867	FAM20A	NM_017565	120.7	72.72	-1.66	-0.32	-47.97	*	72.72	95.14	1.31	0.21	22.42	
8058450	GPR1	NM_005279	100.3	60.57	-1.66	-0.65	-39.73	*	60.57	71.13	1.17	0.74	10.56	
8149574	CSGALNACT1	NM_018371	80.71	48.26	-1.67	-0.49	-32.45	*	48.26	62.21	1.29	0.16	13.95	
7984364	SMAD3	NM_005902	450.74	269.73	-1.67	-1.29	-181.01	*	269.73	249.85	-1.08	-0.94	-19.87	
8134030	STEAP1	NM_012449	650.73	389.94	-1.67	-0.46	-260.79	*	389.94	544.47	1.4	0	154.53	
7905854	ZBTB7B	NM_015872	156.82	94.08	-1.67	-0.67	-62.74	*	94.08	111.5	1.19	1.04	17.41	
8048272	C2orf62	BC052750	124.15	73.88	-1.68	-0.72	-50.26	*	73.88	66	-1.12	-0.69	-7.88	
8130867	THBS2	NM_003247	977.11	582.3	-1.68	-1.29	-394.81	*	582.3	616.1	1.06	0.84	33.8	
7936463	ABLIM1	NM_002313	79.6	47.12	-1.69	-0.5	-32.48	*	47.12	45.09	-1.05	-0.82	-2.03	
8041031	BRE	NM_199193	411.73	243.87	-1.69	-1.04	-167.86	*	243.87	263.85	1.08	0.58	19.98	
8157731	CRB2	NM_173689	197.03	116.56	-1.69	-1.13	-80.47	*	116.56	119.45	1.02	0.87	2.89	
8014115	MYO1D	NM_015194	332.38	197.13	-1.69	-1.03	-135.25	*	197.13	197.38	1	0.77	0.25	
7986446	ALDH1A3	NM_000693	121.87	71.67	-1.7	-0.36	-50.19	*	71.67	82.39	1.15	0.56	10.72	
7919743	C1orf138	BC132992	83.29	49.07	-1.7	0	-34.22	*	49.07	39.81	-1.23	-0.7	-9.26	
8158028	LRSAM1	NM_138361	82.81	48.85	-1.7	-1.06	-33.96	*	48.85	43.47	-1.12	-0.88	-5.38	
8075659	MB	NM_203377	96.91	56.95	-1.7	-0.94	-39.96	*	56.95	57.36	1.01	0.65	0.4	
8025255	STXBP2	NM_006949	195.87	114.95	-1.7	-0.77	-80.91	*	114.95	124.3	1.08	0.79	9.35	
8065400	CST9	NM_001008693	82.58	48.42	-1.71	-0.8	-34.16	*	48.42	61.08	1.26	0.86	12.66	
7909155	AVPR1B	NM_000707	74.35	43.11	-1.72	-0.92	-31.24	*	43.11	37.71	-1.14	-0.92	-5.4	
8073775	FBLN1	NM_006486	462.99	269.52	-1.72	-1.11	-193.47	*	269.52	261.87	-1.03	-0.49	-7.65	
7938485	MICAL2	NM_014632	781.47	453.68	-1.72	-0.64	-327.79	*	453.68	460.15	1.01	0.08	6.47	
8096733	SGMS2	NM_001136258	291.9	169.59	-1.72	-0.69	-122.31	*	169.59	213.5	1.26	0.73	43.92	
8088247	ARHGEF3	NM_001128615	134.82	77.79	-1.73	-0.88	-57.03	*	77.79	89.05	1.14	0.68	11.26	
7986350	ARRDC4	NM_183376	224.97	129.99	-1.73	-0.99	-94.98	*	129.99	157	1.21	0.91	27.01	
7903676	ATXN7L2	NM_153340	165.86	95.69	-1.73	-0.86	-70.17	*	95.69	79.91	-1.2	-0.69	-15.79	
8065412	CST1	NM_001898	324.97	188.16	-1.73	-0.89	-136.81	*	188.16	204.26	1.09	0.63	16.1	
8022295	FAM38B2	AK127627	104.2	60.17	-1.73	0	-44.03	*	60.17	66.22	1.1	0.05	6.05	
7939950	OR5D16	NM_001005496	70.49	40.82	-1.73	-1.05	-29.67	*	40.82	45.8	1.12	0.66	4.98	
8092691	BCL6	NM_001706	358.48	206.03	-1.74	-0.98	-152.45	*	206.03	209.81	1.02	0.88	3.77	
7971126	STOML3	NM_145286	63.04	36.26	-1.74	-1.24	-26.78	*	36.26	34.4	-1.05	-0.7	-1.86	
8172806	XAGE3	NM_133179	139.57	80.34	-1.74	-0.58	-59.23	*	80.34	88.36	1.1	0.7	8.02	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8072710	APOL6	NM_030641	182.04	103.94	-1.75	-0.85	-78.1	*	103.94	78.38	-1.33	-0.16	-25.56	
7957092	C12orf28	AK057785	75.23	43.08	-1.75	-0.81	-32.15	*	43.08	40.35	-1.07	-0.65	-2.73	
8107129	LOC100130703	XM_001715488	64.92	37.12	-1.75	-0.73	-27.8	*	37.12	45.13	1.22	0.62	8.01	
8094372	SOD3	NM_003102	325.99	186.38	-1.75	-1.1	-139.61	*	186.38	170.88	-1.09	-0.8	-15.5	
8129924	TXLNB	NM_153235	94.92	54.09	-1.75	-1.05	-40.83	*	54.09	53.54	-1.01	-0.59	-0.55	
7970954	DCLK1	NM_004734	92.42	52.6	-1.76	-0.59	-39.82	*	52.6	46.41	-1.13	-0.76	-6.19	
7920228	PGLYRP4	NM_020393	116.78	66.26	-1.76	-1.49	-50.52	*	66.26	55.49	-1.19	-0.73	-10.77	
8094228	BST1	NM_004334	212.65	120.19	-1.77	0	-92.46	*	120.19	129.3	1.08	0.2	9.1	
8149927	CLU	NM_001831	1025.87	578.63	-1.77	-0.64	-447.24	*	578.63	628.77	1.09	0.74	50.14	
7919815	CTSK	NM_000396	725.16	410.72	-1.77	0	-314.45	*	410.72	567.64	1.38	0	156.92	
8044605	LOC654433	NR_015377	68.56	38.65	-1.77	-1.38	-29.91	*	38.65	31.52	-1.23	-1	-7.13	
8062948	RBPJL	NM_014276	133.81	75.53	-1.77	-0.64	-58.28	*	75.53	57.37	-1.32	-0.71	-18.16	
8157216	UGCG	NM_003358	295.17	166.55	-1.77	-1.07	-128.62	*	166.55	180.38	1.08	0.95	13.84	
8094911	ATP10D	NM_020453	617.62	346.96	-1.78	-0.68	-270.66	*	346.96	330.86	-1.05	-0.43	-16.1	
8163716	DBC1	NM_014618	213.1	119.6	-1.78	-1.07	-93.5	*	119.6	127.41	1.07	0.27	7.81	
8079167	FLJ36157	ENST00000309765	528.6	296.44	-1.78	-1.03	-232.17	*	296.44	294.1	-1.01	-0.73	-2.34	
8014768	PLXDC1	NM_020405	114.08	64.04	-1.78	-0.87	-50.04	*	64.04	58.68	-1.09	-0.82	-5.36	
8063444	TSHZ2	AF230201	63.9	35.82	-1.78	-1.09	-28.08	*	35.82	36.67	1.02	0.53	0.85	
7943715	ZC3H12C	NM_033390	113.86	63.82	-1.78	-0.91	-50.04	*	63.82	80.55	1.26	0.98	16.73	
8111387	ADAMTS12	NM_030955	111.92	62.55	-1.79	-0.7	-49.37	*	62.55	90.01	1.44	0.73	27.46	
8161166	OR2S2	NM_019897	123.81	69.25	-1.79	-0.7	-54.56	*	69.25	58.2	-1.19	-0.87	-11.05	
8132725	UPP1	NM_003364	79.58	44.46	-1.79	-1.11	-35.11	*	44.46	44.26	-1	-0.8	-0.2	
8139367	NPC1L1	NM_013389	177.29	98.59	-1.8	-0.79	-78.7	*	98.59	119.87	1.22	0.47	21.29	
8135661	CFTR	NM_000492	77.59	42.86	-1.81	-1.24	-34.73	*	42.86	45.39	1.06	0.8	2.53	
7965573	NTN4	NM_021229	435.87	241.46	-1.81	-0.32	-194.4	*	241.46	331.19	1.37	0.63	89.72	
8097829	FHDC1	NM_033393	101.97	55.93	-1.82	-1.21	-46.05	*	55.93	78.64	1.41	0.9	22.71	
8136336	AKR1B10	NM_020299	561.65	307.54	-1.83	-0.69	-254.11	*	307.54	325.25	1.06	0.48	17.7	
8160138	NFIB	NM_005596	121.08	66.28	-1.83	-1.16	-54.8	*	66.28	60.06	-1.1	-0.76	-6.22	
8162934	OR13C5	NM_001004482	88.43	48.27	-1.83	-1.2	-40.16	*	48.27	44.7	-1.08	-0.75	-3.56	
8137112	ZNF212	NM_012256	125.34	68.41	-1.83	-1.08	-56.93	*	68.41	81.38	1.19	0.83	12.97	
7920285	S100A2	NM_005978	704.8	382.61	-1.84	-0.42	-322.19	*	382.61	502.87	1.31	0.87	120.26	
8106660	RASGRF2	NM_006909	127.27	68.74	-1.85	-1.25	-58.53	*	68.74	67.62	-1.02	-0.89	-1.12	
8131263	RNU13P2	X58060	76.66	41.53	-1.85	-0.66	-35.13	*	41.53	55.6	1.34	0.84	14.07	
8177261	TTTY10	NR_001542	100.22	54.23	-1.85	-0.96	-45.99	*	54.23	53.66	-1.01	-0.68	-0.57	
7917850	ARHGAP29	NM_004815	93.3	50.16	-1.86	-0.89	-43.14	*	50.16	68.64	1.37	0.9	18.48	
7993889	C16orf52	BC027604	203.58	109.33	-1.86	-0.88	-94.25	*	109.33	106.65	-1.03	-0.86	-2.69	
8097335	HSPA4L	NM_014278	233.96	126.03	-1.86	-1.18	-107.93	*	126.03	113.65	-1.11	-0.84	-12.38	
8138466	MACC1	NM_182762	71.37	38.41	-1.86	-0.69	-32.96	*	38.41	36.32	-1.06	-0.74	-2.08	
7975482	RGS6	NM_004296	134.22	72.17	-1.86	-0.8	-62.06	*	72.17	73.07	1.01	0.77	0.9	
8155167	HRCT1	NM_001039792	244	130.22	-1.87	-0.93	-113.78	*	130.22	151.76	1.17	0.81	21.54	
7999387	EMP2	NM_001424	553.88	294.34	-1.88	-1.05	-259.54	*	294.34	407.99	1.39	0.57	113.65	
8022283	FAM38B	NM_022068	119.91	63.33	-1.89	0	-56.58	*	63.33	61.89	-1.02	0	-1.44	
8010841	FN3K	NM_022158	97.1	51.46	-1.89	-1.45	-45.64	*	51.46	66.57	1.29	0.8	15.11	
7968015	TNFRSF19	NM_148957	145.04	76.84	-1.89	-1.07	-68.2	*	76.84	62.24	-1.23	-0.39	-14.59	
8132694	IGFBP1	NM_000596	249.96	131.82	-1.9	-1.35	-118.14	*	131.82	127.4	-1.03	-0.77	-4.42	
8095080	PDGFRA	NM_006206	963.09	508.11	-1.9	-0.93	-454.97	*	508.11	508.12	1	0.46	0.01	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8130556	SOD2	NM_001024465	723.16	380.43	-1.9	-1.05	-342.73	*	380.43	412.46	1.08	0.72	32.03	
7963359	KRT83	NM_002282	184.13	96.56	-1.91	-1.17	-87.57	*	96.56	107.73	1.12	0.81	11.17	
8081590	PHLDB2	NM_001134439	446.17	233.45	-1.91	-1.36	-212.72	*	233.45	247.19	1.06	0.43	13.73	
7957819	SLC17A8	NM_139319	64.25	33.7	-1.91	-1.37	-30.55	*	33.7	30.71	-1.1	-0.81	-2.99	
8160260	BNC2	NM_017637	176.3	91.76	-1.92	-1.36	-84.55	*	91.76	112.26	1.22	0.87	20.51	
8122099	ENPP1	NM_006208	1175.55	611.61	-1.92	-1.45	-563.94	*	611.61	615.66	1.01	0.16	4.05	
8148304	TRIB1	NM_025195	204.61	106.67	-1.92	-1.36	-97.94	*	106.67	157.68	1.48	0.63	51.01	
8137468	CCT8L1	ENST00000021776	109.34	56.79	-1.93	-1.18	-52.55	*	56.79	65.31	1.15	0.7	8.52	
7929478	CYP2C19	NM_000769	68.42	35.41	-1.93	-1.05	-33.01	*	35.41	31.77	-1.11	-0.46	-3.64	
7929487	CYP2C9	NM_000771	57.67	29.93	-1.93	-0.39	-27.74	*	29.93	29.52	-1.01	-0.7	-0.42	
7969414	KLF5	NM_001730	486.47	251.72	-1.93	-1.25	-234.76	*	251.72	252.89	1	0.84	1.17	
7968351	C13orf33	NM_032849	82.73	42.65	-1.94	-1.14	-40.07	*	42.65	40.39	-1.06	-0.59	-2.26	
8088047	MUSTN1	NM_205853	574.07	295.89	-1.94	-1.09	-278.18	*	295.89	391.04	1.32	1.01	95.15	
7900409	TMCO2	NM_001008740	80.87	41.72	-1.94	-0.75	-39.15	*	41.72	47.84	1.15	0.59	6.13	
8031084	CACNG8	NM_031895	402	206.66	-1.95	-1.21	-195.34	*	206.66	213.38	1.03	0.9	6.72	
7960427	AKAP3	NM_006422	68.45	35	-1.96	-1.19	-33.45	*	35	32.2	-1.09	-0.86	-2.8	
7981309	BEGAIN	NM_020836	93.78	47.91	-1.96	-0.87	-45.87	*	47.91	57.54	1.2	0.96	9.63	
8085206	CAMK1	NM_003656	332.89	170.09	-1.96	-1.32	-162.8	*	170.09	174.93	1.03	0.9	4.84	
8102877	CLGN	NM_004362	58.05	29.58	-1.96	-1.61	-28.47	*	29.58	33.23	1.12	0.27	3.65	
7905428	TUFT1	NM_020127	98.4	50.14	-1.96	-0.26	-48.27	*	50.14	59.25	1.18	0.75	9.11	
8083409	AADACL2	NM_207365	52.99	26.88	-1.97	-1.39	-26.11	*	26.88	37.02	1.38	0.79	10.14	
8088803	EIF4E3	NM_173359	226.08	114.65	-1.97	-1.07	-111.43	*	114.65	148.36	1.29	1.07	33.71	
8029580	RELB	NM_006509	239.6	121.49	-1.97	-1.43	-118.11	*	121.49	98.07	-1.24	-0.84	-23.42	
8020551	LAMA3	NM_198129	59.92	30.3	-1.98	-1.65	-29.63	*	30.3	43.34	1.43	0.9	13.04	
7939657	DGKZ	NM_001105540	193.07	97.08	-1.99	-0.81	-95.99	*	97.08	109.36	1.13	0.93	12.29	
8097801	FAM160A1	NM_001109977	64.37	32.33	-1.99	-0.79	-32.05	*	32.33	35.16	1.09	0.6	2.84	
7909441	G0S2	NM_015714	742.17	372.19	-1.99	-1.42	-369.99	*	372.19	418.16	1.12	0.69	45.97	
8070286	DSCR4	NM_005867	89.22	44.64	-2	-1.01	-44.58	*	44.64	66.26	1.48	0.94	21.62	
7918913	IGSF3	NM_001542	113.48	56.68	-2	-1.43	-56.8	*	56.68	69.53	1.23	1.07	12.85	
8068024	JAM2	NM_021219	373.09	186.71	-2	-1.49	-186.38	*	186.71	225.43	1.21	1.08	38.71	
7971369	KCTD4	NM_198404	73.73	36.89	-2	-0.85	-36.84	*	36.89	33.08	-1.12	-0.93	-3.81	
7957966	MYBPC1	NM_002465	95.54	47.66	-2	-1.46	-47.88	*	47.66	42.37	-1.12	-0.91	-5.29	
8068361	SLC5A3	NM_006933	388.41	194.08	-2	-0.43	-194.34	*	194.08	272.45	1.4	0.12	78.37	
7976012	NRXN3	NM_004796	53.97	26.9	-2.01	-0.81	-27.07	*	26.9	28.96	1.08	0.86	2.06	
8031253	LILRP2	NR_003061	141.39	69.85	-2.02	-1.14	-71.54	*	69.85	65.09	-1.07	-0.55	-4.76	
8153359	LY6D	NM_003695	168.9	83.46	-2.02	-0.95	-85.44	*	83.46	86.69	1.04	0.91	3.23	
7951807	CADM1	NM_014333	143.41	70.57	-2.03	-0.17	-72.84	*	70.57	63.13	-1.12	-0.12	-7.44	
7971311	ENOX1	NM_017993	89.64	44.13	-2.03	-1.53	-45.51	*	44.13	61.42	1.39	0.96	17.29	
8051133	FTHL3P	NR_002201	54.96	27.01	-2.03	-0.41	-27.95	*	27.01	34.24	1.27	0.62	7.23	
8037755	IGFL3	NM_207393	136.34	67.19	-2.03	-1.64	-69.15	*	67.19	62.87	-1.07	-0.85	-4.32	
7909730	KCNK2	NM_001017425	707.77	348.73	-2.03	-1.52	-359.04	*	348.73	355.67	1.02	0.06	6.94	
8110123	FAM153B	NM_001079529	101.62	49.76	-2.04	-0.76	-51.86	*	49.76	52.03	1.05	0.64	2.26	
8069800	KRTAP24-1	NM_001085455	113.1	55.34	-2.04	-1.08	-57.76	*	55.34	66.19	1.2	1.01	10.85	
7966122	TMEM119	NM_181724	282.28	138.07	-2.04	-0.26	-144.21	*	138.07	131.95	-1.05	-0.17	-6.12	
8132840	DKFZp564N2472	NM_182595	124.04	60.49	-2.05	-1.34	-63.55	*	60.49	67.74	1.12	0.85	7.25	
8014865	NEUROD2	NM_006160	162.54	79.24	-2.05	-1.35	-83.3	*	79.24	103.29	1.3	1.15	24.05	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7931353	PTPRE	NM_006504	109.74	53.47	-2.05	-1.39	-56.27	*	53.47	78.22	1.46	0.97	24.74	
7905233	ADAMTSL4	NM_019032	82.9	40.34	-2.06	-0.17	-42.56	*	40.34	53.27	1.32	0.42	12.93	
8159265	PAEP	NM_001018049	299.09	145.3	-2.06	-1.27	-153.79	*	145.3	171.82	1.18	1.06	26.52	
7937749	TNNT3	NM_006757	347.17	168.21	-2.06	-1.25	-178.96	*	168.21	239.74	1.43	1.02	71.53	
7946069	OR51B2	NM_033180	105.01	50.77	-2.07	-1.29	-54.23	*	50.77	31.55	-1.61	-1.26	-19.22	
7971727	CTAGE3	AF338231	63.63	30.48	-2.09	-1.56	-33.15	*	30.48	23.85	-1.28	-0.86	-6.63	
8069161	KRTAP12-3	NM_198697	451.69	215.73	-2.09	-1.55	-235.95	*	215.73	242.46	1.12	0.99	26.73	
8152764	MTSS1	NM_014751	77.97	37.24	-2.09	-0.92	-40.74	*	37.24	31.45	-1.18	-0.72	-5.79	
7971813	THSD1	NM_018676	135.83	64.98	-2.09	-1.59	-70.86	*	64.98	73.32	1.13	0.7	8.34	
8022531	NPC1	NM_000271	527.42	251.17	-2.1	-0.95	-276.25	*	251.17	334.82	1.33	1.08	83.65	
8047300	AOX1	NM_001159	88.2	41.63	-2.12	-1.46	-46.57	*	41.63	46.61	1.12	0.59	4.98	
8110990	CTNND2	NM_001332	214.95	101.38	-2.12	-1.06	-113.58	*	101.38	92.45	-1.1	-0.88	-8.93	
7940315	C11orf64	BC029583	78.27	36.33	-2.15	-1.37	-41.94	*	36.33	46.71	1.29	0.66	10.38	
8015376	KRT16	NM_005557	164.23	76.29	-2.15	-0.95	-87.94	*	76.29	75.19	-1.01	-0.65	-1.1	
7904726	TXNIP	NM_006472	1739.59	810.9	-2.15	-1.37	-928.69	*	810.9	825.04	1.02	0.76	14.14	
8073513	CCDC134	NM_024821	161.18	74.69	-2.16	-0.98	-86.49	*	74.69	72.46	-1.03	-0.77	-2.23	
7955297	AQP5	NM_001651	243.31	111.91	-2.17	-1.68	-131.39	*	111.91	115.67	1.03	0.84	3.76	
7909503	SERTAD4	NM_019605	92.93	42.77	-2.17	-1.25	-50.16	*	42.77	58.5	1.37	0.76	15.73	
8009602	KIF19	NM_153209	151.93	69.59	-2.18	-1.16	-82.35	*	69.59	70.01	1.01	0.89	0.42	
8020354	OR4K15	NM_001005486	71.69	32.84	-2.18	-0.75	-38.85	*	32.84	41.24	1.26	0.86	8.41	
7943413	BIRC3	NM_001165	71.86	32.86	-2.19	-1.05	-39.01	*	32.86	39.33	1.2	0.85	6.47	
8178193	HLA-DRA	NM_019111	100.11	45.7	-2.19	-0.53	-54.41	*	45.7	46.67	1.02	0	0.97	
7948987	PLA2G16	NM_007069	394	180.05	-2.19	-1.09	-213.95	*	180.05	206.64	1.15	0.79	26.59	
8022653	LOC728606	NR_024259	87.34	39.68	-2.2	-1.53	-47.66	*	39.68	41.14	1.04	0.88	1.45	
7986248	UNQ6190	AY358245	436	198.45	-2.2	-1.11	-237.55	*	198.45	174.63	-1.14	-0.82	-23.82	
8079401	CCR5	NM_000579	112.52	50.84	-2.21	-0.43	-61.68	*	50.84	60.36	1.19	0.87	9.52	
8093298	CCR5	NM_000579	112.52	50.84	-2.21	-0.43	-61.68	*	50.84	60.36	1.19	0.87	9.52	
8145624	EXTL3	NM_001440	292.09	132.33	-2.21	-1.24	-159.76	*	132.33	149.57	1.13	0.91	17.24	
7963289	BIN2	NM_016293	89.18	40.07	-2.23	-1.24	-49.11	*	40.07	63.14	1.58	1.21	23.07	
7921099	CRABP2	NM_001878	342.41	153.29	-2.23	-0.24	-189.11	*	153.29	168.95	1.1	0.23	15.66	
8069269	COL6A1	NM_001848	867.55	383.05	-2.26	-1.41	-484.5	*	383.05	436.16	1.14	0.66	53.12	
8151101	MYBL1	NM_001080416	377.88	167.15	-2.26	-0.37	-210.73	*	167.15	167.45	1	0.77	0.3	
7939492	LOC387763	ENST00000339446	300.9	132.44	-2.27	-1.69	-168.46	*	132.44	138.53	1.05	0.75	6.09	
8005707	MAP2K3	NM_002756	223.15	98.1	-2.27	-0.91	-125.04	*	98.1	98.33	1	0.69	0.23	
7920193	LCE1C	NM_178351	465.08	202.58	-2.3	-1.1	-262.5	*	202.58	211.99	1.05	0.8	9.41	
8011713	CXCL16	NM_022059	165.56	71.1	-2.33	-1.13	-94.45	*	71.1	88.56	1.25	1.11	17.45	
8008237	ITGA3	NM_002204	234.48	100.52	-2.33	-1.77	-133.97	*	100.52	124.86	1.24	0.96	24.35	
7897449	SPSB1	NM_025106	129.48	55.3	-2.34	-1.89	-74.18	*	55.3	68.3	1.24	0.85	13	
8172244	FUNDC1	NM_173794	910.89	383.6	-2.37	0	-527.3	*	383.6	386.03	1.01	0.67	2.43	
8169174	RNF128	NM_024539	119.46	50.14	-2.38	-1.15	-69.32	*	50.14	39.36	-1.27	-0.67	-10.78	
8003667	SERPINF1	NM_002615	379	158.5	-2.39	-1.91	-220.5	*	158.5	174.58	1.1	0.76	16.08	
8163202	SVEP1	NM_153366	168.81	69.64	-2.42	-1.42	-99.16	*	69.64	68.9	-1.01	-0.5	-0.74	
8065569	BCL2L1	NM_138578	348.65	142.84	-2.44	-1.68	-205.81	*	142.84	187.81	1.31	1.1	44.97	
8042769	C2orf78	NM_001080474	94.58	38.72	-2.44	-0.99	-55.86	*	38.72	40.36	1.04	0.74	1.64	
8136248	MEST	NM_002402	217.11	88.93	-2.44	-0.76	-128.18	*	88.93	113.97	1.28	0.64	25.04	
7938072	OR56B4	NM_001005181	98.82	39.5	-2.5	-0.34	-59.32	*	39.5	45.55	1.15	0.92	6.05	

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8021470	PMAIP1	NM_021127	82.02	32.83	-2.5	-1.85	-49.19	*	32.83	29.25	-1.12	-0.67	-3.58	
8066513	SDC4	NM_002999	331.02	132.18	-2.5	-2.06	-198.84	*	132.18	90.68	-1.46	-1.15	-41.5	
8073743	UPK3A	NM_006953	154.34	60.68	-2.54	-0.64	-93.67	*	60.68	62.85	1.04	0.82	2.17	
7958019	DRAM	NM_018370	517.5	195.11	-2.65	-1.95	-322.39	*	195.11	260.16	1.33	0.92	65.05	
8152703	FBXO32	NM_058229	404.38	152.64	-2.65	-1.59	-251.74	*	152.64	185.7	1.22	0.54	33.06	
8118345	CFB	NM_001710	448.66	168.52	-2.66	-1.63	-280.14	*	168.52	159.65	-1.06	-0.37	-8.87	
8178115	CFB	NM_001710	457.39	171.75	-2.66	-1.63	-285.64	*	171.75	162.62	-1.06	-0.37	-9.13	
8100760	UGT2A3	NM_024743	61.27	23	-2.66	-1.17	-38.27	*	23	21.81	-1.05	-0.47	-1.19	
8141228	TMEM130	NM_001134450	186.57	68.91	-2.71	-1.58	-117.66	*	68.91	54.63	-1.26	-0.85	-14.28	
8104022	PDLIM3	NM_014476	129.25	47.45	-2.72	-2.17	-81.8	*	47.45	70.1	1.48	1.24	22.65	
8023497	ATP8B1	NM_005603	357.59	130.16	-2.75	-1.47	-227.43	*	130.16	152.09	1.17	0.9	21.93	
8085138	OXTR	NM_000916	459.89	167.06	-2.75	0	-292.83	*	167.06	209.67	1.26	0	42.6	
8102831	C4orf49	NM_032623	145.59	52.65	-2.76	0	-92.93	*	52.65	75.9	1.44	1.08	23.24	
8013112	RASD1	NM_016084	725.73	262.67	-2.76	-2.05	-463.07	*	262.67	377.61	1.44	1.22	114.94	
7928429	PLAU	NM_002658	145.79	50.42	-2.89	-1.32	-95.37	*	50.42	67.19	1.33	0.9	16.77	
8010614	FSCN2	NM_012418	142.54	47.66	-2.99	0	-94.89	*	47.66	37.9	-1.26	-1.01	-9.76	
7935553	LOXL4	NM_032211	312.15	103.59	-3.01	-0.51	-208.55	*	103.59	93.55	-1.11	-0.54	-10.04	
7955637	KRT18	NM_199187	304.24	100.34	-3.03	0	-203.9	*	100.34	100.13	-1	0	-0.21	
7970329	GAS6	NM_000820	516.37	169.45	-3.05	-1.77	-346.92	*	169.45	220.46	1.3	0.9	51.01	
8101952	DDIT4L	NM_145244	126.1	40.82	-3.09	-1.39	-85.28	*	40.82	50.13	1.23	0.84	9.31	
8138888	PDE1C	NM_005020	269.54	84.01	-3.21	-0.73	-185.53	*	84.01	99.35	1.18	0.74	15.34	
8083494	MME	NM_007288	349.19	108.28	-3.22	-0.55	-240.9	*	108.28	158.78	1.47	0.35	50.5	
8148315	POU5F1P1	NR_002304	115.67	34.23	-3.38	0	-81.44	*	34.23	29.37	-1.17	-0.5	-4.85	
8148070	COL14A1	NM_021110	977.53	286.64	-3.41	-1.58	-690.89	*	286.64	425.61	1.48	0.25	138.97	
7966089	CMKLR1	NM_004072	144.14	40.15	-3.59	-1.97	-103.99	*	40.15	47.88	1.19	0.71	7.73	
8121277	AIM1	NM_001624	311.34	81.05	-3.84	-0.44	-230.29	*	81.05	116.87	1.44	0	35.81	
8124307	CMAH	NR_002174	251.42	62.05	-4.05	0	-189.37	*	62.05	76.04	1.23	0.3	13.99	
8018646	FOXJ1	NM_001454	219.32	50.03	-4.38	0	-169.3	*	50.03	62.11	1.24	0.95	12.08	
7934916	CH25H	NM_003956	164.95	36.26	-4.55	0	-128.7	*	36.26	44.21	1.22	0.43	7.95	
8115664	GLRXL	NM_001123388	440.75	93.1	-4.73	0	-347.65	*	93.1	115.05	1.24	1.09	21.95	
8068083	C21orf7	NM_020152	126.6	26.5	-4.78	-0.2	-100.11	*	26.5	37.61	1.42	0.73	11.11	
8132250	BMPER	NM_133468	185.36	34.6	-5.36	-3.09	-150.76	*	34.6	51.84	1.5	0.73	17.24	
8063839	SS18L1	NM_198935	466.32	78.78	-5.92	0	-387.54	*	78.78	74.11	-1.06	-0.88	-4.67	
7902702	CLCA2	NM_006536	198.83	33.17	-6	-3	-165.67	*	33.17	21.53	-1.54	-0.81	-11.64	
8121768	PKIB	NM_181794	180.42	28.28	-6.38	-3.89	-152.15	*	28.28	42.69	1.51	0.58	14.41	
8033257	C3	NM_000064	282.1	39.72	-7.1	0	-242.38	*	39.72	58.78	1.48	0	19.06	

Genes Differentially Expressed in OSX Null hMSCs from Donors A & C

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
7922130	DPT	NM_001937	209.27	251.49	1.2	0	42.22		251.49	87.38	-2.88	0	-164.12	*
8003814	ASPA	NM_000049	62.21	56.41	-1.1	-0.22	-5.81		56.41	20.61	-2.74	0	-35.79	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8060850	BMP2	NM_001200	297.44	340.82	1.15	0.38	43.38		340.82	125.22	-2.72	-1.2	-215.6	*
8100328	USP46	NM_022832	224.35	283.2	1.26	1.05	58.85		283.2	121.07	-2.34	-1.4	-162.13	*
7960947	A2M	NM_000014	112.37	103.05	-1.09	-0.59	-9.32		103.05	46.01	-2.24	-1.15	-57.04	*
8041467	VIT	NM_053276	187.59	261.57	1.39	1.1	73.98		261.57	122.65	-2.13	-1.63	-138.92	*
8171762	RPS6KA3	NM_004586	374.42	500.25	1.34	1.16	125.82		500.25	239.7	-2.09	-1.7	-260.55	*
8067932	C21orf34	NM_001005732	39.23	60.36	1.54	0.17	21.13		60.36	30.41	-1.98	-0.22	-29.94	*
7921868	FCGR3A	NM_000569	36.64	54.57	1.49	0.78	17.93		54.57	27.86	-1.96	-0.96	-26.71	*
7976443	IFI27	NM_001130080	264.77	352.47	1.33	0.69	87.7		352.47	179.52	-1.96	-1.78	-172.95	*
7985555	LOC727963	ENST00000379369	33.22	51.78	1.56	0.87	18.56		51.78	26.72	-1.94	-1.07	-25.06	*
7951408	CARD16	NM_052889	216.56	212.56	-1.02	-0.76	-4		212.56	111.36	-1.91	-1.09	-101.2	*
7989611	FAM96A	NM_032231	225.89	254.47	1.13	0.86	28.59		254.47	137.63	-1.85	-1.3	-116.85	*
8004184	XAF1	NM_017523	93.38	113.74	1.22	1.03	20.36		113.74	61.59	-1.85	-1.27	-52.15	*
8043583	LOC285033	AK057419	35.52	58.86	1.66	1.3	23.33		58.86	32.57	-1.81	-1.39	-26.29	*
7938225	OLFML1	NM_198474	78.78	86.77	1.1	0.04	7.99		86.77	48.63	-1.78	-0.07	-38.14	*
8073088	APOBEC3G	NM_021822	72.21	86.99	1.2	0	14.78		86.99	49.12	-1.77	0	-37.87	*
7919800	CTSS	NM_004079	72.12	94.57	1.31	0.11	22.45		94.57	53.44	-1.77	-0.14	-41.14	*
8063634	MGC4294	BC002831	186.53	234.76	1.26	0.65	48.22		234.76	132.6	-1.77	-1.14	-102.16	*
8110499	RUFY1	NM_025158	542.72	435.95	-1.24	-0.8	-106.77		435.95	245.79	-1.77	-1.23	-190.16	*
7950391	PGM2L1	NM_173582	314.85	342.6	1.09	0.48	27.75		342.6	199.31	-1.72	-0.67	-143.29	*
8000590	SULT1A1	NM_177534	128.39	150.96	1.18	0.25	22.57		150.96	90.63	-1.67	-0.38	-60.33	*
8157381	ZNF618	NM_133374	77.42	79.05	1.02	0.42	1.63		79.05	47.29	-1.67	-0.68	-31.76	*
7904361	FAM46C	NM_017709	286.8	392.8	1.37	0.91	105.99		392.8	238.18	-1.65	-0.79	-154.61	*
8159521	PTGDS	NM_000954	238.27	176.48	-1.35	-0.42	-61.79		176.48	107.56	-1.64	-0.57	-68.92	*
7968789	C13orf15	NM_014059	205	147.65	-1.39	-0.79	-57.35		147.65	90.8	-1.63	-0.92	-56.84	*
8103601	DDX60L	NM_001012967	116.97	162.81	1.39	0.67	45.84		162.81	99.63	-1.63	-0.76	-63.18	*
8043900	hCG_1790474	NM_001101386	89.65	133.81	1.49	0.86	44.16		133.81	82.67	-1.62	-0.86	-51.13	*
7939559	TSPAN18	NM_130783	203.53	160.99	-1.26	-0.57	-42.54		160.99	100.24	-1.61	-0.87	-60.75	*
8151056	CYP7B1	NM_004820	97.86	107.56	1.1	0.4	9.71		107.56	67.04	-1.6	-0.68	-40.52	*
7986411	MEF2A	NM_005587	413.78	429.57	1.04	0.64	15.79		429.57	269.94	-1.59	-0.84	-159.63	*
7913593	TCEA3	NM_003196	207.42	238.69	1.15	0.59	31.26		238.69	151.07	-1.58	-0.81	-87.62	*
7983679	AP4E1	NM_007347	151.56	188.96	1.25	0.71	37.4		188.96	120.23	-1.57	-1	-68.73	*
8147756	BAALC	NM_024812	95.1	89.42	-1.06	-0.25	-5.68		89.42	57.22	-1.56	0	-32.21	*
8071044	LOC100132288	NM_001033515	222.1	222.74	1	0.47	0.64		222.74	145.65	-1.53	-0.67	-77.09	*
7919984	SELENBP1	NM_003944	242.89	341.01	1.4	0.47	98.12		341.01	222.44	-1.53	-0.48	-118.57	*
8157610	DAB2IP	NM_032552	187.89	203.79	1.08	0.68	15.91		203.79	133.93	-1.52	-0.9	-69.87	*
7958884	OAS1	NM_016816	73.43	96.98	1.32	0.05	23.55		96.98	64.19	-1.51	-0.05	-32.79	*
7930181	AS3MT	NM_020682	213.1	264.56	1.24	0.22	51.46		264.56	176.36	-1.5	-0.27	-88.19	*
8089072	CPOX	NM_000097	169.45	208.16	1.23	0.41	38.71		208.16	138.38	-1.5	-0.5	-69.78	*
8147516	MATN2	NM_002380	293.58	216.74	-1.35	-0.12	-76.85		216.74	144.35	-1.5	0	-72.38	*
8092849	ATP13A3	NM_024524	785.97	650.95	-1.21	-0.51	-135.02		650.95	982.04	1.51	0.44	331.09	*
8108475	LOC492311	NM_001007189	261.7	220.23	-1.19	-0.54	-41.47		220.23	332.91	1.51	0.73	112.68	*
8148059	DEPDC6	NM_022783	148.93	123.24	-1.21	-0.1	-25.7		123.24	189.19	1.54	0.79	65.96	*
8154043	DMRT3	NM_021240	58.19	65.06	1.12	0.6	6.87		65.06	100.45	1.54	1.07	35.39	*
7938295	RPL27A	NM_000990	100.17	108.82	1.09	0.64	8.64		108.82	167.04	1.54	0.61	58.22	*
8022902	INO80C	NM_001098817	161.57	192.63	1.19	0.61	31.06		192.63	298.41	1.55	0.73	105.79	*
7933194	CXCL12	NM_000609	375.73	312.17	-1.2	0	-63.56		312.17	486.31	1.56	0.15	174.14	*

probe set	gene	Accession	Control Mean	10nM BMP6 Mean 20 nM BMP6	fold change	lower bound of FC	difference of means	filtered	10nM BMP6 Mean 20 nM BMP6	10nM BMP6 -OSX Mean	fold change	lower bound of FC	difference of means	filtered
8091972	EVI1	NM_001105078	92.88	120.98	1.3	0.02	28.1		120.98	189.2	1.56	0.27	68.22	*
7982204	2 // HMGN2 // HMGN2 // H	CR542122	336.63	334.52	-1.01	-0.28	-2.11		334.52	523.21	1.56	0.69	188.68	*
7995697	LPCAT2	NM_017839	170.9	162.11	-1.05	-0.62	-8.8		162.11	253.66	1.56	0.92	91.55	*
8135488	LRRN3	NM_001099660	44.2	66.37	1.5	1.15	22.17		66.37	103.55	1.56	1.08	37.18	*
7987165	AVEN	NM_020371	360.57	253.71	-1.42	-0.31	-106.86		253.71	398.37	1.57	0.83	144.66	*
8000409	2 // HMGN2 // HMGN2 // H	CR542122	330.44	328.41	-1.01	-0.26	-2.03		328.41	515.69	1.57	0.69	187.28	*
8116316	MGAT4B	NM_054013	91.41	92.94	1.02	0.59	1.53		92.94	145.82	1.57	0.93	52.88	*
7916986	NEGR1	NM_173808	321.23	413.25	1.29	0.41	92.02		413.25	650.11	1.57	0.88	236.85	*
7951195	ANGPTL5	NM_178127	57.97	48.46	-1.2	-0.46	-9.51		48.46	76.59	1.58	0	28.13	*
8046895	FAM171B	NM_177454	507.86	491.36	-1.03	-0.11	-16.5		491.36	776.6	1.58	0.72	285.24	*
8102950	INPP4B	NM_003866	149.09	122.72	-1.21	-0.49	-26.36		122.72	193.51	1.58	0.4	70.79	*
7906061	SYT11	NM_152280	194.99	217.67	1.12	0.96	22.68		217.67	346.89	1.59	0.61	129.22	*
8014063	EVI2B	NM_006495	72.42	61.24	-1.18	-0.73	-11.19		61.24	98.17	1.6	0.49	36.93	*
8044499	SLC20A1	NM_005415	621.84	557.23	-1.12	-0.67	-64.61		557.23	899.67	1.61	0.45	342.44	*
8123246	SLC22A3	NM_021977	78.6	76.68	-1.03	-0.3	-1.92		76.68	124.07	1.62	0	47.39	*
7997904	ZNF778	AK295122	52.04	57.4	1.1	0.59	5.36		57.4	92.89	1.62	0.58	35.49	*
8037251	PSG7	NM_002783	222.45	222.46	1	0	0.02		222.46	365.01	1.64	0	142.54	*
7903457	PRMT6	NM_018137	100.95	114.36	1.13	0.76	13.41		114.36	189.18	1.65	1	74.82	*
8112971	HAPLN1	NM_001884	271.1	281.94	1.04	0.8	10.85		281.94	472.61	1.68	1.07	190.67	*
7928909	FAM35A	NM_019054	50.29	64.47	1.28	0.64	14.18		64.47	109.48	1.7	1.06	45.01	*
8112622	GFM2	NM_032380	182.46	252.96	1.39	0.59	70.5		252.96	430.68	1.7	1.03	177.72	*
8108905	KCTD16	NM_020768	47.19	71.14	1.51	0.04	23.95		71.14	121.51	1.71	0.38	50.37	*
8060765	PRND	NM_012409	61.11	50.65	-1.21	-0.67	-10.46		50.65	86.74	1.71	0.67	36.09	*
8057599	TFPI	NM_006287	232.6	194.3	-1.2	-0.58	-38.3		194.3	331.84	1.71	1.35	137.53	*
8037246	PSG6	NM_001031850	58.24	62.1	1.07	0	3.85		62.1	106.79	1.72	0	44.7	*
8102594	TNIP3	NM_024873	42.76	44	1.03	0.62	1.23		44	76.3	1.73	0.93	32.3	*
8037283	PSG4	NM_002780	192.92	204.49	1.06	0	11.57		204.49	358.76	1.75	0	154.27	*
8060997	SPTLC3	NM_018327	158.48	108.13	-1.47	-0.59	-50.35		108.13	189.15	1.75	0	81.01	*
8129804	MAP3K5	NM_005923	57.74	85.54	1.48	0.94	27.81		85.54	151.57	1.77	1.2	66.03	*
7995806	MT1A	NM_005946	163.6	160.85	-1.02	-0.31	-2.74		160.85	284.44	1.77	1.42	123.59	*
8037272	PSG5	NM_002781	122.85	153.45	1.25	0	30.61		153.45	271.35	1.77	0	117.9	*
7974697	DAAM1	NM_014992	121.92	99.49	-1.23	-0.62	-22.44		99.49	179.27	1.8	0.82	79.78	*
7995797	MT1E	NM_175617	96.75	100.43	1.04	0.77	3.68		100.43	180.72	1.8	1.32	80.29	*
7918026	EXTL2	NM_001439	172	212.81	1.24	0.69	40.81		212.81	389	1.83	1.33	176.19	*
8019842	TYMS	NM_001071	241.97	193.86	-1.25	-0.25	-48.1		193.86	354.89	1.83	0.02	161.03	*
8102342	ELOVL6	NM_024090	94.57	63.96	-1.48	-0.97	-30.61		63.96	117.54	1.84	0.67	53.58	*
8037290	PSG9	NM_002784	99.65	94.57	-1.05	-0.01	-5.08		94.57	174.65	1.85	0	80.08	*
8095680	IL8	NM_000584	59.82	75.75	1.27	0.14	15.93		75.75	140.85	1.86	0	65.1	*
7995552	CYLD	NM_015247	208.7	246.66	1.18	0.71	37.97		246.66	464.77	1.88	1.41	218.1	*
7914342	FABP3	NM_004102	274.71	263.45	-1.04	-0.15	-11.26		263.45	496.09	1.88	0	232.64	*
7964119	STAT2	NM_005419	128.04	133.79	1.04	0.81	5.75		133.79	253.19	1.89	1.46	119.4	*
7939052	FIBIN	NM_203371	49.1	33.02	-1.49	-0.83	-16.07		33.02	62.9	1.9	1.1	29.88	*
8085665	RFTN1	NM_015150	154.16	175.55	1.14	0.25	21.39		175.55	340.83	1.94	1	165.28	*
7970810	SLC7A1	NM_003045	77.85	69.97	-1.11	-0.48	-7.88		69.97	135.61	1.94	0.92	65.64	*
7951271	MMP1	NM_002421	54.52	34.23	-1.59	-0.78	-20.29		34.23	66.62	1.95	1.1	32.39	*
8113358	ST8SIA4	NM_005668	75.19	55.37	-1.36	-0.13	-19.81		55.37	107.98	1.95	0.22	52.61	*

8037374	PLAUR	NM_002659	254.74	188.3	-1.35	-0.77	-66.45		188.3	368.48	1.96	0.37	180.18	*
8108163	C5orf24	NM_152409	285.89	294.59	1.03	0.59	8.7		294.59	592.06	2.01	1.44	297.47	*
8135763	WNT16	NM_057168	52.83	42.52	-1.24	-0.51	-10.31		42.52	86.84	2.04	0.93	44.32	*
8173933	PCDH19	NM_001105243	35.46	41.66	1.17	0.78	6.2		41.66	85.54	2.05	0.41	43.88	*
7918622	SLC16A1	NM_003051	162.63	162.08	-1	-0.62	-0.55		162.08	335.28	2.07	1.12	173.2	*
8136200	CPA4	NM_016352	64.74	44.37	-1.46	-0.83	-20.37		44.37	92.43	2.08	0.94	48.06	*
8042942	HK2	NM_000189	97.39	90.52	-1.08	-0.78	-6.87		90.52	188.06	2.08	1.25	97.54	*
8056890	CHN1	NM_001822	103.89	106.53	1.03	0.45	2.63		106.53	224.17	2.1	1.04	117.64	*
7970301	TMCO3	NM_017905	158.25	179.95	1.14	0.65	21.7		179.95	379.19	2.11	1.59	199.24	*
7922756	NMNAT2	NM_015039	85.7	88.85	1.04	0.55	3.15		88.85	188.87	2.13	1.59	100.02	*
7938544	TEAD1	NM_021961	379.08	395.09	1.04	0.67	16.01		395.09	841.41	2.13	1.62	446.33	*
7902074	LEPR	NM_002303	249.92	196.99	-1.27	-1.03	-52.93		196.99	421.75	2.14	2.01	224.76	*
8172280	SLC9A7	NM_032591	128.9	91.58	-1.41	-0.82	-37.33		91.58	196.05	2.14	1.07	104.48	*
7993588	TMC7	NM_024847	83.56	68.95	-1.21	-0.37	-14.61		68.95	148.12	2.15	0.43	79.18	*
8138566	IGF2BP3	NM_006547	39.79	54.39	1.37	0.93	14.6		54.39	117.71	2.16	1.32	63.32	*
8147766	FZD6	NM_003506	249.34	176.63	-1.41	-0.73	-72.7		176.63	383.57	2.17	1.31	206.94	*
8089851	HGD	NM_000187	61.08	46.22	-1.32	0	-14.87		46.22	100.26	2.17	0	54.04	*
8093278	HGD	NM_000187	61.08	46.22	-1.32	0	-14.87		46.22	100.26	2.17	0	54.04	*
7899043	SEPN1	NM_020451	115.02	79.67	-1.44	-1.1	-35.34		79.67	173.4	2.18	1.85	93.73	*
8135480	DNAJB9	NM_012328	230.48	242.68	1.05	0.48	12.19		242.68	533.83	2.2	0.85	291.15	*
7951309	MMP13	NM_002427	42.12	22.03	-1.91	0	-20.09		22.03	48.51	2.2	0.26	26.49	*
8023727	DSEL	NM_032160	577.1	406.33	-1.42	-1.08	-170.76		406.33	898.74	2.21	1.65	492.4	*
8059852	MSL3L2	NR_024322	43.62	61.18	1.4	0.43	17.56		61.18	135.78	2.22	0.86	74.6	*
8142814	OPN1SW	NM_001708	55.05	40.49	-1.36	-0.85	-14.56		40.49	90.84	2.24	1.64	50.35	*
8138857	GGCT	NM_024051	274.79	230.65	-1.19	-1.02	-44.13		230.65	557.66	2.42	2.03	327	*
8086028	GLB1	NM_000404	115.21	155.23	1.35	1.14	40.02		155.23	427.29	2.75	2.25	272.06	*
7943293	ENDOD1	NM_015036	90.6	88.32	-1.03	-0.53	-2.28		88.32	251.72	2.85	1.85	163.4	*
7930882	FAM45A	NM_207009	238.38	178.52	-1.34	-0.96	-59.86		178.52	658.85	3.69	2.94	480.33	*
8169928	FAM45A	NM_207009	84.3	62.25	-1.35	0	-22.05		62.25	293.46	4.71	2.78	231.21	*

Appendix 2.3 Enriched Biological Process (Genes) Activated by OSX

Probe Set	Gene	Accension	10nM BMP6 Mean	10nM BMP6 -OSX Mean	Fold Change
OSX Activated Genes 148 out of 13,528					
GO:0000902~Cell Morphogenesis (10 out of 356, p = 0.0157)					
8104901	IL7R	NM_002185	330.33	52.67	-6.27
7972239	SLITRK6	NM_032229	170.93	50.31	-3.4
8060850	BMP2	NM_001200	340.82	125.22	-2.72
8140668	SEMA3A	NM_006080	208	97.64	-2.13
7933772	ANK3	NM_020987	230.07	123.23	-1.87
8099746	CCKAR	NM_000730	406.31	218.3	-1.86
8011214	RTN4RL1	NM_178568	91.13	50.15	-1.82
8130505	EZR	NM_003379	490.17	285.15	-1.72
8141140	DLX5	NM_005221	1021.05	640.5	-1.59
8088919	ROBO1	NM_133631	502.04	334.24	-1.5
GO:0007155~Cell Adhesion (14 out of 148, p = 0.0413)					
8162388	OMD	NM_005014	786.15	125.36	-6.27
7922130	DPT	NM_001937	251.49	87.38	-2.88
8077270	CHL1	NM_006614	94.19	49.46	-1.9
8046695	ITGA4	NM_000885	488.18	279.52	-1.75
8130505	EZR	NM_003379	490.17	285.15	-1.72
7985786	ACAN	NM_013227	301.23	176.26	-1.71
8088866	CNTN3	NM_020872	117.73	68.69	-1.71
8162404	ECM2	NM_001393	257.1	158.28	-1.62
7952036	MPZL3	NM_198275	190.68	118.94	-1.6
7917370	COL24A1	NM_152890	75.9	48.62	-1.56
7988713	TRPM7	NM_017672	522.85	336.17	-1.56
8177222	CD24	NM_013230	142.05	93.51	-1.52
8108697	PCDHB5	NM_015669	329.7	219.45	-1.5
8088919	ROBO1	NM_133631	502.04	334.24	-1.5
GO:0030178 Negative Regulation of Wnt Receptor Signaling Pathway (3 out of 30, p = 0.0418)					
8057506	FRZB	NM_001463	843.66	351.7	-2.4
8161919	TLE1	NM_005077	157.38	87.99	-1.79
7927631	DKK1	NM_012242	1433.13	928.68	-1.54

Appendix 2.4 Enriched Biological Process (Genes) Repressed by OSX

Probe Set	Gene	Accension	10nM BMP6 Mean	10nM BMP6 -OSX Mean	Fold Change
OSX Repressed Genes 181 out of 13,528					
GO:0001944 Vasculature Development (10 out of 251, p = 0.0064)					
8066214	TGM2	NM_004613	63.32	191.69	3.03
7902074	LEPR	NM_002303	196.99	421.75	2.14
7972713	EFNB2	NM_004093	40.79	78.35	1.92
7933469	ARHGAP22	NM_021226	107.55	205.77	1.91
8135594	CAV1	NM_001753	525.64	984.44	1.87
8114805	FGF1	NM_000800	66.66	124.25	1.86
8095680	IL8	NM_000584	75.75	140.85	1.86
7992789	TNFRSF12A	NM_016639	300.02	473.62	1.58
7933194	CXCL12	NM_000609	312.17	486.31	1.56
8095723	EPGN	NM_001013442	356.88	542.67	1.52
GO:0042127 Regulation of Cell Proliferation (23 out of 787, P = 7.72E-4)					
8066214	TGM2	NM_004613	63.32	191.69	3.03
8083690	IL12A	NM_000882	73.61	213.25	2.9
8006433	CCL2	NM_002982	124.33	320.99	2.58
7903358	VCAM1	NM_001078	204.6	509.64	2.49
7914342	FABP3	NM_004102	263.45	496.09	1.88
8135594	CAV1	NM_001753	525.64	984.44	1.87
8131803	IL6	NM_000600	177.01	331.74	1.87
8114805	FGF1	NM_000800	66.66	124.25	1.86
8095680	IL8	NM_000584	75.75	140.85	1.86
7958202	CHST11	NM_018413	88.38	158.58	1.79
7962689	VDR	NM_001017535	36.59	64.97	1.78
8105040	OSMR	NM_003999	159.63	280.51	1.76
7973067	NP	NM_000270	184.19	319.08	1.73
7960821	APOBEC1	NM_001644	52.49	85.92	1.64
7904137	HIPK1	NM_198268	146.73	238.92	1.63
8046488	CDCA7	NM_031942	48.74	78.27	1.61
8012896	PMP22	NM_000304	487.19	779.12	1.6
8010061	SPHK1	NM_182965	110.8	176.9	1.6
7936661	PRDX3	NM_006793	580.37	918.08	1.58
7953291	CD9	NM_001769	265.89	417.5	1.57
8091972	EVI1	NM_001105078	120.98	189.2	1.56
8095723	EPGN	NM_001013442	356.88	542.67	1.52
7947230	BDNF	NM_170732	132.8	199.54	1.5

Appendix 3.1 Shape Factors and Surfaces Areas of MSCs from the Two Rats

Week 2								
Rat	**Surface**	**Sample Size (n)**	**Average Cell Area (μm2)**	**Standard Deviation**	**Standard Error**	**Average Shape Factor (l/w)**	**Standard Deviation**	**Standard Error**
W	Smooth PCL	29	9384.26	5475.4	1810.13	1.84	0.33	0.06
SD	Smooth PCL	22	12867.22	5992.7	1277.65	2.35	0.56	0.12
W	Nanopillar	29	1916.46	792.08	147.09	6.84	2.5	0.46
SD	Nanopillar	16	3563.89	1551.56	387.89	9.06	4.82	1.2

Week 3								
Rat	**Surface**	**Sample Size (n)**	**Average Cell Area (μm2)**	**Standard Deviation**	**Standard Error**	**Average Shape Factor (l/w)**	**Standard Deviation**	**Standard Error**
W	Smooth PCL	22	10752.7	5587.63	1191.29	2.46	0.41	0.09
SD	Smooth PCL	14	16087.09	10212.45	2729.39	2.84	1.44	0.39
W	Nanopillar	24	1328.73	483.13	98.62	7.07	3.1	0.63
SD	Nanopillar	12	2194.01	1174.82	339.14	5.73	1.66	0.48

Week 4								
Rat	**Surface**	**Sample Size (n)**	**Average Cell Area (μm2)**	**Standard Deviation**	**Standard Error**	**Average Shape Factor (l/w)**	**Standard Deviation**	**Standard Error**
W	Smooth PCL	27	11219.25	4204.64	809.18	1.79	0.31	0.06
SD	Smooth PCL	22	26072.34	18916.8	4033.08	2.18	0.67	0.14
W	Nanopillar	43	1580.92	814.55	124.22	7.5	3.68	0.56
SD	Nanopillar	25	3308.24	1875.36	375.07	7.44	3.71	0.74